

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 312 shows 95.6% identity over a 451 aa overlap with a predicted ORF (ORF 312.ng) from *N. gonorrhoeae*:

m312/g312

m312.pep	MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTGVKDLVTT
g312	MSIQSGEILETVKMVADRNFDVRTITIGIDLHDCISTDIDVLNQNIYNKITTGVKDLVAT
m312.pep	AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVQAQTLDKAAKAIGVSFIGGFSALV
g312	AKHLSAKYGVPIVNQRISVTPIAQIAAATKADSYVSVQAQTLDKAAKAIGVSFIGGFSALV
m312.pep	QKGMSPSDEVLIRSIPEAMKTTDIVCXSNIGSTRAGINMDAVKLAGETVKRTAEITPEG
g312	QKGMSPSDEVLIRSVPEAMKTTDIVCSSINIGSTRAGINMDAVKLAGETIKRTAEITPEG
m312.pep	FGCAKIVVFCNAVEDNPF XAGAFHSGS--DAVINVGVS GPGVVKAALENS DATLTLEVAE
g312	FGCAKIVVFCNAVEDNPF MAGAFHSGSEADAVINVGVS GPGVVKAALENS DAVSLTEVAE
m312.pep	VVKKTAFK ITRVGELIGREASKMLNIPFGILDLS--PTPPVGD SVARILEEMGLSVC GTH
g312	VVKKTAFK ITRVGELIGREASKMLNIPFGILDLSLAPT PAVGDSVARILEEMGLSVC GTH
m312.pep	GTTAALALLND AVKKGGMMASSAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV
g312	GTTAALALLND AVKKGGMMASSAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV
m312.pep	CSVGLDMIAVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDTVEFGGLLG
g312	CSVGLDMIAVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG
m312.pep	YAPVMPVKEGSCEVFVNRGGRI PAPVQSMKNX
g312	YAPVMPAKEGSCEVFVNRGGRI PAPVQSMKNX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1305>:

a312.seq

```

1  ATGAGTATCC AATCCGGCGA AATTTTAGAA ACCGTCAAAA TGGTTGCCGA
51  CCAGAATTTC GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
101 GCATCAGCAC CGACATCGAC GTGTTGAACC AAAATATTTA CAACAAAATT
151 ACCACGGTCG GCAAAGACTT GGTGGCGACA GCAAATATC TGTCTGCCAA
201 ATACGGCGTG CCGATTGTGA ATCAGCGCAT TTCTGTCACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATTCTT ACGTCAGCGT GCGCGAAACT

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706 x 1

719

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301 TTGGATAAGG CTGCCAAAGC CATCGGCGTG TCTTTTATTG GCGGCTTTTC
351 CGCGCTGGTG CAAAAGGTA TGTGCGCTTC TGACGAGGTG TTAATCCGTT
401 CCATTCCCGA AGCGATGAAG ACTACTGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGTA CGCGCGCCGG TATCAATATG GACGCGGTCA GACTGGCGGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACTAGAAGGT TTCGGCTGCG
551 CAAAATCGT CGTGTCTGTC AACGCGGTGG AAGACAACCC GTTTATGGCG
601 GGCGCGTTTC ACGGCTCAGG CGAAGCGGAT GCTGTGATTA ATGTCGCGCT
651 ATCCGGCCCCG GGTGTCGTAA AAGCCGCGTT GGAATTCG GATGCAACGA
701 CATTGACCGA AGTTGCGGAA GTTGTGAAGA AAACCGCCTT CAAAATTACC
751 CGCGTGGGCG AACTCATCGG CCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTTGGTATT CTCGACTTGT CGCTGGCACC GACCCCTGCC GTCGGCGACT
851 CCGTGGCGCG CATTCTTGAA GAAATGGGTT TGAGCGTCTG CCGTACGCAC
901 GGCACAACAG CAGCTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCGAGCGCGG TTGGCGGTTT GAGTGGCGCG TTTATCCCCG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCGG CCGAAGCAGG CGTGCTGACG
1051 TTGGATAAAC TCGAAGCGAT GACCGCCGTT TGTTGCGTGC GCTTGGATAT
1101 GATTGCCGTT CCCGGCGACA CACCCGCGCA CACCATTTC GGCATCATTG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC TGCCGTGCGC
1201 ATTATCCGG TAACCGGTAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 CCTGTTGGGC TACGCGCCTG TAATGCCGGT AAAAGAAGGC TCATGCGAAG
1301 TGTTCTGCAA CCGGGCGCGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1306; ORF 312.a>:

```

a312.pep
1  MSIQSGEILE TVKMOVADQNF EVRTITIGID LHCISTDID VLNQNIYNKI
51  TTVGKDLVAT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVVAQT
101 LDKAAGAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVRLAGETI KRTAEITLEG FGCAKIVVFC NAVEDNPFMA
201 GAFHGSSEAD AVINVGVSGP GVVKAALENS DATTLTEVAE VVKTAFAKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCETH
301 GTTAALALLN DAVKKGMMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIIV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

m312/a312 96.7% identity in 451 aa overlap

```

              10      20      30      40      50      60
m312.pep    MSIQSGEILETVKMOVADQNFVVRTITIGIDLHCISSDINVLNQNINYNKITTVGKDLVTT
              |||
a312        MSIQSGEILETVKMOVADQNFVVRTITIGIDLHCISTDIDVLNQNINYNKITTVGKDLVAT
              10      20      30      40      50      60

              70      80      90      100     110     120
m312.pep    AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVVAQTLDKAAGAIGVSFIGGFSALV
              |||
a312        AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVVAQTLDKAAGAIGVSFIGGFSALV
              70      80      90      100     110     120

              130     140     150     160     170     180
m312.pep    QKGMSPSDEVLIRSIPEAMKTTDIVCXNIGSTRAGINMDAVKLAGEVTKRTAEITPEG
              |||
a312        QKGMSPSDEVLIRSIPEAMKTTDIVCSSINIGSTRAGINMDAVRLAGETIKRTAEITLEG
              130     140     150     160     170     180

              190     200     210     220     230
m312.pep    FGCAKIVVFCNAVEDNPFAGAFHGS--DAVINVGVS GPGVKAALENS DATTLTEVAE
              |||
a312        FGCAKIVVFCNAVEDNPFMAGAFHGSGEADAVINVGVSGPGVKAALENS DATTLTEVAE
              190     200     210     220     230     240

              240     250     260     270     280     290
m312.pep    VVKTAFAKITRVGELIGREASKMLNIPFGILDLS--PTPPVGDSVARILEEMGLSVCETH
              |||
a312        VVKTAFAKITRVGELIGREASKMLNIPFGILDLSLAPTPAVGDSVARILEEMGLSVCETH

```


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	250	260	270	280	290	300
	300	310	320	330	340	350
m312.pep	GTTAALALLNDVKKGGMMASAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
a312	GTTAALALLNDVKKGGMMASAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
	360	370	380	390	400	410
m312.pep	CSVGLDMIIVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDTVEFGGLLG					
a312	CSVGLDMIIVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
	370	380	390	400	410	420
	420	430	440			
m312.pep	YAPVMPVKEGSCEVFVNRGGRIAPAPVQSMKNX					
a312	YAPVMPVKEGSCEVFVNRGGRIAPAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1307>:

g313.seq

```

1   atggacgacc  cgcgcaccta  cggatcgggc  aatcccggcg  cgaccaatgt
51  tttagcgagc  ggcaaaaaaa  aggcggccgc  gctgacgctc  ttgggcatgt
101 cgcgcaaagg  tttagttgcc  gttttgcttg  cagcggtgct  tcaagaacgg
151 ctcggtttat  cgcacagcgc  aatcgccgcc  gtcgcactcg  ccgcgctggt
201 cgggcatatg  tggccggtgt  ttttcggatt  taaggcgccg  aaaggcgtgg
251 caacggcatt  gggcggtgct  ctggcactct  ctctgcaac  tgccttggtc
301 tgccggttga  tttggcttgt  gatggcatct  ggcttcaaag  tatcctccct
351 tgccgcgctg  gtcgccacaa  ccgccgcccc  ccttgccgca  ctgtttttta
401 tgccgcatac  ttcttggtat  ttgcgaaccc  tcgcaatcgc  catattggtg
451 ttgtccgcc  ataagagcaa  catcctcaac  ctgattaaag  gcaaaagaaag
501 caaatcggc  gaaaaacgct  ga

```

This corresponds to the amino acid sequence <SEQ ID 1308; ORF 313.ng>:

g313.pep

```

1   MDDPRTYSG  NPGATNVLRS  GKKKAAALTL  LGDAAKGLVA  VLLARVLOEP
51  LGLSDSAIAA  VALAALVGHM  WPVFFGFKGG  KGVATALGVL  LALSPATALV
101 CALIWLVMFA  GFKVSSLAAL  VATTAPLAA  LFFMPHTSWI  FATLAIALLV
151 LLRHKSNILN  LIKGESKIG  EKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1309>:

m313.seq

```

1   ATGGACGACC  CGCGCACCTA  CGGATCGGGC  AATCCGGGGG  CAACCAATGT
51  TTTACGCAGC  GGCAAAAAAA  AGGCGGCCGC  GCTGACGCTC  TTGGGCSATG
101 CCGCCAAAGG  TTTAGTTGCC  GTTTTGCTTG  CACGCGTGCT  TCAAGAACCG
151 CTCGGTTTAT  CCGACAGCGC  AATCGCGGCC  GTCGCACTCG  CCGCGCTGGT
201 CGGGCATATG  TGGCCGGTGT  TTTTCGGATT  TAAAGGCGGC  AAAGGCGTGG
251 CAACGGCATT  GGGCGTGCTT  CTGGCACTCT  CTCCCGCAAC  TGCTTTGGTC
301 TGC CGTTGA  TTTGGCTTGT  TATGGCATTC  GGCTTCAAGG  TGCTCTCCCT
351 TGCCGCATTA  ACCGCCACAA  TCGCCGCACC  GGTCCGCCGA  TCCTTCTTTA
401 TGCCGCACGT  CTCGTGGGTT  TGGGCGACCG  TCGCCATTGC  TTTGCTGGTG
451 TTGTTCCGCC  ACAAAGTAA  TATCGTCAAG  CTGCTCGAAG  GCAGAGAAAG
501 CAAAATCGGC  GGCAGCCGCT  GA

```

This corresponds to the amino acid sequence <SEQ ID 1310; ORF 313>:

m313.pep

```

1   MDDPRTYSG  NPGATNVLRS  GKKKAAALTL  LGDAAKGLVA  VLLARVLOEP
51  LGLSDSAIAA  VALAALVGHM  WPVFFGFKGG  KGVATALGVL  LALSPATALV
101 CALIWLVMFA  GFKVSSLAAL  TATIAAPVAA  SFFMPHVSWV  WATVAIALLV
151 LFRHKSNIIV  LEGRESKIG  GSR*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N. gonorrhoeae*

ORF 313 shows 90.2% identity over a 173 aa overlap with a predicted ORF (ORF 313.ng) from *N. gonorrhoeae*:

m313/g313

	10	20	30	40	50	60
m313.pep	MDDPRTYSGNPGATNVLRS GKKKAAAL TLLGDAAGL VAVLLARVLQEP LGLSDSAIAA					
g313	MDDPRTYSGNPGATNVLRS GKKKAAAL TLLGDAAGL VAVLLARVLQEP LGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMF GFKVSSLAAL					
g313	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMF GFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVS WWATVAIALLV LFRHKSNI VKLLEGRESKIGGSRX					
g313	VATTAAPLAALFFMPHTSWIFATLAIILV LLRHKSNI LNLIKGESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1311>:

a313.seq

1	ATG	GAC	GACC	CGC	GAC	CTA	CGG	ATC	GGG	GGC	AAT	CCG	GGG	GGG	CAAC	CAAT	GT
51	TTT	ACG	CAG	C	GG	CAAAAA	AGG	CGG	CCG	CGC	GCT	GAC	GCT	C	TTG	GGC	GAT
101	CCG	CAA	AAG	TTT	GTT	TGCC	GTT	TGCT	TG	CAC	CGT	GTCT	TCA	AAG	AACCG		
151	CTC	GGT	TTAT	CCG	ACG	CGC	AAT	CGC	GGC	GTC	GCA	CTCG	CCG	CGT	GGT		
201	CGG	CAT	ATG	TGG	CGG	TGT	TTT	TCG	GAT	TAA	AGG	CGG	CAA	AGG	CGT	GG	
251	CAAC	GCAT	TG	GGC	GTG	CTT	CTG	GCA	CTCT	CTC	CCACA	CAAC	TGC	CTT	GGT	C	
301	TGC	CGT	TGA	TTT	GCT	TGT	GAT	GCA	TTC	GGC	TCA	AAG	TGC	TCT	CCCT		
351	TGCC	GATTA	ACG	CCACA	TCG	CCGCC	CCT	TGCC	CGCA	CTG	TTTTTT	TA					
401	TGCC	GATTA	TTCT	TGGAT	TTG	CAACCC	TCG	CAAT	CGC	CAT	ATTGGT	G					
451	TTG	CTCCG	CC	ATA	AGCA	AA	CAT	CCTCA	AC	CTG	ATTAA	AG	GCA	AAGAA	AG		
501	CAAA	ATCGG	C	GAAA	ACG	CT	GA										

This corresponds to the amino acid sequence <SEQ ID 1312; ORF 313.a>:

a313.pep

1	MDDPRTYSG	NPGATNVLRS	GKKKAAAL	TL	LGDAAGLVA	VLLARVLQEP
51	LGLSDSAIAA	VALAALVGHM	WPVFFGFKGG	KG	VATALGVL	LALSPTTALV
101	CALIWLVMF	GFKVSSLAAL	TATIAAPLAA	LF	FMPTSWI	FATLAIILV
151	LLRHKSNI	LN	LIKGESKIG	EKR*		

m313/a313 90.8% identity in 173 aa overlap

	10	20	30	40	50	60
m313.pep	MDDPRTYSGNPGATNVLRS GKKKAAAL TLLGDAAGL VAVLLARVLQEP LGLSDSAIAA					
a313	MDDPRTYSGNPGATNVLRS GKKKAAAL TLLGDAAGL VAVLLARVLQEP LGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMF GFKVSSLAAL					
a313	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMF GFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVS WWATVAIALLV LFRHKSNI VKLLEGRESKIGGSRX					
a313	TATIAAPLAALFFMPHTSWIFATLAIILV LLRHKSNI LNLIKGESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1313>:

```
g401.seq
1  atgaaattac aacaattggc tgaagaaaaa atcggcggtc tgattgtgtt
51  cagcgtgctt gtagtcagtg tcggtctgtt gattgaagtt gtgcccttgg
101 cctttaccac ggccggcaaca cagccggcgc cgggcgtgaa gccttacaat
151 gccctgcagg ttgccggacg cgatatttac atccgtgagg gctgttacaa
201 ctgccactct caaatgattc gtccgttccg tgcggaaacc gagegttacg
251 gtcattactc tgttgccgga gagtcgggtt acgaccatcc gttccaatgc
301 ggttccaaac gtaccgggtc tgatttgcca cgtgtggggc gccgctattc
351 cgacgaatgg caccgcatcc acctgctgaa tccccgtgat gtcgtgcctg
401 agtccaatat gccggcattc ccgtggcttg cagcgaataa agtcgatgtc
451 gatgcaaccg ttgccaacat gaaggctttg cgtaaagtag gtactcctta
501 cagtgatgag gaaattgcga aagcgctga ggctttggca aacaaatccg
551 agctggatgc tgtagtgcgc tatctgcaag gattgggtct ggctttgaaa
601 aacgtaaggt aa
```

This corresponds to the amino acid sequence <SEQ ID 1314; ORF 401.ng>:

```
g401.pep
1  MKLQQLAEEK IGVLIVFTLL VSVGLLIEV VPLAFTKAAT QPAPGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYCHYSVAG ESYDHPFQW
101 GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDAVVA YLQGLGLALK
201 NVR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1315>:

```
m401.seq
1  ATGAAATTAC AaCAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101 CCTTTACCAA GGCGGCAACA CAGCCGGCGC CGGGCGTGAA GCCTTACAA
151 GCCCTGCAGG TTGCCGGACG CGATATTAC ATCCGTGAGG GCTGTTACAA
201 CTGCCACTCG CAAATGATTG GTCCGTTCG TCGGAAACC GAGCGTTACG
251 GTCATTACTC TGTGCGGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301 GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGGCG GTCGCTATTG
351 CGACGAATGG CACCGTATCC ACCTGTGTA TCCCCGTGAT GTCGTGCCTG
401 AGTCCAATAT GCCGGCATTG CCGTGGCTTG CACGCAATAA AGTCGATGTC
451 GATGCAACCG TTGCCAATAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501 CAGTGATGAG GAAATTGCGA AAGCACCTGA GGCTTTGGCA AACAAATCCG
551 AGCTGATGTC TGTAAGTCCG TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601 AACGTAAGGT AA
```

This corresponds to the amino acid sequence <SEQ ID 1316; ORF 401>:

```
m401.pep
1  MKLQQLAEEK IGVLIVFTLL VSVGLLIEV VPLAFTKAAT QPAPGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESYDHPFQW
101 GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDAVVA YLQGLGLALK
201 NVR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 401 shows 100.0% identity over a 203 aa overlap with a predicted ORF (ORF 401.ng) from *N. gonorrhoeae*:

m401/g401

	10	20	30	40	50	60
m401.pep	MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY					
g401	MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m401.pep	IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW					

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      |||
g401  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
      70      80      90      100     110     120

      130     140     150     160     170     180
m401.pep HRIHLLNPRDVPESNMPAFWLRNKNVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
      |||
g401  HRIHLLNPRDVPESNMPAFWLRNKNVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
      130     140     150     160     170     180

      190     200
m401.pep NKSELDVVAYLQGLGLALKNVRX
      |||
g401  NKSELDVVAYLQGLGLALKNVRX
      190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1317>:

```

a401.seq
  1  ATGAAATTAC AACAAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
 51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101  CCTTTACCAA GCGCGCAACA CAGCCGGCGT CGGGCGTGAA GCCTTACAA
151  GCCCTGCAGG TTGCCGGACG CGATATTAC ATCCGTGAGG GCTGTTACAA
201  CTGCCACTCG CAAATGATTC GTCCGTTCG TGCGGAAACC GAGCGTTACG
251  GTCATTACTC TGTGCGCGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301  GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGCG GTGCGTATTC
351  CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCGTGAT GTCGTGCTG
401  AGTCCAATAT GCCGGCATT CCGTGGCTTG CACGCAATAA AGTCGATGTC
451  GATGCAACCG TTGCCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501  CAGTGATGAG GAAATTGCGA AAGCGCCTGA GGCTTTGGCA AACAAATCCG
551  AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAA
601  AACGTAAGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1318; ORF 401.a>:

```

a401.pep
  1  MKLQQLAEK IGVLIVFTLL VSVGLLIEV VPLAFTKAAT QPASGVKPYN
 51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101  GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF WLRNKNVDV
151  DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDVVA YLQGLGLALK
201  NVR*

```

m401/a401 99.5% identity in 203 aa overlap

```

      10      20      30      40      50      60
m401.pep MKLQQLAEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
      |||
a401  MKLQQLAEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPASGVKPYNALQVAGRDIY
      10      20      30      40      50      60

      70      80      90      100     110     120
m401.pep IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
      |||
a401  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
      70      80      90      100     110     120

      130     140     150     160     170     180
m401.pep HRIHLLNPRDVPESNMPAFWLRNKNVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
      |||
a401  HRIHLLNPRDVPESNMPAFWLRNKNVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
      130     140     150     160     170     180

      190     200
m401.pep NKSELDVVAYLQGLGLALKNVRX
      |||
a401  NKSELDVVAYLQGLGLALKNVRX
      190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1319>:

g402.seq

```

1  ATGGATATGG TGAACACTAA Accgaatact agtgtgatta atatgctttc
51  tttcccttacc ggattATTGA GCTTGGGTat agaagtCtTg tGGGTAAAGGA
101 TGtttttcgTT CGCagcAcag tccgtgcctc aggCATTtTC atttattcctt
151 gcctGttttc tgACCGgtat cgcctgcggc gCgTATTtTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCCctT TATCGGGCAG TgcttcttgT
251 GGGCGGGTAT TgccgaTttt ttgatTTTGG GTGCTGCGTG GTTGTGACG
301 G3TTTTTccg gtttcGTCCA CCACGCCGGT AtttTCATTA CCCTgtctgc
351 C3tcGTCAGG GGGTTGATTT TCCCACCTGT ACACCATgtg GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTCGC CAACGTTGCC
451 G3CAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATttgtt
501 gTCCACCCAA CAGATTtacc tgctcatCTG TTTGATTtCT CTGctgtctc
551 cTTTGTtTTg tacaCTGtTC CAAAAAAGTC TCCGACTGAA TGCAGTGTGCG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTTAC TGCCGGATTG
651 TGTCTTTCAA AATATTGCTG GCCGTCCGGA TAGGTTGATT GAAAACAAAC
701 ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTtTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATATATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCC GGCATACGCG
851 GCATTtTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGAcg agccgcAAAT CGCACCgCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAATAGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTtTGATG AATTGCACTT GGTACTGGCG
1101 TGCCTATTTC ACTAACCTGT TGAGTGCAGA ATTTTAAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATgctTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTACGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCcct AATAAAGAAC
1301 TGCTCaagca aCGCCTTtcc cgGTTGATTt GCCCGGAAAG CGGCAGgcac
1351 gTATTTGACA GCAGCACCGT G3ATGCTGCA GCACAAAAGG TTGctctctCG
1401 TATGCTGATT CGGATGACGG AAcctTCGGC TGGGGCGGAA GTCATTACTG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1320; ORF 402.ng>:

g402.pep

```

1  MDMVNTKPNT SVINMLSFLT GLLSLGIEVL WVRMFSFAAQ SVPQAPSFIL
51  ACFLTGIavg AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDLLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFO NIAGRPDRLI ENKHGIVAVY HRDGDKVVYG
251 ANVYDGAYNT DIFNSVNGIE RAYLLPSLKS GIRRI FVVGL STGSWARVLS
301 AIPEMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NSTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATFVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSSTVDA A QKVVSRLI RMTEPSAGAE VITDDNMIVE YKYGRGI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1321>:

m402.seq

```

1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATTt ATATGCnTTC
51  TTTCCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTGAGGA
101 TGTTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTtTC ATTTACCCTT
151 GCCTGTTTTTC TGACCGGTAT CGCCGTTCGGC GCGTATTtTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCCCTT TATCGGGCAG TGCTTCTTGT
251 TGGCGGGTAT TGCCGACTTT TTGATTtTG GTGCTGCGTG GTTGTGACG
301 GGTTTTTCCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTCAsa sGGTTGATTT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTCGC CAACGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTtCTT
501 GTCCACCCAA CAGATTtACC TGCTCATCTG TwTGATTtCT GCTGCTGTCC
551 CTTTGTtTTTg TACACTGTTT CAAAAAAGTC TCCGACTGAA TGCAGTGTGCG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTyTAC TGCCGGATTG

```

```

651 TGTCTTTCAA AATATTGCTG ACCGTCCGGA TagGCTGATT GAAAACAAAC
701 ACGGCATTGT TGC GGTTTAC CATAGAGATG GTGATAAGGT TGTTTATGGG
751 GCGAATGTAT ACGACGCGC ATACAATACC GATGTATTCA ATAGTGTCAC
801 CGGCATCGAA CGTGCCATC TGCTACCCCT CCTGAAGTCT GGCAATCGCC
851 GCATTTTCGT CGTTGGACTG AGTACAGGTT CGTGGGCGCG CGTCTTGCTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAAT CGCCCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCTATTCC ACCAACCTGT TGAGTGC GGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCCT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATTT GGCCGGAAAG CGGCAGGCAC
1351 GTATTTGACA GCAGCACCGT GGATGCTGCA GCACAAAAGG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG aAcCTTCGGC TGGGGCGGAA GTTATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1322; ORF 402>:

m402.pep

```

1 MDIVNTKPNT SLIYMXSFLS GLLSLGLIEVL WVRMFSFAAQ SVPOAFSFTL
51 ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
101 GFSGFVHHAG IFITLSAVVX XLIFPLVHHV GTDGNKSGRQ VSNVYFAXVA
151 GSALGPVLIG FVILDFLSTQ QIYLLICXIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DVFNVSNGIE RAYLLPSLKS GIRRI FVVGL STGSGWARVLS
301 AIPMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NTTWYWRAYS TNLSSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSSTVDA A QKVVSRLMI QMTEPSAGAE VITDDNMIVE YKYGRGI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 402 shows 97.0% identity over a 497 aa overlap with a predicted ORF (ORF 402.ng) from *N. gonorrhoeae*:

m402/g402

	10	20	30	40	50	60
m402.pep	MDIVNTKPNTSLIYMXSFLSGLLSLGLIEVLWVRMFSFAAQSVPOAFSFTLACFLTGIAVG					
g402	MDMVNTKPNTSVINMLSFLTGLLSLGLIEVLWVRMFSFAAQSVPOAFSFTLACFLTGIAVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADF LILGAAWLLTGFSGFVHHAGIFITLSAVVX					
g402	AYFGKRICRSRFVDIPFIGQCFLWAGIADF LILGAAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m402.pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQQIYLLICXIS					
g402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDLLSTQQIYLLICLIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m402.pep	AAVPLFCTLFQKSLRLNAVS VAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
g402	AAVPLFCTLFQKSLRLNAVS VAVSLMFGILMFLLPDSVFQNIAGRDPDRLIENKHGIVAVY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m402.pep	HRDGDKVYVGANVYDGAYNTDVFNVSNGIERAYLLPSLKS GIRRI FVVGLSTGSGWARVLS					

726

```

g402      |||||:|||||
          HRDGDKVYGANVYDGYNTDIFNSVNGIERAYLLPSLKSGIRRIFFVVLSTGSWARVLS
          250      260      270      280      290      300

m402 . pep      310      320      330      340      350      360
          AIPQMISMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM
g402      |||||:|||||
          AIPQMISMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM
          310      320      330      340      350      360

m402 . pep      370      380      390      400      410      420
          NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
g402      |||||:|||||
          NSTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
          370      380      390      400      410      420

m402 . pep      430      440      450      460      470      480
          VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSTVDAQAQKVVSRMLIQMTEPSAGAE
g402      |||||:|||||
          VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSTVDAQAQKVVSRMLIRMTEPSAGAE
          430      440      450      460      470      480

m402 . pep      490
          VITDDNMIVEYKYGRGIX
g402      |||||:|||||
          VITDDNMIVEYKYGRGI
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1323>:

```

a402 . seq
1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATTT ATATGCTTTT
51  TTTCCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTAAGGA
101 TGTTCCTCGT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACTCTT
151 GCCTGTTTTC TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTCCTCGG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGCTGTC
351 CGTCGTCAGA GGGTTGATTT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTCGC CAACGTTGCC
451 GGCAGTGATC TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTTCTT
501 GTCACCCCAA CAGATTACCT TGCTCATCTG TTTGATTTCT GCTGCTGTCC
551 CTTTGTTCCT TACACTGTTC CAAAAAAGTC TCCGACTGAA TGCAGTGTCT
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTCTC TGCCGGATTC
651 TGTCTTTCAA AATATTGCTG ACCGTCCGGA TAGGCTGATT GAAACAAAC
701 ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTTCATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATGTATTCA ATAGTGTCAT
801 CGGCATCGAA CGTGCTATAT TGCTACCTCT CCTGAAGTCT GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAAT CGCCCGCTT TTGCAGGACA
1001 AACGTGTGTA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCTATTCC ACCAACCTGT TGAGTGGCGA ATTTTAAAG CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCCTT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATTT GGCCGGAAG CCGCAGGCAC
1351 GTATTTGACA GCAGACCGT GGATGCTGCA GCACAAAAGG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG AACCTTCGGC TGGTGCGGAA GTCATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1324; ORF 402.a>:

```

a402 . pep
1  MDIVNTKPNT SLIYMLSFLS GLLSLGIEVL WVRMFSFAAQ SVPQAFSFTL

```

```

51 ACFLTGIavg AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDFLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFFVGL STGSWARVLS
301 AIPMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NTTWYWRAYS TNLSSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLQRLS RLIWPESGRH
451 VFDSSTVDAA AQKVSRMLI QMTEPSAGAE VITDDNMIVE YKYGRGI*

```

m402/a402 99.0% identity in 497 aa overlap

	10	20	30	40	50	60
m402.pep	MDIVNTKPNSTLIYMXSFLSGLLSLGIEVLWVRMFSAFAQSVPAFSTLACFLTGIavg					
a402	MDIVNTKPNSTLIYMLSFLSGLLSLGIEVLWVRMFSAFAQSVPAFSTLACFLTGIavg					
	10	20	30	40	50	60
m402.pep	70	80	90	100	110	120
a402	70	80	90	100	110	120
	70	80	90	100	110	120
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX					
a402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
m402.pep	130	140	150	160	170	180
a402	130	140	150	160	170	180
	130	140	150	160	170	180
m402.pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQIYLLICXIS					
a402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDFLSTQIYLLICLIS					
	130	140	150	160	170	180
m402.pep	190	200	210	220	230	240
a402	190	200	210	220	230	240
	190	200	210	220	230	240
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
a402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
	190	200	210	220	230	240
m402.pep	250	260	270	280	290	300
a402	250	260	270	280	290	300
	250	260	270	280	290	300
m402.pep	HRDGDKVYGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSWARVLS					
a402	HRDGDKVYGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSWARVLS					
	250	260	270	280	290	300
m402.pep	310	320	330	340	350	360
a402	310	320	330	340	350	360
	310	320	330	340	350	360
m402.pep	AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM					
a402	AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM					
	310	320	330	340	350	360
m402.pep	370	380	390	400	410	420
a402	370	380	390	400	410	420
	370	380	390	400	410	420
m402.pep	NTTWYWRAYSTNLSSAEFLKQVQSHLTPDGIVMNTTHSPHAFATAVHSIPYAYRYGHMV					
a402	NTTWYWRAYSTNLSSAEFLKQVQSHLTPDGIVMNTTHSPHAFATAVHSIPYAYRYGHMV					
	370	380	390	400	410	420
m402.pep	430	440	450	460	470	480
a402	430	440	450	460	470	480
	430	440	450	460	470	480
m402.pep	VGSATPVVFPNKELLQRLSRLIWPESGRHVFDSSSTVDAAAQKVSRMLIQMTEPSAGAE					
a402	VGSATPVVFPNKELLQRLSRLIWPESGRHVFDSSSTVDAAAQKVSRMLIQMTEPSAGAE					
	430	440	450	460	470	480
m402.pep	VITDDNMIVEYKYGRGIX					
a402	VITDDNMIVEYKYGRGIX					
	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1325>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TC GCGGTGCGA ACAAGAACTT GTGGCGGCTT CTGCCAGAGC TGCCGTAAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGCGGC GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCTTGC GCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAAC TGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCCA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC AACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1326; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPREYET AETTSGLTGT LTSSLSTLNA PALSRQSDG SGRSSSLGLN
151 IGGMGDYRNE TLTINPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK FTEGLMVDFFS DIQPYGNHTG NSAPSVEADN
301 SHEGYGYSDE AVRQHRQGP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1327>:

m406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA CGTAAACGCT
101 TTGCGGTGCGA ACAAGAACTT GTGGCGGCTT CTGCCAGAGC TGCCGTAAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCTTGC GCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAAC TGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAG CCGACGGAAG GATTAATGGT CGATTTCTCC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGCAC AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1328; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIFSHGG GKRFAVEQEL VAASARAAVK

```

729

```

51 DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPREYETT AETTSGLTGC LTSLSTLNA PALSRQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSF ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDFS DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGP *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406 .pep	MRARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA AVKMDLQALHGR					
	:					
m406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA AVKMDLQALHGR					
	10	20	30	40	50	60
	70	80	90	100	110	120
g406 .pep	KVALYIATMGDQSGSLTGG RYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGLTGC					
m406	KVALYIATMGDQSGSLTGG RYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGLTGC					
	70	80	90	100	110	120
	130	140	150	160	170	180
g406 .pep	LTSLSTLNA PALSRQSDGSGSRSSGLNIGGMGDYRNETLT TNPRDTAFLSHLVQTVF					
m406	LTSLSTLNA PALSRQSDGSGSKSSLNIGGMGDYRNETLT TNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
g406 .pep	FLRGIDVVS PANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
m406	FLRGIDVVS PANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
g406 .pep	IKPKTNAFEAAYKENYALWMGPYKVSIGIKPTEGLMVDFS DIQPYGNHTGNSAPSVEADN					
m406	IKPKTNAFEAAYKENYALWMGPYKVSIGIKPTEGLMVFS DIRPYGNHTGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
g406 .pep	SHEGYGYSDEAVRQHRQGPX					
m406	SHEGYGYSDEVVRQHRQGPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1329>:

a406 .seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAG3TT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGT3GC CAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAAT3CC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG

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501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACASAAG GATTAATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC GACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1330; ORF 406.a>:

```

a406.pep
  1 MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK
  51 DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
 101 DYTYPRIYET AETTSGLTGT LTSLSTLNA PALSRQSDG SGSKSSLGLN
 151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVS ANADTDVFIN
 201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
 251 AYKENYALWM GPYKVSIGIK PTEGLMVD FS DIQPYGNHMG NSAPSVEADN
 301 SHEGYGYSDE AVRRHRQGQP *

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m406/a406 98.8% identity in 320 aa overlap

	10	20	30	40	50	60
m406.pep	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFVEQELVAASARAAVK DMDLQALHGR					
a406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFVEQELVAASARAAVK DMDLQALHGR					
	10	20	30	40	50	60
m406.pep	70	80	90	100	110	120
	KVALYIATMGDQSGSLTGG RYSIDALIRGEYINSPAVRTDYTYPRIYET AETTSGLTGT					
a406	KVALYIATMGDQSGSLTGG RYSIDALIRGEYINSPAVRTDYTYPRIYET AETTSGLTGT					
	70	80	90	100	110	120
m406.pep	130	140	150	160	170	180
	LTSLSTLNAPALSRQSDGSGSKSSLGLNIGGMGDYRNETLTNPRDTAFLSHLVQTVF					
a406	LTSLSTLNAPALSRQSDGSGSKSSLGLNIGGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
m406.pep	190	200	210	220	230	240
	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
a406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
m406.pep	250	260	270	280	290	300
	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVD FS DIRPYGNHTGNSAPSVEADN					
a406	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVD FS DIQPYGNHMGNSAPSVEADN					
	250	260	270	280	290	300
m406.pep	310	320				
	SHEGYGYSDEVVRQHRQGQPX					
a406	SHEGYGYSDEAVRRHRQGQPX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1331>:

```

g501.seq
  1 atggtcggac ggaccttgac cgcagatacc gacatatattg ttctgcttgc,
  51 ggcaggcgga gatggcaaga tgcagcatca ctttgacggc aggggtgcgt

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101  tcgtcaaacg attcggacac caagccgctg tctcggtcga ggccgagggg
151  cagctgggtc atgtcggtcg agccgatgga gaagccgtcg aagtattgca
201  ggaattgttc cgccaataacc gcgttgctcg gcagctcgca catcataatc
251  aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcaatgcctt
301  aaccactgct tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351  cgacgttggg cagacccatt tcgtcacgaa cgcgtttcaa ggctttgcat
401  tccaaggcga aacagtcttt gaagctctcg gcaacataac gcgccgcacc
451  acggaagccc aacatcgggg tttcttcatt cggttcgtat acgctgccgc
501  cgaccaggtt ggcgatttcg ttggatttga agtcggacat acggacgatg
551  gttttacgcg gataaaccga tgcggcaagc gttgccacgc cttcggcgat
601  tttatcgacg tagaagtcga caggggatgc gtaaccggcg atcgggcgga
651  taatttccgc tttcagttcg tcgtcttgtt tgtcaaattc caacaaggct
701  ttcgggtgga tgccgatttg gcggttgatg ataaattcca tacgcgcaa
751  gccgatgcct tcgctgggca gattggcgaa gctgaatgcg agttcgggat
801  tgccgacgtt catcatgact ttgacgggtg cttttggcat attgtccaag
851  gcgacatcgg taatttgtac gtccagcagg ccggcataga taaagccggt
901  atcgcttcg gcacaggata cggtaacttc ctgaccgttt tccaagagtt
951  cggtcgcatc gccgcagccg acgacggcag gaatacccg ttcgcgcgcg
1001 atgatggcgg cgtggcaggt gcgtccgcgg cggttggtca cgtatggcga
1051 agcacgtttc atcacgggtt cccaatccgg atcggtcatg tcggtacca
1101 gtacgtcgcc ggcttcgacg gaatccatct cggaagcatc tttaatcagg
1151 cgcaccttgc cctgaccgac tttttgaccg atggcacgac cttcgacaa
1201 gacggttttt tcgcccgttg tggcgtagcg gcgcaggttg cggtgcctt
1251 cttcttggga tttgacgggt tcggggcggg cttgcaggat gtatagtttg
1301 ccgtccaggc cgtcgcgtcc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagcgcgt agtgtgcaa ctcggtgatt tcttcgtcgg
1401 taatggagaa gcggttgagg tcttcttcgg ggacttcgac gttggttacc
1451 gatttgccgg cttcggcttt gtcggtgaaa atcattttga tgtgtttcga
1501 acccatgggtc ttgcgcagga tggcgggttt gcctgctttg agcgtgggtt
1551 tgaacacata aaattcgtcc ggggtgaccg cgccttgatc gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acttggttgt agccggattc
1651 ggtgtcagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1332; ORF 501.ng>:

```

g501.pep
1  MVGRITLTADT DIFVLLAAGG DGKMQHHFDG RFAVVKRFGH QAAVSVEAEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQCL
101 NHCFCGFAQSA DERNHDFDVG QTHFVTNAFQ GFAFQGETVF EALGNITRRT
151 TEAQHRVFFM RFVYAAADQV GVFGFPEVGH TDDGFTRINR CGKRCHAFGD
201 FIDVEVDRGC VTGDAADNFR FQFVVLVVKF QQGFVRDADL AVDDKFHTRQ
251 ADAFAGQIGE AECEFGIADV HHDFDGCFWH IVQGDIGNLY VQAGIDKAG
301 IAFGTGYGNF LTVFQEFGR I AAADDGRNTQ FARDDGGVAG ASAAVGHDDG
351 STFHHGFPIR IGHVGNQYVA GFDGIHLGSI FNQAHALTD FLTDGTTFAQ
401 DGFFAVDQVA AQVAAFFFLG FDGFGAGLQD VEFVQAVAS PFDIHRAAVV
451 PFDGQRVVCQ LGDFFVGNCE AVAVFFGDFD VGYRFAGFGF VGENHFDVFR
501 THGLAQDGGF ACFERGF EHI KFVRVLRALY DVFAQTVRGG NKDDLTVVAGF
551 GVEGEHHT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1333>:

```

m501.seq
1  atggctcgac sggccttgac cgcagatgcc gacatatttg ttctgcttgc
51  ggcaggcgga gatggcaagg tgcagcatca ctttgacggc aggggttcgt
101 tcgtcaaacg attcggatac caagccgctg tcgcggtcga gaccgagggg
151 cagttgggtc atgtcggtcg agccgatgga gaagccgtcg aagtattgca
201 ggaattgttc cgccaataacc gcgttgctcg gcagctcgca catcataatc
251 aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcagggtttt
301 gacaacggmt tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351 caacgttggg caacccatt tcatcgcgga cgcgtttcaa ggctttgcat
401 tccaaggcga aacagtcttt gaagttgtcg gcgacataac gcgccgcacc
451 acggaagccc aacatcgggg tttcttcatt cggttcgtat acgttgccgc
501 cgaccaggtt ggcgatttcg ttggatttga agtcggacat acggacgatg
551 gttttacgcg gataaaccga tgcggccaat gtcgccacgc cttcggcgat
601 tttatcgacg tagaagtcga caggggacgc gtaaccggcg atacggcgga
651 taatttccgc ttttaattcg tcgtcttgtt tgtcaaaatc caacaargct

```

m501.pep

1	MVGXALTADA	DIFVLLAAGG	DGKVQHHFDG	RVAFVKRFGY	QAQAVAVETEG
51	QLGHVVRADG	EAVEVLQELF	RQYRVARQLA	HHNQAQAVFA	AFQAVFFQGF
101	DNGFGFAQSA	DERNHDFNVG	QPHFIADAFO	GFAFOGETVF	EVVGDITRRT
151	TEAQHRVFFM	RFVYVAADQV	GXFVGFVEVH	TDDGFTRINR	CGQCRHAFQD
201	FIDFVEVDRG	VTGDITAGNR	GVFVVLVFKF	QXQFGVDTDL	AVDDKKFTRG
251	ADAFAGQVGE	ABCEFGIADV	HHDFYRCFRH	IVXGDIIGNLY	VQQTGIDTKAG
301	IAFGTGYGNF	LTVFQQFGCI	AAADNGRNAQ	FTRDDGGVAG	TAAAVGNDGR
351	STFHHGFPPI	IGHVGNEYVA	GFDGIHLGSI	FNQAHLALTD	FLTDGAAPAX
401	<u>YGFAVVDGEA</u>	<u>AQVAVALFLG</u>	FYGFGTGLQD	VEFAVQAVAS	PFDIHRAAVV
451	FFDGQDCMRL	LSNFFVGNGE	AVAVFLGDDI	VGYGFTGFCF	VGKNEFDVFX
501	THGFTQVGGQ	ARFERGFEHX	KFVRVDRTLY	DVFAQTVRGG	NKDDLIIVXGF
551	GVEGEHHT*				

Homology with a predicted ORF from *N. gonorrhoeae*

m501/q501

	10	20	30	40	50	60
m501.pep	MVGXALTADADIFVLLAAGGDGKGVQHFDGRVAFVKRFGYQA	AAVAVETEGQLGHVVRADG				
	: :	:	:	:	:	
g501	MVGRTLTDITDIFVLLAAGGDGKMQHFDGRVAFVKRFGHQA	AVSVEAEGQLGHVVRADG				
	10	20	30	40	50	60
	70	80	90	100	110	120
m501.pep	EAVEVLQELFRQYRVARQLAHHNQAQAVFAAFQAVFFQ	QGFDFGFGFAQSADERNHDFNVG				
				:		
g501	EAVEVLQELFRQYRVARQLAHHNQAQAVFAAFQAVFFQ	CLNHCFCGFAQSADERNHDFVNG				
	70	80	90	100	110	120
	130	140	150	160	170	180
m501.pep	QPHFIADAFQGFAPQGETVFEVVGDI	TRRTTEAQHRVFFMRFVYAADQVG	VFGFVGVGH			
	:	:				
g501	QTHFVTNAFCGFAPQGETVFEALGNI	TRRTTEAQHRVFFMRFVYAADQVG	VFGFVGVGH			
	130	140	150	160	170	180
	190	200	210	220	230	240
m501.pep	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGN	FRFXFVVLVFKVQXFXGVD	TDL			
		:		:		:

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g501	TDDGFTRINRCGKRCHAFGDFIDVEVDRGCVTGDAADNFRFQFVVLFVKFQOQGFVRDADL
	190 200 210 220 230 240
m501.pep	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHIVXGDIIGNLYVQQTGIDKAG
g501	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFDGCFWHIVQGDIGNLYVQQAGIDKAG
	250 260 270 280 290 300
m501.pep	IAFGTGYGNFLTTFVQFGCIAAADNGRNAQFTRDDGGVAGTAAAVGNDGRSTFHHGFPIR
g501	IAFGTGYGNFLTTFVQFGRIAAADDGRNTQFARDDGGVAGASAAVGHGSGSTFHHGFPIR
	310 320 330 340 350 360
m501.pep	IGHVGNQYVAGFDGIHLGSI FNQAH LALTDFLTDGAAFA XYGFVAVDGEAAQVAVALFLG
g501	IGHVGNQYVAGFDGIHLGSI FNQAH LALTDFLTDGTTFAQDGF FAVDGVAAQVAAAFVLG
	370 380 390 400 410 420
m501.pep	FYGFGLQDVEFAVQAVASPFDIHRAAVVFFDGCQVMRQLSNFFVNGEAVAVFLGDID
g501	FDGFGAGLQDVEFAVQAVASPFDIHRAAVVFFDQQRVVCQLGDFVNGEAVAVFFGDFD
	430 440 450 460 470 480
m501.pep	VGYGFTGF CFVGNHFDVFXTHGFTQDGLARFERGF EHXKFVRVDR TLYDVFAQTVRGG
g501	VGYRFAGFGFVGENHFDVFRTHGLAQDGGFACFERGF EHIKFVRVDRALYDVFAQTVRGG
	490 500 510 520 530 540
m501.pep	NKDDLIVXGFGVEGEHHT
g501	NKDDLIVVAGFGVEGBHHT
	550

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1335>:

a501.seq (partial)

```

1  ATGGTCGGAC GGCCTTGAC CGCAGATGCC GACATATTTG TTCTGCTTGC
51  GGCAGGCGGA GATGGCAAGG TGCAGCATCA CTTTGACGGC AGGGTTGCGT
101 TCGTCAAACG ATTCGGATAC CAAGCCGCTG TCGCGGTCGA GACCGAGGGT
151 CAGTTGGGTC ATGTCGTTCC AGCCGATGGA GAAGCCGTCG AAGTATTGCA
201 GGAATTGTTC CGCCAATACC GCGTTGCTCG GCAGCTCGCA ATCATAATC
251 AGGCGCAGGC CGTTTTTGCC GCGTTCCAAG CCGTTTTCTT TCAGGGCTTT
301 GACAACGGCT TCGGCTTCGC CCAAAGTGCG GACGAACGGA ATCATGATTT
351 CAACGTTGGT CAACCCATT TCATCGCGGA CGCGTTTCAA GGCTTTGCAT
401 TCCAAGGCGA AACAGTCTTT GAAGTTGTCG GCGACATAAC GCGCCGACCC
451 ACGGAAGCCC AACATCGGGT TTCTTTCATG CCGTTCGTAT ACGTTGCCCG
501 CGACCAGGTT GCGTATTTCG TTGGATTGTA AGTCGGACAT ACGGACGATG
551 GTTTTACCGG GATAAACCGA TGCGGCCAAT GTCGCCACGC CTTCCGCGAT
601 TTTATCGACG TAGAAGTCGA CAGGGGACGC GTAACCGGCG ATACGGCGGG
651 TAATTTCCGC TTTTAATTCC TCGTCTTGTT TGTCAAATTC CAACAAGGCT
701 TTGGGGTGGA TACCGATTTC GCGGTTGATG ATAAATTCCA TACGCGCCAA
751 GCCGATGCCT TCGCTGGGCA GGTGGCGGAA GCTGAATGCG AGTTCGGGAT
801 TGCCGACGTT CATCATGACT TTACAGGTG CTTTAGSCAT GTTGTCCTAAA
851 GCAACATCGG TAATTTGTAC GTCCAGCAGG CCGGAGTAGA TGAAGCCGGT
901 ATCGCCTTCG GCACAGGATA CGGTAAC TTCGACCGTTT TTCAGCAATT
951 CGGTTGCATT GCCGCAGCCG ACAACGGCAG GAATACCCAG TTCGCGCGCG

```

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1001 ATGATGGCGG CGTGGCAGGT ACGTCCGCCC CTGTTGGTCA CGATGGCGGA
1051 AGCGCGTTTC ATCACCAGTT CCCAATCTGG GTCGGTCATG TCGGTAACCA
1101 GTACGTCGCC GGCTTCGACG GAATCCATCT CGGAAGCATC TTTAATCAGG
1151 CGTACCTTGC CCTGACCGAC TTTCTGACCG ATGGCGCGGC CTTCGCACAA
1201 GACGGTTTTT TCGCCGTTGA TAGAAAAGCG GCGCAGGTTG CGGCTGCCTT
1251 CTTCTGGGGA TTTGACGGTT TCGGGACGGG CTTGCAGGAT GTAGAGTTTG
1301 CCGTCCAAGC CGTCGCGTCC CCATTCGATG TCCATCGGGC GGCCGTAAGT
1351 TTTTTCGATG GTCAGTGCCT AATGCGCCAA CTCGGTGATT TCTTCGTCGG
1401 TAATGGAGAA GCGGTTGCGG TCTTCTTCGG GGACATCGAC GTTGGTTACC
1451 GATTTGCCGG CTTCTGCTTT GTCGGTAAAA ATCATTTTGA TGTGTTTTGA
1501 GCCCATGGTT TTGCGCAGGA TGGCAGGTTT GCCTGCTTTC AGCGTGGGTT
1551 TGAACACATA GAATTCGTCG GGATTGACTG CGCCTTGAC GACGTTTTCG
1601 CCCAGACCGT AGGATGAAGT GACAAAGACG ACTTGGTCGT AACCGGATTG
1651 GGTATCGAGG GTGAACATCA C

```

This corresponds to the amino acid sequence <SEQ ID 1336; ORF 501.a>:

a501.pep

```

1  MVGRALTADA DIFVLLAAGG DGKVQHFDG RFAFVKRFGY QAAVAVETEG
51  QLGHVVRADG EAVEVLQELF RQYRVAROLA HHNQAQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151 TEAQHRVFFM RFVYVAADQV GVFGFEVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNER F*FVVLVFKF QQGFVVDLTL AVDDKFHTRQ
251 ADAFAGQVGE AECEFGIADV HHDFYRCFRH VVQSNIGNLY VQAGVDEAG
301 IAFGTGYGNF LTVFQQFGCI AAADNGRNTQ FARDDGGVAG TSAPVGHGDDG
351 SAFHHRFPIW VGHVGNQYVA GFDGIHLGSI FNQAYLALTD FLTDGAFAAQ
401 DGFFAVDRKA AQVAAFFLG FDGFGTGLQD VEFVAVAVAS PFDVHRAAVV
451 FFDGQCVMRQ LGDFFVGNGE AVAVFFGDDI VGYRFAGFCF VGKNHFDVF*
501 AHGFAQDGRF ACFQRGFEHI EFVGIDCALY DVEAQTVG*S DKDDLVTGTF
551 GIEGEHH

```

m501/a501 90.3% identity in 557 aa overlap

	10	20	30	40	50	60
m501.pep	MVGXALTADADIFVLLAAGGDGKVQHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
a501	MVGRALTADADIFVLLAAGGDGKVQHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m501.pep	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG					
a501	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m501.pep	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFGFEVGH					
a501	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFGFEVGH					
	130	140	150	160	170	180
	190	200	210	220	230	240
m501.pep	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVFKFQQXFGVDTDL					
a501	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVFKFQQXFGVDTDL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m501.pep	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHIVXGDIIGNLYVQQTGIDKAG					
a501	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHVQSNIGNLYVQAGVDEAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m501.pep	IAFGTGYGNFLTVEFQQFGCIAAADNGRNAQFTRDDGGVAGTAAAVGNDGRSTFHHGFPIR					
a501	IAFGTGYGNFLTVEFQQFGCIAAADNGRNTQFARDDGGVAGTAAAVGNDGRSTFHHGFPIW					
	310	320	330	340	350	360

g502.seq

g502.pcp

m502.seq

m502 . pep

1 MMKPHNLQFQ LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQXVQ
51 XKKKTQTAHG TFKILRPGLF KWEYTKLYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIgx SPAAILSNKX ALESSYTLKE DGSSNGIDYV GNAQTQRRRL
151 PIHPHRLORR OPRRHAAX

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 502 shows 95.8% identity over a 168 aa overlap with a predicted ORF (ORF 502.ng) from *N. gonorrhoeae*:

m502/g502

	10	20	30	40	50	60
m502.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
g502	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502.pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGXSPAAILSNKX					
g502	TFKILRPGLFKWEYTLPRYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502.pep	ALESSYTLKEDGSSNGIDYV-GNAQTQORRLPIHPHRLQRRQPRRHAA					
g502	ALESSYTLKEDGSSNGIDYVRGNAQTQORRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1341>:

a502.seq

1	ATGATGAAC	CGCACACCT	GTTCCAATTC	CTCGCCGTTT	GCTCCCTGAC
51	CGTCTCCGTC	GCTTCCGCAC	AGGCGGGCGC	GGTGGACGCG	CTCAAGCAAT
101	TCAACAACGA	TGCCGACGGT	ATCAGCGGCA	GCTTCACCCA	AACCGTCCAA
151	AGCAAAAAGA	AAACCCAAAC	CGCGCACGGC	ACGTTCAAAA	TCCTGCGCCC
201	GGGCTCTTT	AAATGGGAAT	ACACTTCGCC	TTACAAACAG	ACTATTGTCG
251	GCGACGGTCA	AACCGTTTGG	CTCTACGATG	TCGATTGGC	ACAAGTGACC
301	AAGTCGTCCC	AAGACCAGGC	CATAGGCGGC	AGCCCCGCCG	CCATCTGTG
351	GAACAAAACC	GCCCTCGAAA	GCAGCTACAC	GCTGAAAGAG	GACGGTTCGT
401	CCAACGGCAT	CGATTATGTG	GGCAACGCC	AAACGCAACA	ACGCCGGCTA
451	CCAATACATC	CGCATCGGCT	TCAAAGGCGG	CAACCTCGCC	GCCATGCAGC
501	TTAA				

This corresponds to the amino acid sequence <SEQ ID 1342; 502 217.a>:

a502.pep

1	MMKPHNLFQF	LAVCSLTVS	ASAQAGAVDA	LKQFNNDADG	ISGSFTQTVQ
51	SKKKTQTAHG	TFKILRPGLF	KWEYTSYKQ	TIVGDGQTVW	LYDVDLAQVT
101	KSSQDQAIGG	SPAAILSNKT	ALESSYTLKE	DGSSNGIDYV	GNAQTQORRL
151	PIHPHRLQRR	QPRRHAA*			

m502/a502 95.2% identity in 167 aa overlap

	10	20	30	40	50	60
m502.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
a502	MMKPHNLFQFLAVCSLTVSVAASQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502.pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGXSPAAILSNKX					
a502	TFKILRPGLFKWEYTSYKQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502.pep	ALESSYTLKEDGSSNGIDYVGNAQTQORRLPIHPHRLQRRQPRRHAAX					
a502	ALESSYTLKEDGSSNGIDYVGNAQTQORRLPIHPHRLQRRQPRRHAAX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1343>:

g502-1.seq

```
1 ATGatGAAAc cgcaCaacct gttccaaTtc CTCGCCGTTT GCTCCCTGAC
51 CGTCGCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTC AAATGGGAAT ACACTTGCC CTACAGACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TTGATTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATCGGCGGC AGCCCCGCCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGTTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CGGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ACCAAACCTC CATCAGTTTC GCGGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAA
601 GCGGTGGACG TGTGAGCAA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1344; ORF 502-1.ng>:

g502-1.pep

```
1 MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTVO
51 SKKKTQTAHG TFKILRPGLF KWEYTLPRQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQAIIG SPAAILSNKT ALESSYTLKE DGSSNGIDYV RATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSSIF GGLNTNPQLS RGAFFKTPPK
201 GVDVLSN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1345>:

m502-1.seq

```
1 ATGATGAAAC CGCACAACT GTTCCAATTC CTCGCCGTTT GCTCCCTGAC
51 CGTCGCCGTC GCTTCCGCAC AGGCGGGCGC GGTAGACGCG CTTAAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGACC
201 GGGCCTTTTC AAATGGGAAT ACACCAAACC TTACAGGCAA ACCATCGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TTGATCTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGGCGGC AGCCCCGCCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ACCAAACCTC CATCAGTTTC GCGGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAA
601 GCGGTGGACG TGTGAGCAA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1346; ORF 502-1>:

m502-1.pep

```
1 MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTVO
51 SKKKTQTAHG TFKILRPGLF KWEYTKPRQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQAIIG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSSIF GGLNTNPQLS RGAFFKTPPK
201 GVDVLSN*
```

m502-1/g502-1 99.0% identity in 207 aa overlap

	10	20	30	40	50	60
m502-1.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDAL	LKQFNNDADGISGSFTQT	VQSKKKTQTAHG			
g502-1	MMKPHNLFQFLAVCSLTVAVASAQAGAVDAL	LKQFNNDADGISGSFTQT	VQSKKKTQTAHG			
	10	20	30	40	50	60
m502-1.pep	TFKILRPGLFKWEYTKPYRQTIVGDGQTVW	LYDVLDAQVTKSSQDQAIIGGSPAAILSNKT				
g502-1	TFKILRPGLFKWEYTLPRQTIIVGDGQTVW	LYDVLDAQVTKSSQDQAIIGGSPAAILSNKT				
	70	80	90	100	110	120
m502-1.pep	ALESSYTLKEDGSSNGIDYVLRATPKRNNAG	YQYIRIGFKGNLAAMQLKDSFGNQTSSIF				
g502-1	ALESSYTLKEDGSSNGIDYVRATPKRNNAG	YQYIRIGFKGNLAAMQLKDSFGNQTSSIF				
	130	140	150	160	170	180
m502-1.pep	ALESSYTLKEDGSSNGIDYVLRATPKRNNAG	YQYIRIGFKGNLAAMQLKDSFGNQTSSIF				
g502-1	ALESSYTLKEDGSSNGIDYVRATPKRNNAG	YQYIRIGFKGNLAAMQLKDSFGNQTSSIF				
	130	140	150	160	170	180

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```

                190      200
m502-1.pep    GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                |||
g502-1        GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1347>:

```

a502-1.seq
1  ATGATGAAAC CGCACAACT GTTCCAATTC CTCGCCGTTT GCTCCCTGAC
51 CGTCTCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTT AAATGGGAAT AACTTCGCC TTACAAACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TCGATTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGGCGGC AGCCCCGCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAACGCAA CAACGCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ATCAAACCTC CATCAGTTTC GCGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTAC CCCGCCAAA
601 GGCSTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1348; ORF 502-1.a>:

```

a502-1.pep
1  MMKPHNLFQF LAVCSLTVSV ASAQAGAVDA LKQFNNDADG ISGSFTQTQVQ
51 SKRKTQTAHG TFKILRPLGF KWEYTSPLYKQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQT SIF GGLNTNPQLS RGAFTKTPPK
201 GVDVLSN*

```

a502-1/m502-1 98.6% identity in 207 aa overlap

```

                10      20      30      40      50      60
a502-1.pep    MMKPHNLFQFLAVCSLTVSVASQAQAVDALKQFNNDADGISGSFTQTQVQSKKKTQTAHG
                |||
m502-1        MMKPHNLFQFLAVCSLTVAVASQAQAVDALKQFNNDADGISGSFTQTQVQSKKKTQTAHG
                10      20      30      40      50      60

                70      80      90      100     110     120
a502-1.pep    TFKILRPLGFKWEYTSPLYKQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT
                |||
m502-1        TFKILRPLGFKWEYTKPYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT
                70      80      90      100     110     120

                130     140     150     160     170     180
a502-1.pep    ALESSYLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQT SIF
                |||
m502-1        ALESSYLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQT SIF
                130     140     150     160     170     180

                190     200
a502-1.pep    GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                |||
m502-1        GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1349>:

```

g503.seq
1  atgtccgcgc cgtcggcadc ggtaatcatt ttgttccatg ccgcttcgat
51 ttcggcatcg agctgttcgg ggaagggcgt gtccaaaatc cattggcgga
101 tttctttgcc gacgcgtgcc agttcgaaa cgtcttcgat atccaatttt
151 gccagagcgg cggaaatgcg ttcgttcaga ccgttgtgtg cgagaaatgc
201 gcggttag

```

This corresponds to the amino acid sequence <SEQ ID 1350; ORF 503.ng>:

```

g503.pep
1  MSAPSASVII LFHAASISAS SCSGKGVSKI HWRISLPTRA SSETSSTSNF
51 ARAAEMRSFR PLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1351>:

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```

m503.seq
1  atgtccgcac cgcgggcac ggcaaccatt ttgttccatg ccgcttcgat
51  ttcggcatcg agctgttcgg ggaaggcgt atccaaaatc cattggcgga
101 tttctttgcc gacgcgtgcc agttcggcaa cgtcttcgac atccaatttt
151 gccagtgcgg cggaaatgcg ttcgctcaga ccgttggtgt cgaggaatgc
201 gcggtag

```

This corresponds to the amino acid sequence <SEQ ID 1352; ORF 503>:

```

m503.pep
1  MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNF
51  ASAAEMRSLR PLCARNAR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 503 shows 91.2% identity over a 68 aa overlap with a predicted ORF (ORF 503.ng) from *N. gonorrhoeae*:

```

m503/g503
          10      20      30      40      50      60
m503.pep  MSAPPASATILFHAASISASSCSGKGVSKIHWRIPLTRASSATSSTSNFASAAEMRSLR
          ||||| ||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g503      MSAPSASVILFHAASISASSCSGKGVSKIHWRIPLTRASSETSTSNFARAAEMRSFR
          10      20      30      40      50      60

          69
m503.pep  PLCARNAR
          ||||| ||
g503      PLCARNAR

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1353>:

```

a503.seq
1  ATGTCCGCGC CGCCGGCATC GGCAACCATT TTGTTCATG CCGCTTCGAT
51  TTCGGCATCG AGCTGTTCGG GGAAGGGCGT GTCCAAAATC CATTGGCGGA
101 TTTCTTTGCC GACGCGTGCC AGTTCGGCAA CGTCTTCGAC ATCTAATTTT
151 GCCAGTGCGG CGGAAATGCG TTCGCTCAGA CCGTTGTGTG CGAGGAATGC
201 GCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1354; ORF 503.a>:

```

a503.pep
1  MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNF
51  ASAAEMRSLR PLCARNAR*

```

m503/a503 100.0% identity in 68 aa overlap

```

          10      20      30      40      50      60
m503.pep  MSAPPASATILFHAASISASSCSGKGVSKIHWRIPLTRASSATSSTSNFASAAEMRSLR
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a503      MSAPPASATILFHAASISASSCSGKGVSKIHWRIPLTRASSATSSTSNFASAAEMRSLR
          10      20      30      40      50      60

          69
m503.pep  PLCARNARX
          ||||| ||
a503      PLCARNARX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1355>:

```

g503-1.seq
1  ATGGCGCGGT CGTTGTACAG GGAGGCGAAA ACGTGGCGCA TCGCTTTTTT
51  AACGTTATCC AAGCCATTGA TATTCAGGAA GGTTCCTGT TGGCCGGCRA
101 ATGATGCGTC GGCAGGTCT TCGCGGTTG CGGAAGAGCG TACGGCAACG
151 GAAATGTCCG CGCCGTCGGC ATCGGTAATC ATTTGTTC ATGCCGCTTC
201 GATTCGGCA TCGAGCTGTT CGGGGAAGGG CGTGTCCAAA ATCCATTGGC
251 GGATTTCTTT GCCGACGCGT GCCAGTTCGG AAACGTCTTC GACATCCAAT
301 TTGCCAGAG CGGCGGAAAT GCCTTCGTT AGACGTTGT GTGCGAGAAA
351 TCGCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1356; ORF 214.ng>:

g503-1.pep
 1 MARSLYREAK TWRIAFITLS KPLIFRKVSC WPANDASGRS SAVAEERTAT
 51 EMSAPSASVI ILFHAASISA SSCSGKGVSK IHWRI SLPTR ASSETSSTSN
 101 FARAAEMRSF RPLCARNAR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1357>:

m503-1.seq
 1 ATGGCAGCGT CGTTATACAG GGAAGCGAAT ACATGGTGCA TCGCTTCTTT
 51 AACGTTATCC AAGCCGTTGA TGTTCAGAA GGTTCCTGT TGTCCAGCGA
 101 ATGATGCGTC CGGCAGGTCT TCGGCAGTTG CGGAAGAAGC TACGGCAACG
 151 GAAATGTCCG CACCGCCGGC ATCGGCAACC ATTTGTTC ATGCCGCTTC
 201 GATTTGCGCA TCGAGCTGTT CGGGGAAAGG CGTATCCAAA ATCCATTGGC
 251 GGATTTCITT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCCAAT
 301 TTTGCCAGTG CGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
 351 TGC GCGGTAG

This corresponds to the amino acid sequence <SEQ ID 1358; ORF 503-1>:

m503-1.pep
 1 MARSLYREAN TWCIASTLS KPLMFKKVSC CPANDASGRS SAVAEERTAT
 51 EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRI SLPTR ASSATSSTSN
 101 FASAAEMRSL RPLCARNAR*

g503-1 / m503-1 89.9% identity in 119 aa overlap

	10	20	30	40	50	60
g503-1.pep	MARSLYREAKTWRIAFITLSKPLIFRKVSCWPANDASGRSSAVAEERTATEMSAPSASVI					
m503-1	MARSLYREANTWCIASTLSKPLMFKKVSCCPANDASGRSSAVAEERTATEMSAPPASAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
g503-1.pep	ILFHAASISASSCSGKGVSKIHWRI SLPTRASSETSSTSNFARAAEMRSFRPLCARNARX					
m503-1	ILFHAASISASSCSGKGVSKIHWRI SLPTRASSATSSTSNFASAAEMRSLRPLCARNARX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1359>:

a503-1.seq
 1 ATGGCGCGGT CGTTGTACAG GGAGGCGAAT ACATGGCGCA TCGCTTCTTT
 51 AACGTTTTCC AAGCCGTTGA TATTCAGGAA GGTTCCTGT TGGCCGGCAA
 101 ATGATGCGTC GGGCAGGTCT TCGGCGGTTG CGGAAGAGCG TACGGCAACG
 151 GAAATGTCCG CGCGCCGGC ATCGGCAACC ATTTGTTC ATGCCGCTTC
 201 GATTTGCGCA TCGAGCTGTT CGGGGAAGGG CGTGTCCAAA ATCCATTGGC
 251 GGATTTCITT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCTAAT
 301 TTTGCCAGTG CGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
 351 TGC GCGGTAG

This corresponds to the amino acid sequence <SEQ ID 1360; ORF 503-1.a>:

a503-1.pep
 1 MARSLYREAN TWRIASLTFS KPLIFRKVSC WPANDASGRS SAVAEERTAT
 51 EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRI SLPTR ASSATSSTSN
 101 FASAAEMRSL RPLCARNAR*

a503-1 / m503-1 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
a503-1.pep	MARSLYREANTWRIASLTFSKPLIFRKVSCWPANDASGRSSAVAEERTATEMSAPPASAT					
m503-1	MARSLYREANTWCIASTLSKPLMFKKVSCCPANDASGRSSAVAEERTATEMSAPPASAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
a503-1.pep	ILFHAASISASSCSGKGVSKIHWRI SLPTRASSATSSTSNFASAAEMRSLRPLCARNARX					
m503-1	ILFHAASISASSCSGKGVSKIHWRI SLPTRASSATSSTSNFASAAEMRSLRPLCARNARX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1361>:

```

g504.seq
1   atgttggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgatttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 taacggacaa ggcaaccggg gagaaactcg agcgaccat ccgcgtgaac
151 catcctttga ccttgacagg catcacgatt tatcaggcga gttttgccga
201 cggcgggtcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgaacctgt cgtgttgaag gcaacctcca tacaccagtt tccgttggaa
301 atcggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gtgcggaacg ggaaaaaagc ctgaaatcca
401 ctctgaacga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccattcggtg ccgcatccgt gatgcggcag ggcaggcggg
501 cgaatataaa aactatatgc tgccggtttt gcaggacaaa gattattttt
551 ggctgaccgg cacgcgcagc ggcttgacgc agcaataacc ctggctgcgt
601 atccccttgg acaagcagtt gaaagcggac acctttatgg cattgctgta
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aagacgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaaa
751 acgctgaata tctttgcgca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag ggcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatgta aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga accgtttcct
951 gctgcacagt atggatgcct atacggggct gacggaatat cccgcgccta
1001 tgctgctcca gcttgacggg ttttccgagg tgcgttcctc aggtttgcag
1051 atgacccggt cgccgggtgc gcttttggtc tatctcggct cggatttgtt
1101 ggttttggtt acagtattta tgttttatgt gcccaaaaaa cgggcgtggg
1151 tattgttttc aaacdgc aaa atccgttttg ctatgtcttc ggcccgcagc
1201 gaacgggatt tgcagaagga atttccaaaa cagctcgaga gcctgcaacg
1251 gctcggcaag gacttgaatc atgactga

```

This corresponds to the amino acid sequence <SEQ ID 1362; ORF 504.ng>:

```

g504.pep
1   MLVQDLPEFV KLKFKHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51  HPLTLHGITI YQASFADGGS DLTFKAWNLR DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPILQDK DYFWLTGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKDAPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKGQDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQDD EARNRFLHLS MDAYTGLTEY PAPMLQLDQG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVFMFYVPKK RAWVLFNKKI RFAMSSARSE
401 RDLQKEFPKH VESLQRLGKD LNHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1363>:

```

m504.seq..
1   atattggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgatttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 tgacggacaa ggcaaccggg gagaaactcg agcgaccat ccgcgtgaac
151 catcctttga ccttgacagg catcacgatt tatcaggcga gttttgccga
201 cggcgggtcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgagcctgt cgtgttgaag gcaacatcca tacaccagtt tccgttggaa
301 attggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gcgcggaacg ggaaaaaagc ctgaaatcca
401 cgctgmmcga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccattgttta ccgtatccgt gatgcggcag ggcaggcggg
501 cgaatataaa aactatatgc tgccggtttt gcaggacaa gattattttt
551 ggattaccgg cacgcgcagc ggcttgacgc agcaataacc ctggctgcgt
601 atccccttgg acaagcagtt gaaagcggac acctttatgg cattgctgta
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aaggcgcaac tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaaa
751 acgctgaaca tctttgcaca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag agcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatgta aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga atcgtttctt
951 gctgcacagt atggatgcgt acacgggttt gaccgaatat cccgcgccta
1001 tgctgctgca acttgatggg ttttccgagg tgcgttcgctc ggggttgcag

```

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```

1051 atgaccggtt ccccggtg cgttttggtc tatctcggt cgggtctggt
1101 ggtattgggt acggtattga tgttttatgt gcgcgaaaaa cgggcgtggg
1151 tattgttttc agacggcaaa atccggtttg ccatgtcttc ggccgcagc
1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gtctgcaacg
1251 gctcggcaag gacttgaatc atga

```

This corresponds to the amino acid sequence <SEQ ID 1364; ORF 504>:

```

m504.pep..
1  ILVQDLPEFEV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51  HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLXDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKEQDDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQQD EARNRFLHLS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
401 ERDLQKEFPK HVESLQRLGK DLNHD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 504 shows 96.7% identity over a 425 aa overlap with a predicted ORF (ORF 504.ng) from *N. gonorrhoeae*:

m504/g504

m504.pep	10	20	30	40	50	60
	ILVQDLPEFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLETRIRVNHPLTLHGITI					
g504	10	20	30	40	50	60
	MLVQDLPEFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLETRIRVNHPLTLHGITI					
m504.pep	70	80	90	100	110	120
	YQASFADGGSDLTFKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
g504	70	80	90	100	110	120
	YQASFADGGSDLTFKAWNLRDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
m504.pep	130	140	150	160	170	180
	MSEGAREKSLKSTLXDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ					
g504	130	140	150	160	170	180
	MSEGAREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPILQDK					
m504.pep	190	200	210	220	230	240
	DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLDGEGRKRLVADATKGAPAEI					
g504	190	200	210	220	230	240
	DYFWLTGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLDGEGRKRLVADATKDAPAEI					
m504.pep	250	260	270	280	290	300
	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQDDKMQGYFYEMLYGVMNAALDETIR					
g504	250	260	270	280	290	300
	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQDDKMQGYFYEMLYGVMNAALDETIR					
m504.pep	310	320	330	340	350	360
	RYGLPEWQQDEARNRFLHLSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV					
g504	310	320	330	340	350	360
	RYGLPEWQQDEARNRFLHLSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV					
m504.pep	370	380	390	400	410	420
	YLGSVLLVLGTVMFYVREKRAWVLFSDGKIRFAMSSARSDRLQKEFPKHVESLQRLGK					

743

g504 YLGSVLLVLGTVFMFYVPPKKRAWVLSN-KIRFAMSSARSERDLQKEFPKHVESLQRLGK
 370 380 390 400 410

m504.pep DLNHD
 |||||
 g504 DLNHD
 420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1365>:

a504.seq
 1 ATATTGGTTC AGGACTTGCC TTTTGAAGTC AAAGTAAAA AATTCCATAT
 51 CGATTTTAC AATACGGGTA TGCCGCGCGA TTTTGCCAGT GATATTGAAG
 101 TAACGGATAA GCAACCGGT GAGAACTCG AGCGCACCAT CCGCGTGAAC
 151 CATCCTTTGA CCTTGCACGG CATCACGATT TATCAGGCGA GTTTTGCCGA
 201 CGCGGTTTCG GATTTGACAT TCAAGGCGTG GAATTTGGGT GATGCTTCGC
 251 GCGAGCCTGT CGTGTGAAG GCAACATCCA TACACCAGTT TCCGTTGGAA
 301 ATTGGCAAAC ACAATATCG TCTTGAGTTC GATCAGTTTA CTTCTATGAA
 351 TGTGGAGGAC ATGAGCGAGG GCGCGGAACG GGAAGAAAGC CTGAAATCCA
 401 CGCTGAACGA TGTCGCGGCC GTTACTCAGG AAGGTAAAA ATACACCAAT
 451 ATCGGCCCTT CCATTGTTTA CCGTATCCGT GATGCGGCAG GGCAGGCGGT
 501 CGAATATAAA AACTATATGC TGCCGGTTT GCAGGAACAG GATTATTTT
 551 GGATTACCGG CACGCGCAGC GGCTTGCAGC AGCAATACCG CTGGCTGCGT
 601 ATCCCCTTGG ACAAGCAGTT GAAAGCGGAC ACCTTTATGG CATTGCGTGA
 651 GTTTTGAAG GATGGGGAAG GCGCAAACG TCTGGTTGCC GACGCAACCA
 701 AAGGCGCACC TGCCGAATC CCGAACAAT TCATGCTGGC TCGGGAAC
 751 ACGCTGAACA TCTTGCACA AAAAGGCTAT TTGGGATTGG ACGAATTTAT
 801 TACGTCCAAT ATCCCGAAG AGCAGCAGGA TAAGATGCAG GGCTATTCT
 851 ACGAATGCT TTACGGCGTG ATGAACGCTG CTTTGGATGA AACCATACGC
 901 CGGTACGCT TGCCGAATG GCAGCAGGAT GAAGCGCGGA ATCGTTTCT
 951 GCTGCACAGT ATGGATGCGT ACACGGGTTT GACCGAATAT CCGCGCCTA
 1001 TGCTGCTGCA ACTTGATGGG TTTTCCGAGG TCGCTTCGTC GGCTTGCAG
 1051 ATGACCCGTT CCGCGGTC GCTTTTGGTC TATCTCGGCT CGGTGCTGT
 1101 GGTATTGGGT ACGGTATTGA TGTTTTATGT GCGCAAAAA CCGGCGTGGG
 1151 TATTGTTTTC AGACGGCAAA ATCCGTTTTC CCATGCTTC GGCCCGCAGC
 1201 GAACGGGATT TGCAGAAGGA ATTTCCAAAA CACGTCGAGA GTCTGCAACG
 1251 GCTCGGCAAG GACTTGAATC ATGACTGA

This corresponds to the amino acid sequence <SEQ ID 1366; ORF 504.a>:

a504.pep
 1 ILVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
 51 HPLTLHGITI YQASFADGGS DLTFFKAWN LG DASREPVVLK ATSIHQFPLE
 101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTQEGKKYTN
 151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQYRWLR
 201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMALAEEN
 251 TLNIFAQKGY LGLDEFITSN IPKEQQDKMQ GYFYEMLYGV MNAALDETIR
 301 RYGLPEWQQD EARNRFLHS MDAYTGLTEY PAPMLQLDG FSEVRSSGLQ
 351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
 401 ERDLQKEFPK HVESLQRLGK DLNHD*

m504/a504 99.8% identity in 425 aa overlap

	10	20	30	40	50	60
m504.pep	ILVQDLPEFVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLE	IRVNHPLTLHGITI				
a504	ILVQDLPEFVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLE	IRVNHPLTLHGITI				
	10	20	30	40	50	60
m504.pep	YQASFADGGSDLTFFKAWN LGDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
a504	YQASFADGGSDLTFFKAWN LGDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
	70	80	90	100	110	120
m504.pep	MSEGAREKSLKSTLXDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ					
a504	MSEGAREKSLKSTLXDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ					
	130	140	150	160	170	180
m504.pep						
a504						

744

```

|||||
a504      MSEGAREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ
          130      140      150      160      170      180

          190      200      210      220      230      240
m504.pep  DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
          |||||||
a504      DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
          190      200      210      220      230      240

          250      260      270      280      290      300
m504.pep  REQFMLAENTLNIFAQKGYLGLDEFITSNIPKEQODKMQGYFYEMLYGVMNAALDETER
          |||||||
a504      REQFMLAENTLNIFAQKGYLGLDEFITSNIPKEQODKMQGYFYEMLYGVMNAALDETER
          250      260      270      280      290      300

          310      320      330      340      350      360
m504.pep  RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMRSPGALLV
          |||||||
a504      RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMRSPGALLV
          310      320      330      340      350      360

          370      380      390      400      410      420
m504.pep  YIGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
          |||||||
a504      YIGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
          370      380      390      400      410      420

m504.pep  DLNHDH
          |||||
a504      DLNHDH

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1367>:

```

g505.seq
1  atgtttcggt tacaattcag gctgtttccc cctttgcgaa ccgccatgca
51  catcctgttg accgcccctgc tcaaattgcct ctcctctgtg tcgctttcct
101 gtctgcacac gctgggaaac cggctcggac atctggcgtt ttacctttta
151 aaggaagacc gcgcgcgcat cgtcgccaat atgcggcagg cgggtttgaa
201 ccccgacacg cagacggtca aagccgtttt tgcggaaacg gcaaaatgcg
251 gtttggaact tgccccgcg tttttcaaaa aaccggaaga catcgaaaca
301 atgttcaaag cggtagacag ctgggaacac gtgcagcagg ctttggaaca
351 gggcgaaggg ctgctgttca tcacgccgca catcggcagc tacgatttgg
401 gcggacgcta catcagccag cagcttcctg tccacctgac cgccatgtac
451 aagccgccga aaatcaaagc gatagacaaa atcatgcagg cgggcagggt
501 gcgcggcaaa ggcaaaaccg cgcccaccgg catacaaggg gtcaaacaaa
551 tcatcaaggc cctgcgcgcg ggcgaggcaa ccatcatcct gcccgaccac
601 gtcccttctc cgcaggaagg cggcggcgtg tggcgaggatt ttttcggcaa
651 acctgcatac accatgacac tggcgcaaaa attggcacac gtcaaaggcg
701 tgaaaaccct gtttttctgc tgcgaacgcc tgcggacagg acaaggcttc
751 gtgttgaca tccgccccgt ccaaggggaa ttgaacggca acaaagccca
801 cgatgccgcc gtgttcaacc gcaataccga atattggata cgcggttttc
851 cgacgcagta tctgtttatg tacaaccgct ataaaacgcc gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1368; ORF 505.ng>:

```

g505.pep
1  MFRLLQRLFP PLRTAMHILL TALLKCLSL SLSCLHTLGN RLGHAFYLL
51  KEDRARIVAN MRQAGLNPDT QTVKAVFAET AKCGLELAPA FFKKPEDIET
101 MFKAVHGEH VQALDKGEG LLFITPHIGS YDLGGYISQ QLPFHLTAMY
151 KPPKIKAIK IMQAGVRVGK GKTAPTGIQG VKQIIKALRA GEATIILPDH
201 VPSPQEGGGV WADFFGKPAY TMTLAAKLAH VKGVKTLFFC CERLPDQGQF
251 VLHIRPVQGE LNGNKAHDA VFNRTYEWI RRFTQYLFM YNRYKTP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1369>:

m505.seq (partial)

```

1  GGCATGTTTC GTTTACAATT CAGGCTGTTT CCCCCTTTGC GAACCGCCAT
51  GCACATCCTG TTGACCGCCC TGCTCAAATG CCTCTCCCTG CTGCCGCTTT
101 CCTGTCTGCA CACGCTGGGA AACCGGCTCG GACATCTGGC GTTTTACCTT
151 TTAAGGAAG ACCGCGCGCG CATCGTCGCC AATATGCGGC AGGCGGGTTT
201 GAACCCCGAC CCCAAAACGG TCAAAGCCGT TTTGCGGAA ACGGCAAAAG
251 GCGGTTTGGG ACTTGCCCCC GCGTTTTTCA GAAAACCGGA AGACATAGAA
301 ACAATGTTCA AAGCGGTACA CGGCTGGGAA CATGTGCAGC AGGCTTTGGA
351 CAAACACGAA GGGCTGCTAT TCATCACGCC GCACATCGGC AGTACGATT
401 TGGGCGGACG CTACATCAGC CAGCAGCTTC CGTTCCTGCT GACCGCCATG
451 TACAAACCGC CGAAAATCAA AGCGATAGAC AAAATCATGC AGGCGGGCAG
501 GGTTGCGGCG AAAGGAAAAA CCGCGCCTAC CAGCATACAA GGGGTCAAAC
551 AAATCATCAA AGCCTGCGT TCGGGCGAGC AACCATCGTC CTGCCCGACC
601 ACGTCCCCTC CCCTCAAGAA GCGGGGGAAG GCGTATGGGT GGATTTCTTC
651 GGCAAACCTG CCTATACCAT GACGCTGGCG GCAArATTGG CACACGTCAA
701 AGGCGTGAAA ACCCTGTTTT TCTGCTGCGA ACGCCTGCCT GGCGGACAA
751 GTTTCGATTG GCACATCCGC CCCGTCCAAG GGAATTGAA CGGCGACAAA
801 GCCCATGATG CCGCGTGTG CAACCGCAAT GCCGAATATT GGATACGCCG
851 TTTCCGACG CATATC....

```

This corresponds to the amino acid sequence <SEQ ID 1370; ORF 505>:

m505.pep (partial)

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSLP LSLCLHTLGN RLGHAFYLL
51  KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLLELAPA FFRKPEDIET
101 MFKAVHGW EHVQQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAI D KIMQAGRVRGK GKTAPT SIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGG EG VVWVDFGKPA YMTLAAXLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQ G ELNGDKAHD AAVFNRAEY WIRRFPTHI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 505 shows 93.7% identity over a 287 aa overlap with a predicted ORF (ORF 505.ng)

from *N. gonorrhoeae*:

m505/g505

	10	20	30	40	50	60
m505.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSLCLHTLGNRLGHAFYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSLCLHTLGNRLGHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLLELAPAFRRKPEDIETMFKAVHGW EHVQQALDKHEG					
g505	MRQAGLNPDQTQTVKAVFAETAKGGLLELAPAFRRKPEDIETMFKAVHGW EHVQQALDKHEG					
	70	80	90	100	110	120
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLLELAPAFRRKPEDIETMFKAVHGW EHVQQALDKHEG					
g505	MRQAGLNPDQTQTVKAVFAETAKGGLLELAPAFRRKPEDIETMFKAVHGW EHVQQALDKHEG					
	70	80	90	100	110	120
m505.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPT SIQG					
g505	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPT SIQG					
	130	140	150	160	170	180
m505.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPT SIQG					
g505	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPT SIQG					
	130	140	150	160	170	180
m505.pep	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVVWVDFGKPAYTMTLAAXLAHVKGVKTLFF					
g505	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVVWVDFGKPAYTMTLAAXLAHVKGVKTLFF					
	190	200	210	220	230	240
m505.pep	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVVWVDFGKPAYTMTLAAXLAHVKGVKTLFF					
g505	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVVWVDFGKPAYTMTLAAXLAHVKGVKTLFF					
	190	200	210	220	230	240
m505.pep	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRAEYWIRRFPTHI					
g505	CCERLPGGQGFVLHIRPVQGEELNGDKAHDAAVFNRAEYWIRRFPTHI					
	240	250	260	270	280	290
m505.pep	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRAEYWIRRFPTHI					
g505	CCERLPGGQGFVLHIRPVQGEELNGDKAHDAAVFNRAEYWIRRFPTHI					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1371>:

a505.seq

```

1   ATGTTTCGTT TACAATTCAG GCTGTTTCCC CTTTTCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGTCAGG CAGGCATGAA
201 TCCCGACCCC AAAACGGTCA AAGCCGTTT TCGGAAACG GCAAAAGCGG
251 GTTTGGAAct TGCCCCGCG TTTTTCAGAA AACCGGAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGTT
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GAAAAACCG CGCCTACCAG CATACAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTCG GCGGAAGCAA CCATCGTCCT GCCCGACCAC
601 GTCCCTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAAAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTGTC ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1372; ORF 505.a>:

a505.pep

```

1   MFRLLQFRLFP PLRTAMHILL TALLKCLSL PLSCSLHTLGN RLGHlafYLL
51  KEDRARIVAN MRQAGMNPDP KTVKAVFAET AKGGLLELAPA FFRKPEDIET
101 MFKAVHGWEH VQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VWVDFGKPA YMTLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHDA AVFNRNAEYW IRRFPTQYLF MYNRYKMP*

```

m505/a505 99.0% identity in 287 aa overlap

	10	20	30	40	50	60
m505.pep	MFRLLQFRLFP	PLRTAMHILL	TALLKCLSL	PLSCSLHTLGN	RLGHlafYLL	KEDRARIVAN
a505	MFRLLQFRLFP	PLRTAMHILL	TALLKCLSL	PLSCSLHTLGN	RLGHlafYLL	KEDRARIVAN
	10	20	30	40	50	60
m505.pep	MRQAGLNPD	PKTVKAVFAET	AKGGLLELAPA	FFRKPEDIET	MFKAVHGWEH	VQALDKHEG
a505	MRQAGMNPDP	KTVKAVFAET	AKGGLLELAPA	FFRKPEDIET	MFKAVHGWEH	VQALDKHEG
	70	80	90	100	110	120
m505.pep	LLFITPHIGS	YDLGGYISQ	QLPFPLTAMY	KPPKIKAIK	IMQAGRVRGK	GKTAPTSIQG
a505	LLFITPHIGS	YDLGGYISQ	QLPFPLTAMY	KPPKIKAIK	IMQAGRVRGK	GKTAPTSIQG
	130	140	150	160	170	180
m505.pep	VKQIIKALRS	GEATIVLPDH	VPSPQEGGEG	VWVDFGKPA	YMTLAAKLA	HVKGVKTLFF
a505	VKQIIKALRS	GEATIVLPDH	VPSPQEGGEG	VWVDFGKPA	YMTLAAKLA	HVKGVKTLFF
	190	200	210	220	230	240
m505.pep	CCERLPGGQG	FDLHIRPVQ	GELNGDKAHDA	AVFNRNAEY	WIRRFPTHI	
a505	CCERLPGGQG	FDLHIRPVQ	GELNGDKAHDA	AVFNRNAEY	WIRRFPTQYLF	MYNRYKMPX
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1373>:

747

m505-1.seq

```

1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAATGCCT CTCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGGCAGG CGGGTTTGAA
201 CCCCGACCCC AAAACGGTCA AAGCCGTTTT TGCGGAAACG GCAAAAGGCG
251 GTTTGGAAct TGCCCCCGCG TTTTTCAGAA AACCGGAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGA AAAACCG CGCCTACCAG CATACAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTGG GCGGAAGCAA CCATCGTCCT GCCCGACCAC
601 GTCCCTCTCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAAGC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CCGACAAGGT
751 TTCGATTGTC ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1374; ORF 505-1>:

m505-1.pep

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSLP LSLCLHTLGN RLGHAFYLL
51  KEDRARIVAN MRQAGLNPD KTVKAVFAET AKGGLLELAPA FFRKPEDTET
101 MFKAVHGEH VQALDKHEG LLFITPHIGS YDLGGYISQ QLPPPLTAMY
151 KPPKIKAIK IMQAGRVGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPOEGGEG VWVDFFGKPA YMTLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHDA AVFNRAEYV IRRFPTQYLF MYNRYKMP*

```

m505-1/g505 94.3% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSLCLHTLGNRLGHAFYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSLCLHTLGNRLGHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MRQAGLNPDPTVKAVFAETAKGGLLELAPAFRRKPEDTETMPKAVHGEHVQALDKHEG					
g505	MRQAGLNPDPTVKAVFAETAKGGLLELAPAFRRKPEDTETMPKAVHGEHVQALDKHEG					
	70	80	90	100	110	120
m505-1.pep	MRQAGLNPDPTVKAVFAETAKGGLLELAPAFRRKPEDTETMPKAVHGEHVQALDKHEG					
g505	MRQAGLNPDPTVKAVFAETAKGGLLELAPAFRRKPEDTETMPKAVHGEHVQALDKHEG					
	70	80	90	100	110	120
m505-1.pep	LLFITPHIGSYDLGGYISQQLPPPLTAMYPKPKIKAIKIMQAGRVGKGKTAPTSIQG					
g505	LLFITPHIGSYDLGGYISQQLPPPLTAMYPKPKIKAIKIMQAGRVGKGKTAPTSIQG					
	130	140	150	160	170	180
m505-1.pep	LLFITPHIGSYDLGGYISQQLPPPLTAMYPKPKIKAIKIMQAGRVGKGKTAPTSIQG					
g505	LLFITPHIGSYDLGGYISQQLPPPLTAMYPKPKIKAIKIMQAGRVGKGKTAPTSIQG					
	130	140	150	160	170	180
m505-1.pep	VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDFFGKPAYTMTLAAKLAHVKGKTLFF					
g505	VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDFFGKPAYTMTLAAKLAHVKGKTLFF					
	190	200	210	220	230	240
m505-1.pep	VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDFFGKPAYTMTLAAKLAHVKGKTLFF					
g505	VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDFFGKPAYTMTLAAKLAHVKGKTLFF					
	190	200	210	220	230	240
m505-1.pep	CCERLPGGQGFVLDHIRPVQGEELNGDKAHDAAVFNRAEYVIRRFPTQYLFMYNRYKMPX					
g505	CCERLPGGQGFVLDHIRPVQGEELNGDKAHDAAVFNRAEYVIRRFPTQYLFMYNRYKMPX					
	240	250	260	270	280	290

m505-1/a505 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSLCLHTLGNRLGHAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSLCLHTLGNRLGHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
	70	80	90	100	110	120

q506.seq

1	ATGGCGGTAT	TTGATGAAGT	CGGGCGCATC	GCCCATGGCT	GCGGCGGTGT
51	TGTCAAACAA	AGCCTGTTTC	TGCGCGTCGT	TCATCAGGTT	GAACAAGGCG
101	CGCGGTTGGC	TGAAGTAGTC	GTCATCGCTT	TGGCGGTAGT	CCCATGTGTG
151	CGCGTCGCCG	TTGATTTTCA	AAGCGGGTTC	GGCGAAGTCG	GGTTGTGTCT
201	GCCATTGGCC	GAAAGCTGTG	GGTTCGTAGT	CGCGCAGGCT	CCCGTAGTTG
251	CCGTGCGGCG	GGCCTTGTC	GTCGCGCTGG	TTGCTGTGAA	CAGGGCAACG
301	CGGACGATTG	ACGGGGATT	GGCGGAAGT	CACACCCAAG	CGGTAACGTT
351	GCGCGTCGGC	GTAATTGAAC	AAACCGGGCT	GCAACATTTT	ATCCCGGGTC
401	GCGCCGATAC	CGGGAACGAG	GTGTCTCGGT	GCGAAGCGCG	ATTGTTCCAT
451	ATCGGCGAAG	AAGTTTTCGG	GATTGCGGTT	CAACTCGAAT	TCGCCCCTTT
501	CAATCAGCGG	ATAGTCTTTT	TTCGGCCAAA	CTTTGGTCAA	GTCAAACGGA
551	TGATAAGGCA	CTTTTTCCGC	ATCGGCTTCA	GGCATGACAT	GGATGTACAT
601	CGTCCATTTC	GGGAACCTGC	CGCGCTCGAT	GGCTTCGTAC	AGGTGCGCGT
651	GATGCGTTTC	CGCGTCGTGC	GCGATGATT	TTGCAGCTTC	TTCGTTGGTC
701	AGGTTTTTAA	TCCCTTGCTG	GCTGCGGAAA	TGGAATTTCA	CCCAAAAACG
751	TTCGCCCGCT	TCGTTCCAGA	AGCTGTAGAT	ATGCGAACCG	AAGCCGTGCA
801	TATGGCGGTA	GCTGGCGGGA	ATACCGCGGT	CGCTCATCAC	GATGGTAACT
851	TGGTGCAGGG	TCTGCGGCAG	CAGCGTCCAG	AAGTCCACAT	TGTTTGTGCG
901	GGAACGCATA	TTGGTGCGCG	GATCGCGTTT	GACGGCTTTG	TTCAGGTCGG
951	GGAATTTGCG	CGGTCGCGC	AGGAAGAACA	CGGGCGTGTT	GTTGCCGACC
1001	ACATCCCAAT	TGCCTTTCTC	GGTATAGAAT	TTCAACGCAA	AACCCGCGAT
1051	GTGCGGTTCC	GCATCGGCTG	CGCCGCGCTC	GCCTGCCACG	GTGGGTGAAAC
1101	GGGCGAACAT	CTCGGTTTTT	TGCGGCACTT	CGCTGAAAAT	TTTGGCGCGG
1151	GTGTATTTGG	TGATGTCGTG	TGTTACGGTA	AACGTACCGA	ACGCGCCCCG
1201	ACCTTTGGCG	TGCATACGGC	GTTCCGGGAT	GACTTCGCGC	ACGAAGTCGG
1251	CGAGTTTTTC	ATTCAAGCAC	AAATCTTGCG	TACGACGGGG	GCCGCGCGGG
1301	CGCGGGTTCA	GCTGTTTTTG	ATTGTGCGCA	ACGGGCGCGC	GCTGTGTCAT
1351	GGTCAGATGG	GTTACGGGGC	ATTTGGAGGT	AGTCATCGCT	CTTGTTCCCT
1401	TTCTCAGGTT	GGTCAAAATG	GGGGCAAACG	GCTTACAGTA	CGATTTTGGCG
1451	GAAAGCGTAT	TCGTAACCGG	TTTCTTGATT	GTAATAAATT	TCCTGAATCG
1501	ACATTTTATT	TTCTCTTTGC	AAAAACTATG	GATGCGATTA	TACGCCAAGA
1551	TTTTCGTTAT	TAA			

q506 . pep

1 MAVFDEVGRI AHGCGGVVKQ SLFLRVVHVQ EQGARLAEVV VIVLAVVPVC
51 RVAVDFQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGAALS VALVAVNRAT
101 RTIDGDIAEV HTQAVTLRVG VIEQTGLQHF IRARADTNE VARCEGGLFH
151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGO VKRMIRHFFG IGRHDLDVH

m506.seq

m506.ppt

m506/g506

m506 . pep MAVFDEVGVRVAHCGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRAVADFQRRF
 |||||:::||:|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
g506 MAVFDEVGRIGHCGGVVKQSFLRVVHQVEQGARLAEVVIVLAVVPVCRAVADFQRRF
 10 20 30 40 50 60

750

	70	80	90	100	110	120
m506.pep	GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
g506	GEVGLLLPLAEAVGFVVRQAQAVVAVGAALSVALVAVNRATRTIDGDLAEVHTQAVTLRVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m506.pep	VIEQTRLQHFIXAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
g506	VIEQTGLQHFIRARADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m506.pep	VKRMIRYFFRVCFRHDLVHRPFRKLAAFDGFXXVALMAFAVVGDGFGGFVGVFNALL					
g506	VKRMIRHFFGIGFRHDLVHRPFRRELAALDGFVQVALMAFAVVGDGFCFFVGVFNPLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m506.pep	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVCG					
g506	AAEMEFHPKTFARFVPEAVGMRTEAVHMAVAGGNTAVAHHDGNLVQGFQQRPEVPVVCG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m506.pep	RAHIGARVAFDGFVQVGEELTRVAQEEHGRVVADHIPVAFPGIKFQKGTADVAFCIGCAAF					
g506	GTHIGARIAFDGFVQVGEFARVAQEEHGRVVADHIPVAFPGIEFQKGTADVAFRIGCAAL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m506.pep	ACHGGTGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
g506	ACHGGTGEHLGFFADFAENFGAGVFGDVVCYGKRTERARTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m506.pep	IQPQILRQQAARTGGQAVLIVGNRAVVHGMGYRAFGGSHRSCSFSQVGMGKRLTV					
g506	IQPQILRQQAARAGGQAVLIVGNRAVVHGMGYGAFGGSHRSCSFSQVGMGKRLTV					
	430	440	450	460	470	480
	490	500	510	520		
m506.pep	RFGGKRIRNRFLDCNKFLESTFYFPFVKTMDATIRQDFRY					
g506	RFGGKRIRNRFLDCNKFLESTFYFPFAKTMDAIRQDFRY					
	490	500	510	520		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1379>:

a506.seq

```

1  ATGGCGGTAT TTGATGAAGT CCGGCGCGTC GCCCATTGCG GCGGCGGTGT
51  TGCCGAACAA TGCTGTTTC TGCGCGTCGT TCATCAGGTT GAACAGGGCG
101 CGCGGTGGC TGAAATAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGCGC
151 CGCGTCGCGG TTGATTTTCA AAGGCGGTTC GCGGAAGTCG GGCTGCTGCT
201 GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
251 CCGTCGGCGC GTCCTGTCC GTCGCGCTGG TTGCTGTGAA CAGGGCAACG
301 CCGACGGTTG ACAGGGATTG GCGGAAGTT CACGCCAAG CGGTAGCGTT
351 GCGGTCGCGC GTAATTGAAC AAACGCGCCT GCAACATTTT ATCTGGGCTG
401 GCGCGACAC CGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
451 ATCGGCGAAG AAGTTTTCGG GATTGCGGTT CAACTCGAAT TCGCCCACTT
501 CAATCAGCGG ATAGTCTTTT TTCGCCCAA CTTTGGTCAA GTCAAACGGA
551 TGATACGGCA CTTTTCCGC ATCGGCTTCA GGCATGACTT GGATGTACAT
601 CGTCCATTTC GGAAACTCGC .CGCGCTCGAT GGCTTCGTAC AGGTCGCGCT

```

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```

651 GATGGCTTTC ACGGTCCTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC
701 AGGTTTTTAA TGCCTTCTTG GGTGCGGAAA TGGAAATTTCA CCCAAAAACG
751 CTCGCCTGCT TCGTTCCAGA AGCTGTAGGT ATGCCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCCGGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCAGTG CTTCGGGCAG CAGCGTCCAG AAGTCCCAGT TGT'TGTGGC
901 AGAGCGCATA TTGGTGC GGTGCGGTTT GACGGCTTTG TTCAGGTCGG
951 GGAACCTACG CGGGTCGCGC AGGAAGAAC ACGGCGTGTT GTTGCCGACC
1001 ACATCCAGT TGCCTTCTTC GGTATAGAAC TTCAACGCAA AACCGCGGAT
1051 GTCGCGTTCT GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAGAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG CGTTACGGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTC ATTACGCCAC AAATCCTGCG CCAGCAGAGG GCCGCGAGGA
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACAGGCGCGC CGTTGTTTAT
1351 GGTCAGATGG GTTACAGGGC ATTTGGAGGT ANTATCGCT CTTGTTCTCT
1401 TTCTCAGGTT GGTCAAAT.G GGGGTAAACG GCTTACAGTA CGATTTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GCAATAAAT TCTTGAATCG
1501 ACATTTTATT TCCCTTTTGT AAAAATATG GATGCGACTA TACGCCAAGA
1551 TTTTCGCTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1380; ORF 506.a>:

```

a506.pep
1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHQV EQGARLAEIV VIVLAVVPVR
51 RVAVDFQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGASLS VALVAVNRAT
101 RTVDRDLAEV HAQAVALRVG VIEQTRLQHF IWAGADTGNE VARCEGGLFH
151 IGEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFR IGFRLDLVH
201 RPFRLAALD GFVQVALMAF TVVGDDFGGF FVGQVFNALL GAEMEFHFKT
251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFGQ QRPEVPVVCG
301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFV GIELQRKTAD
351 VAFICGAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGRTERAR
401 TFGVHTAFGD DFAEVGGEFF IQPQILRQOR AARTGGQAVL IVGNRRVAVH
451 GQMGYRAFGG XHRSCSFSQV GQXGKRLTV RFGGKRIRNR FLDCNKFLS
501 TFFFPFVKTM DATIRQDFRY *

```

m506/a506 94.8% identity in 520 aa overlap

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQRRF					
a506	MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVRRVAVDFQRRF					
	10	20	30	40	50	60
m506.pep	GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
a506	GEVGLLLPLAEAVGFVVRQAAXVAVGASLSVALVAVNRATRTVDRDLAEVHAQAVLRVG					
	70	80	90	100	110	120
m506.pep	VIEQTRLQHFIXAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
a506	VIEQTRLQHFIWAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
m506.pep	VKRMIRYFFRVCFRHLVDVHRPFRKLAAFDGFXVALMAFAVVGDDFGGFFVGQVFNALL					
a506	VKRMIRHFRIGFRHLVDVHRPFRKLAAALDGFVQVALMAFTVVGDDFGGFFVGQVFNALL					
	190	200	210	220	230	240
m506.pep	GAEMEFHFKTLACFVPEAVGMRTAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVCG					
a506	GAEMEFHFKTLACFVPEAVGMRTAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVCG					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m506.pep	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVDHI PVAFFGIKFGKGTADVAFCIGCAAF					
a506	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVDHI PVAFFGIELQRKTADVAFCIGCAAF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m506.pep	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
a506	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m506.pep	IQPQILRQQRARTGGQAVLIVGNRRRAVVHGMGYRAFGGSHRSCSFSQVGMGGKRLTV					
a506	IQPQILRQQRARTGGQAVLIVGNRRRAVVHGMGYRAFGGXHRSCSFSQVGMGXGGKRLTV					
	430	440	450	460	470	480
	490	500	510	520		
m506.pep	RFGGKRIRNRFLDCNKFLESTFYFPFVKTMDATIRQDFRYX					
a506	RFGGKRIRNRFLDCNKFLESTFYFPFVKTMDATIRQDFRYX					
	490	500	510	520		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1381>:

g507.seq

```

1  ATGCTCTTGC CGGCTTTGCA ACAAGGCGGC GGCTTCCTGA GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTCAGGGCTT GGTTTTCTCG CTTCAGACGG
101 CCTTTGCGCT CTTCTGTGCTT GGCAACGGTT TGTTCCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGAA GGCAGCGTTG AGCGTGGCTT GGACTTCTTC CAATTGCGGC
251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCCATTCGG CCAATTGCGT
301 TTGCTTTTCT TCGACCTGCA ACTCGTTTTC CTCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC CTGCCGGATG CGTTGCAACT GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTCA TCGCTTGGTG CAGGTTTTCG CCGTGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTTC CTCAATTGCT
501 GTACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TTATTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1382; ORF 507.ng>:

g507.pep

```

1  MLLPALQQGG GFLSGGGFGL VGQVQGLVFL LQTAFALFVL GNLFMGMKL
51  LLLQRQFAAD AVCLVLLGLE GSVERGLDFF QPGOTLFPVG NLHRPFROFG
101 LLFFDLQLVF LKLHADLLL LPDALQLRLR CLLVAFDALV QVLPVADLFF
151 QTGNLLAQHA AFVAQFVYCL LLRLFGSLQG VYFVI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1383>:

m507.seq

```

1  ATGCTCTTGC TGACTTTGCA ACAAGGCGGC TGCTTCCTGC GCGGCGGCGG
51  TTTCGGCTTC GTCGGGCAGG TTAAAGGCTT GGTTTTCTCG TTTAGACGA
101 CCTTTGCGCT CTTCTGTGCTT GGCAATCGTT TGTTCCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGAA GGCAGCGTTG AGCGTGGCTT GGGCTTCTTC CAATTGCGGC
251 AGACGCTCCT CGTGTTCGGC AACCTGCATC GCCCATTCGG CCAGCTCGGT
301 TTGTTTTTCT TCGACCTGCA ACTCGTTTTC TTCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC TTGATGAATG CGTTGTAAC TCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTCA TCGCTTGGTG CAGGTTTTCG TGATGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGCTTGTTC CTCAATTGCT
501 GCACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TCGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1384; ORF 507>:

m507.pep

```

1  MLLLTLLQGG CFLRGGGFGF VGQVXGLVFL FQTTAFALFVL GNRLFMMGKL

```

51 LLLQRQFAAD AVCLVLLGLE GGVERGLGFF QFGQTLVFG NLHRPFRQLG
101 LFFFDLQLVF FKLHADLLLL LMNALXLRLR CLLVAFDALV QVLLMADLFF
151 QTGNLLAQHA ALVAQFMHCL LLRLFGSLQG VYFVV*

Homology with a predicted ORF from *N. gonorrhoeae*

m507/g507

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1385>:

```
a507.seq
  1  ATGCTCTTGC  TGGCTTTGCA  ACAAGGCGGC  AGCTTCCTGC  GCGGCGGCGG
51  TTTCCGGCTTC  GTCAGGCAGA  TTCAGGGCTT  GGTTTTCCTG  TTTCAGACGA
101 CTTTTCGGCT  CTTCTGCTT  GGCACAGGTT  TGTTCCGGAT  GTTCAGCTG
151 CTGCTGCTTC  AACGCCAGTT  CGCGGCGGAT  GCGGTTTGCC  TCGTCTGTCT
201 GGGTTTGGAA  GGCGGCATTG  AGTGTGGCTT  GGTTTCTTC  CAATTCGGGC
251 AGACGCTCTT  CGTGTTCCGC  AACTGCATC  GCCCATCCG  CCAATTCGGT
301 TTGCTTTTCT  TCCGCCTGCA  ACTCGTTTTC  TTCAAGCTGC  ACGCGGATTT
351 GCTGCTGCTC  CTGATGGATG  CGCTGEATCT  GCGCCTCGGC  CGCCTGCTTG
401 TCGCGTTTCA  TGCGTTGGTG  CAGSTTTTGC  TGATGGCGGA  TTTGTTCTTC
451 CAAACGGGCA  ATCTGTTCCG  GCAACACGCC  GCSTTTGTTG  CCCAATTCGT
501 GCACCGCCTG  CTGCTGCGAC  TGTTCGGCAG  TCTGCAAGGC  GTGTACTTCG
551 TCGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1386; ORF 507.a>:

a507.pep

1	MLLLALQGGG	SFLRGGGFGF	VRQIQGLVFL	<u>FQTTFALFVL</u>	GNGLFGMGKL
51	LLLRQRFAD	AVCLVLLGLE	GGIECGLGFF	QFGQTLFVFG	NLHRPFRQFG
101	LLFTRLQLV	FKLHADLLLL	LMDALHLRLR	RLLVAFDALV	<u>QVLLMADLFF</u>
151	OTGNLFAOHA	AFVAOFVHRL	LLRLFGSLOG	VYFVV*	

m507/a507 89.7% identity in 185 aa overlap

	10	20	30	40	50	60
m507.pep	MLLLTLQQGGCFLRGGGFGFVGQVXGLVFLFQTTTFFALFVLGNRLF	GMGKLLLLLQRF	AAAD			
	:		:			
a507	MLLLALQQGGSFLRGGGFGFVVRQIQGLVFLFQTTTFFALFVLGNLFG	MGKLLLLLQRF	AAAD			
	10	20	30	40	50	60
	70	80	90	100	110	120

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```

m507.pep  AVCLVLLGLEGGVERGLGFFQFGQTLFVFGNLHRPFRQGLFFFDLQLVFFKLHADLLLL
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a507       AVCLVLLGLEGGIECGLGFFQFGQTLFVFGNLHRPFRQGLFFFDLQLVFFKLHADLLLL
              70      80      90      100     110     120

              130     140     150     160     170     180
m507.pep  LMNALXLRRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRFLGSLQG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a507       LMDALHLRLRLLVAFDALVQVLLMADLFFQTGNLFAQHAAAFVAQFVHRLLLRFLGSLQG
              130     140     150     160     170     180

m507.pep  VYFVVX
|||||
a507      VYFVVX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1387>:

```

g508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TCGGCAGCT TGGTTGCAG GGTTCGTACG
101 CGGGCGTATT GCTCCCTGCC CTGTTCTGA ATCTGCGCGA GTTTTCCTG
151 CACGGCGATG TATTCTTCGT CCAGCGTGTG TACGGTTTCG GTCAACTCGT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCCGCGCTTC CTGCCAGTCC AGGGTTTGCT GTTCGAGCCG
301 GGCGATTGTC TGCCGGTAGT TTTGTTTTTG CGGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAGTA GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1388; ORF 508.ng>:

```

g508.pep
1  MVAFGVDQGL LLLQQGGLGG GLKLRQLGLQ GLYAGVLLPA LFLNLRFFFL
51  HGDVFFVQRV YFGQLVELD VLLVLELGF IGEGKLLPAF LPVQGLLFEP
101 GDLLPVVFL RVEFVDGDFG KPVLA VGFOQ GKLRLFOTAL LLLAAVRGGL
151 LLVFEFGGGF LQSSDVV

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1389>:

```

m508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TCGGCAGCT TGGTTGCAG GGTTCGACT
101 TTAGCGTATT GCTCCCTGCC CTGTTCTGA ATCTGCGCGA GTTTCCTTG
151 CACAACAATA TATTCTTCGT CCAAGGTCTG TACGGCTTCG CTTAATCTT
201 CAAGCTTGAT GTGCTGCTCG TCGTTTGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAGTCG AGGGTTTGCT GTTCAAGCTG
301 GGCGATTGTC TGCCGGTAGT TTTGTTTTTG CTGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAGTA ACGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1390; ORF 508.ng>:

```

m508.pep
1  MVAFGVDQGF LLLQQGGLGG GLKLRQLGLQ GLHFSVLLPA LFLNLRFFLL
51  HNNIFFVQGL YGFAEFKLD VLLVLELGF IGEGKLLAF LPVEGLLFKL
101 GDLLPVVFL LVEFVDGDFG KPVLA VGFOQ GKLRLFOTAL LLLAAVRGGL
151 LLVFEFGGGF LQGNDDV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 508 shows 86.8% identity over a 167 aa overlap with a predicted ORF (ORF 508.ng) from *N. gonorrhoeae*:

m508/g508

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	10	20	30	40	50	60
m508 . pep	MVAFGVDQGFLL	LLQQGGLGGLKLRQLGLQGLHFSVLLPALFLNLREFLLHNNIFFVQGL				
g508	MVAFGVDQGLLL	LLQQGGLGGLKLRQLGLQGLYAGVLLPALFLNLREFFLHGDVFFVQRV				
	10	20	30	40	50	60
	70	80	90	100	110	120
m508 . pep	YGFAFFKLDVLL	VVLELGFIGEGKLLLAFLPVEGLLFLKGLDLPVVLFLLVFVDGDFG				
g508	YGFQQLVELDVLL	VVLELGFIGEGKLLPAFLPVQGLLFPDGLLPVVLFLRVEFVDGDFG				
	70	80	90	100	110	120
	130	140	150	160		
m508 . pep	KPVLAVGFQQGLR	LFQTALLLLAAVRGGLLVFEFGGFLQGNDDV				
g508	KPVLAVGFQQGLR	LFQTALLLLAAVRGGLLVFEFGGFLQSSDVV				
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1391>:

```

a508 . seq
1  ATGGTAGCGT TTGGCGITGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TCGGCAGCT TGGTTGCAG GGTTCGTACG
101 CGGGCGTATT GTTCCCTACC CTGCTCCTGA ATCTGCGCGA GTTTCCTCTG
151 TACGACAATA TATTCTCGT CCAAACTCTG TACGGCTTCG CTCAACTCTT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTGGG ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAATCG AAGGTTTGT GTTCAAGCTG
301 GGCAATTGTC TGTGTGTA GTTGTGTTT CTGGTTGAGC TTGTGGACGG
351 CGACTTCGGC AAGCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGACCTTG CTGCTCTTGG CGGCTGTGCG CGGCGGTTTG
451 CTGCTGCTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAATG GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1392; ORF 508.a>:

```

a508 . pep
1  MVAFGVDQGF LLLQQGGLGG GLKLRQLGLQ GLYAGVLFPT LLLNLREFLL
51  YDNIFVQTL YGFAQLFELD VLLVVLELGF IGEGKLLAF LPIEGLLFLK
101 GNLLLVVFL LVELVDGDFG KPVLAVGFQ GKRLRFQTL LLLAAVRGL
151 LLVFEFGGF LQNGDVV*

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m508/a508 88.6% identity in 167 aa overlap

	10	20	30	40	50	60
m508 . pep	MVAFGVDQGFLL	LLQQGGLGGLKLRQLGLQGLHFSVLLPALFLNLREFLLHNNIFFVQGL				
a508	MVAFGVDQGFLL	LLQQGGLGGLKLRQLGLQGLYAGVLFPTLLNLREFLLYDNIFVQTL				
	10	20	30	40	50	60
	70	80	90	100	110	120
m508 . pep	YGFAFFKLDVLL	VVLELGFIGEGKLLLAFLPVEGLLFLKGLDLPVVLFLLVFVDGDFG				
a508	YGFAQLFELD	VLLVVLELGFIGEGKLLLAFLPIEGLLFLKGNLLLVVFLLVVELVDGDFG				
	70	80	90	100	110	120
	130	140	150	160		
m508 . pep	KPVLAVGFQQGLR	LFQTALLLLAAVRGGLLVFEFGGFLQGNDDVX				
a508	KPVLAVGFQQGLR	LFQTLALLAAVRGGLLVFEFGGFLQNGDVVX				
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1393>:

g509 . seq

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1  atggtcgctg tatgtgatga acgggctgta cagcggaagt tggtagccca
51  attcgcgcaa caaggcggct tgtttttgct cttcgttcag gctgtttag
101 tcttccaagc ctgctgtgtg gaaaagctcg gcaaccacat cggcgtgttt
151 gcctgcgtgt tggcgaggt cgagcggcat catgtggaag ccgaacacgg
201 acacggaacg gatgaggtct gccaaacggc cttcggcaag caggcggtg
251 ccgttgtcga taagggaacg ttgcaatttt ttcaaatcat cgagaaattt
301 ttgggcccga gcataacgct cgagaaagcc gaatttgca cccatgccc
351 aaccgagcga gcgcgctttg cccatagcgc gcgccataat gtaggcaatg
401 gcgcggcggt aagggttctt ggtgcggcg atttcttcgt caggcgagag
451 cgctgccagt gccattacgt cgtcgttgac ttgacgcgg cggtatggaa
501 gcggcagttc gcggtaaagt ttgtcgagtt cgctgcggt aaaaacgga
551 acggcatcgg cgtggcggcg gaaggcaaag cgcagggttt cggcagaaac
601 aaacggaatt cgctcgcggt cgccgcgcat ccagccgcg attttaagga
651 tatteggaac gcggacatcg ggataggccg tctgaaagtc gtgttccatc
701 ttgcggtaga gtttgggcag ggcttcaaaa aagctcatcg gyaagatgga
751 cagccggtt ttgatttcgt cgttgacgct gagtttggt cggcgcttt
801 cgctggtctg ccacaagccc agaagcacgg tgcgatttc gcggcgagc
851 cgtgccagcg cgtcgcgatt ggtgcagcgt tcgcgttgcg gcagcagcg
901 gcggatgcgg cggttgaaat tcaaaacggc ttggcggtgc acttcggtcg
951 ggtgcgcggc caaaacggcg gtaacggagc tattgtccaa ctgccgctgc
1001 accgatttgc cgtcggtttt ccccgctttg agcctgcgga cgggttccgt
1051 caggctgcct tctgctgcgt tgtggcggcg atcttcgtgg atttgcggg
1101 ggcgttcgtg gtgcacgtct tcggcgatat tcagaatctg ggcgaaacagc
1151 ccgcaggcaa gcgtcagatc gtaggtctgc cgttcgtcca atttcggcaa
1201 tactttttca atcaatgccg cgctgtcgtc ggaagtggac aagagtttga
1251 ccgtttcgac aaccaacggc gaggttctt cgtgcaggag gttgaacag
1301 gactgtttca aaaattccgc gtccgcgcgc aaagccgcgt ccttcggatt
1351 gttcaggata tgcagttgca tgattttcct ctcattgccg taaatactgt
1401 aaatgtacct caaatgccgc atccgtgcc aaccgttcac actttaacca
1451 ctcagtcccc gaaatgccgt ctgaagtga acgcgcgcc acggcgcgct
1501 tacaatcgcc cgcaactgtt tttttccgaa catcatcatg acccgagccg
1551 aacacgacaa cgacgacgca ctctgctgc ggtacagccg ccacatcttc
1601 ttggacgaaa tcggcatcga agggcagcag aagctttccg ccgcgcatat
1651 tttggtcgtc ggctgcggcg gattgggcgc cgccgccctt gccctatctc
1701 gccgcctcgg gggtcggcac gctga

```

This corresponds to the amino acid sequence <SEQ ID 1394; ORF 509.ng>:

g509.pep

```

1  MVAVCDERAV ORTLVAQFAQ OGGLFLLFVQ AVVVFQACVL BKLGNHIGVF
51  ACVLAQVERH HVEAEHGHGT DEVCQTAFGK QAAAVVDKGT LQFFQIIEKF
101 LGRSIRLEKA EFAAHQTER ARFAHSARHN VGNGAAVRFF GAGDFFVRRE
151 GCQCHYVVVD FDAADGKRQF AVKFVEFAAV KTEHGIGVAA BGKAQGFAFN
201 KRIAVAAAD PAADFKDIRN ADIGIGRLKV VFHLAVEFGQ GFKKAHREDG
251 HAVVDVFVDA EFVAARFAGL PQAQKHGVDF AAQPCQRVGI GAAFALRQQR
301 ADAAVEIQNG LALHFGRVRG QNGGNRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFCCVVAG IFVDLAAAFV VHVFGDIQNL GEQPAKROI VGLPFVQLRQ
401 YFFNQCRVV GSGQEFDRFD NRRGFFVQE VEQGLFQKFR VRRQSRVLR
451 VQDMQLHDFP LIAVNTVNVP QMPHPCQTVH TLTHVPKCR LKLNAARRRR
501 YNRPQLFFSE HHDRDRTRQ RRRTPAAVQP PHPLGRNRHR RAEEAFRRAY
551 FGRLRRRIGR RRPCISPFR GSAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1395>:

m509.seq

```

1  ATGGTCGCTG TATGTGATAA ACGGGCTGTA CAGAGGACGT TGATGGCTCA
51  ATTCGCGCAA CAGGGCGGTT TGTTTTGTCT CTTCTTCAG GCGGTGTAG
101 TCTTCCAAGC CTGCGTGTGG GAAAAGCTCG GCAACCACAT CGGCGTGTG
151 GCCTGCGTGT TGGCGCAAGT CGAGCGGCAT CATGTGAAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTGCGCAAG CAGACGGCTG
251 CCGTTGTGCG TAAGGGAACG TTGCAATTTT TTCAAATCAT CCAGAACTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCCATACCCA
351 AACCAGACGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCGATG
401 GCGCGGCGGT AGGGTTCTTC GCGCGGGCG ATTTCTTCGT CGGGCGATTT
451 GTCGGACAAC GCCGTACAT CGCCGTTGAC TTTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTCGAGTT CGCCGCGATA GAACCGGAAC

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551 ACGGCATCGG CGTGGCGGCG GAAGGCAAAG CGCAGGGTTT CGGCAGAAAC
601 AAACGGATTG CCGTCGCGGT CGCCGCCGAT CCAGCCGCCG ATTTTGAGGA
651 TGTCCGGAAC GCGGACGCCG GGATAGGCCG TCTGAAAGTC GTGTTCATC
701 TTGCGGTAGA GCTTGGGCAG GGCTTCGAAA AAGCTCATCG GGAAGATGGA
751 CACGCCGTTG TTGATTTCGT CGTTGACGCT GAGTTGTGG CGGCGCGTTT
801 CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTGATTtC GCgGCGCAGC
851 CGTGCCAGCG CGTCGCGATT GGTGACGCGT TCgCGTTGCG GCAACAGTGC
901 GCGGATGCGG CGGTTGAAGC TTAAGACGGT TTGGCGTTGC ACTTCGGTCG
951 GGTGCGCGGT CAAAACG3CG GTAACGGACG TATTGTCCAA CTGCCGCTGC
1001 ACCGATTTCG CGTCGCGCTTT CCCCCTTTG AGCCTGCGGA CGGTTCCGT
1051 CAGGCTGCCT TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTTGGCGGC
1101 GCGCTTCGTG GTGCACGTCT TCGGCGATGT TCAAAATCTG GGCGAACAGG
1151 CCGCAGGCCA AGGTTAAATC GTGGGTTTGT TGTTCGTCCA ATTGCGGCCA
1201 TACTTTTTCA ATCAATGCCG CGCTGTCGTC GGAAGTGGAC AAGAGTTTGA
1251 CTGTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAGGAG GTTGAACAGG
1301 GATTGTTTCA GAAATTCCGC GTCCGCCGCC AAAGCCGCGT CCTTTGATT
1351 GTTCAGAATA TGCAGTTGCA TGATTTTCT CTCTCGTCTG CCGTAAATAT
1401 TGTAATATGTA CCCCATAATG CGCATCCGTG CCAAACCGTT CACACTTTAA
1451 CCGCCCGTGT CCCGAAATGC CGTCTGAAGT TGAACGCCGC CCGACGGCAG
1501 CGTTACAATC GCCCGCAACT GTTTTtTTCC GAACATCATC ATGACCACGA
1551 CCGAACACGA CAACGACGAT GCATTCCCTGC TGCAGTACAG CCGCCACATC
1601 CTCTTGACG AAATCGGCAT CGAAGGGCAG CAGAACTTT CCGCCGCGCA
1651 TATTTTGGTC GTCGCTGCG GCGGTTGGG TGCCGCCGCA CT.GCCCTAC
1701 CTTGCCGCTT CGGGTGTCGG CACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1396; ORF 509>:

m509.pep

```

1  MVAVCDKRAV QRTLMAQFAQ QGGLFLLFVQ AVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVKAEHGYGT DEVCQAFGK QTAAVVDKGT LQFFQIIQKL
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VGDGAAGVFF GAGDFFVGRF
151 VGQRRYIAVD FDAADGERQF AVEFVEFAAI EAEHGIGVAA EGKAQGFGRN
201 KRIAVAVAAD PAADFEDVRN ADAGIGRLKV VFHLAVELGQ GFBAHREDG
251 HAVVDFVUDA EFVAARFAGL PQAQDSVDF AAQPCQRVGI GAAAFALRQC
301 ADAAVEAXDG LALHFGRVRG QNGGNRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFRAAASG FFVDLAAAFV VHVFGDVQNL GEQAAGQGX I VGLLFVQLRQ
401 YFFNQCRADV GSGQEFDCFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI
451 VQNMQLHDFS LSSAVNIVNV PQMPHPCQTV HTLTARVPKC RLKLNARRQ
501 RYNRPQLFFS EHHHDHRT RRCIPAAVQ PPHPLGRNRH RRAAETFRRA
551 YFGRRLRRFG CRRTXPTLPL RVSAR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 509 shows 87.8% identity over a 575 aa overlap with a predicted ORF (ORF 509.ng) from *N. gonorrhoeae*:

m509/g509

	10	20	30	40	50	60
m509.pep	MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVFQACVLEKLGNHIGVFACVLAQVERH					
g509	MVAVCDERAVQRTLVQAQFQQGGLFLLFVQAVVVFQACVLEKLGNHIGVFACVLAQVERH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m509.pep	HVKAHGYGTDEVCQAFGKQTAAVVDKGTLQFFQIIQKL LCRSIRLEKA EFAAHTQTER					
g509	HVEAEHGHGTDEVCQAFGKQAAAVVDKGTLQFFQIIQKL LGRSIRLEKA EFAAHTQTER					
	70	80	90	100	110	120
	130	140	150	160	170	180
m509.pep	ARFAHSARHNVDGAAGVFFGAGDFFVGRFVGQRRYIAVD FDAADGERQFAVEFVEFAAI					
g509	ARFAHSARHNVDGAAVRFFGAGDFFVRREGQCHYVVD FDAADGKRQFAVKFEFAAV					
	130	140	150	160	170	180

	190	200	210	220	230	240
m509 .pep	EAEHGIGVAAEGKAQGFGRNKRIAVAVAADPAADFEDVRNADAGIGRLKVVVHFLAVELGQ					
g509	KTEHGIGVAAEGKAQGFARNKRIAVAVAADPAADFIDIRNADIGIGRLKVVVHFLAVEFCQ					
	190	200	210	220	230	240
m509 .pep	250	260	270	280	290	300
g509	GFEKAHREDGHAVVDFVVDAEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGAAAFALRQQC					
	250	260	270	280	290	300
m509 .pep	310	320	330	340	350	360
g509	ADA AVEAXDGLALHFGVRVGRQNGGNRIVQLPLHRFAVGFPFRFEPADGFRQAAFRAAASG					
	310	320	330	340	350	360
m509 .pep	370	380	390	400	410	420
g509	FFVDLAAAFVHVHFGDVQNLGEQAAGQGXI VGLL FVQLRQYFFNQCRAVVSGSQEFDCFD					
	370	380	390	400	410	420
m509 .pep	430	440	450	460	470	480
g509	NQRRGFFVQGEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFLS SAVNIVNV PQMPHP CQTV					
	430	440	450	460	470	
m509 .pep	490	500	510	520	530	540
g509	HTLTARVPKCRLLKNAARRQRYNR PQ LFFSEHHHDH DRTRQRRCI PAAVQPPHPLGRNRH					
	480	490	500	510	520	530
m509 .pep	550	560	570			
g509	RRAAETFRRAYFGRRLLRRFGCRRTCPTLPLRV SAR					
	540	550	560	570		

a509.seq

1	ATGGTCGCTG	TATGTGATGA	ACGGACTGTA	CAGTGGACGT	TGATGGCTCA
51	ATTCCGCGAA	CAGGGCGGCT	TGTTTTTGCT	CTTCGTTGAG	GCCTCTTGTA
101	TCTTCCAAGC	TGCGCTGTTT	GAAAAGCTCG	GCAACCAGAT	CGGCGTGTTT
151	GCGTCGCTGT	TGGCGCAGGT	CGAGCGGCAT	CATGTGGGAAG	CCGAAACACGG
201	ATACGGAACG	GATGAGGTCT	GCCAAACGCG	CTTCGGCAAG	GAGCGCGCTG
251	CGGTTGTCGA	TAAAGGGAATG	TTGCAATTTT	TTCAAATCAT	CGAGAAATTC
301	TTGTGCGCCA	GCATAAGGCT	CGAGAAAGCC	GAATTTGACG	CCCATACCCA
351	AACCGAGCGC	GCGCGCTTTG	CCCATAGGCG	CGGCCATAAT	GTAGGCAATG
401	GCGCGACGCT	ACGGTTCCTC	GCGCGCGGCG	GTTCCTTCGT	CGGGCGAATT
451	GTCGGACAAC	GCCATCACAT	CGCCGTTGAC	TTTGACGCGG	CGGATGGAGA
501	GCGGCGAGTT	GCGGTAGAGT	TTGTGAGATT	CGCCACGCTA	AAAACGGAAC
551	ACGGCATCGG	CGTGCGCGCG	GAAAGCAAAA	CGCAAGGTTT	CGGCAGAAAC
601	GAAACGATTG	CCGTGCGGGT	CGCCGCGCAT	CCAGCGCGCG	ATTTTGAGGA
651	TGTCCGGAAC	GCGGACATCG	GGATAGGCCG	TCTGAAAGTC	GTGTTCCATC
701	TTGCGGTAGA	GTTGTTGCGAG	GGCTTCAAAA	AAGCTCATCG	GAAAGATGGA
751	CAGCCGCTTG	TTCATTTTCGT	CGTTGACGCT	GAGTTTGTGG	CGGCGCGCTT
801	CGCTGCTGTC	CCACAAGCCC	AGCAGGATAG	TGTCGATTTC	GCGGCGCAGC
851	CGTGCCACGG	CGTCGGCATT	GCTACAGCGT	TGCGGTTGCG	GACGACGCGC

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901 GCGGATGCGG CGGTTGAAAT TCAAGACGGT CTGGCGTTGC ACTTCGGTCG
951 GGTGCGCGGT CAAAACGGCG GTAACGGACG TATTGTCCAA CTGCCGCTGC
1001 ACCGATTTGC CGTTCGGCTT CCCCGCTTTG AGCCTGCGGA CGGTTTCCGT
1051 CAGGCTGCCT TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTTGGCGGC
1101 GCGGTTTCGT GTGCACGTCT TCGGCGATGT TCAAAATCTG GCGGAACAGG
1151 CCGCAGGCCA AGGTTAAATC GTGGGTTTGT TGTTCGTCCA ATTGCGGCAA
1201 TACTTTTTC AATCAATGCCG CGCTGTCTGC GGAAGTGGAC AAGAGTTTGA
1251 CCGTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAGGAG GTTGAACAGG
1301 GATTGTTTCA GAAATTCGGC GTCCGCGGCC AAAGCCCGCT CCTTTGGATT
1351 GTTCAGAATA TGCAGTTGCA TGATTTTCT CTCATTGCCG TAAATACTGT
1401 AAATGTACCT CAAATGCCGC ATCCGTGCCA AACCGTTCAC ACTTTAACCG
1451 CCCGTGTCCC GAAATGCCGT CTGAAGTTGA ACGCCGCCCG ACGGCAGCGT
1501 TACAATCGCC CACAACGTGT TTT.TCCGAA CATCATCATG ACCACGACCG
1551 AACACGACAA CGACGATGCA TTCCTGCTGC GGTACAGCCG CCACATCCTC
1601 TTGGACGAAA TTGGCATCGA AGGGCAGCAG AAACCTTCCG CCGCGCATAT
1651 TTTGGTCGTC GGCTGCGGCG GTTTGGGTGC CGCCG.CCCT GGCCTATCTC
1701 GCCGTTCCG GCATCGGCAC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1398; ORF 509.a>:

```

a509.pep
1  MVAVCDERTV QWTILMAQFAQ QGGLFLLFVE AVVVFOACVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGYGT DEVCQTAFGK QAAAVVDKGM LQFFQIIIEKF
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VNGATVGGFF GAGGFFVGRF
151 VGQRHHIAVD FDAADGERQF AVEFVEFATV KTEHGIGVAA EGKTQGFGRN
201 ERIAVAVAAD PAADFEDVRN ADIGIGRLKV VFHLAVELGQ GFKAHRKDG
251 HAVVDFVVD AEFVAARFAGL PQAQDSDVDF AAQPCQRVGI GTAFALRQQR
301 ADAAEVIQDG LALHFGRVRG QNGNGRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFRAAASG FFDVLAFAFV VHVFGDVQNL GEQAAGQG*I VGLLFVQLRQ
401 YFFNQCRVV GSGQEFDRFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI
451 VQNMQLHDFS LIAVNTVNVP QMPHPCQTVH TLTARVPKCR LKLNAARRQR
501 YNRQQLFXSE HHHHDHRTRO RRCIPAAVQP PHELGRNWHR RAAETFRRAY
551 FGRRLLRRFGC RXPCPISPLP ASAR*

```

m509/a509 93.0% identity in 575 aa overlap

m509.pep	10	20	30	40	50	60
	MVAVCDKRAVQRTILMAQFAQ	QGGLFLLFVQAVVVFOACVLEK	LG	GNHIGVFACVLAQVERH		
a509	MVAVCDERTVQWTILMAQFAQ	QGGLFLLFVEAVVVFOACVLEK	LG	GNHIGVFACVLAQVERH		
m509.pep	70	80	90	100	110	120
	HVKAEGHYGTDEVCQTAFGKQ	TAAVVDKGT	LQFFQIIQKLLCRSIRLEKAEFAAHTQTER			
a509	HVEAEHGYGTDEVCQTAFGKQ	AAVVDKGM	LQFFQIIIEKFLCRSIRLEKAEFAAHTQTER			
m509.pep	130	140	150	160	170	180
	ARFAHSARHNVGDGA	AVGFFGAGDFFVGRFVGRQRRYIAVD	FDAADGERQFAVEFVEFAAI			
a509	ARFAHSARHNVGNGATV	GFFGAGGFFVGRFVGRQRRHIAVD	FDAADGERQFAVEFVEFATV			
m509.pep	190	200	210	220	230	240
	EAEHGIGVAAEGKAQGFGRNKRI	AVAVAADPAADFEDVRNADAGIGRLKVV	FHLAVELGQ			
a509	KTEHGIGVAAEGKTQGFGRNERI	AVAVAADPAADFEDVRNADAGIGRLKVV	FHLAVELGQ			
m509.pep	250	260	270	280	290	300
	GFKAHREDGHAVVDFVDAEF	VAARFAGLPQAQDSDVDFAAQPCQRVGIG	AAAFALRQQR			
a509	GFKAHRKDGHAVVDFVDAEF	VAARFAGLPQAQDSDVDFAAQPCQRVGIG	TAFAALRQQR			
	310	320	330	340	350	360

m509.pep	ADA AVEAXDGLALHFGSRVRGQNGGNRIVQLPLHRFAVGFPRFEPADGFRQAAFRAAASG					
a509	ADA AVEIQDGLALHFGSRVRGQNGGNRIVQLPLHRFAVGFPRFEPADGFRQAAFRAAASG	310	320	330	340	350 360
m509.pep	FFVDLAAAFVHVHFGDVQNLGEQAAGQGXI VGLLFVQLRQYFFNQCRAVVSGSQEFD	370	380	390	400	410 420
a509	FFVDLAAAFVHVHFGDVQNLGEQAAGQGXI VGLLFVQLRQYFFNQCRAVVSGSQEFD	370	380	390	400	410 420
m509.pep	NQRRGFFVQEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLS SAVNIVNVPQMPHP	430	440	450	460	470 480
a509	NQRRGFFVQEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFS LI-AVNTVNVPQMPHP	430	440	450	460	470
m509.pep	HTLTARVPKCR LKLNAARRQRYNRPQLFFSEHHHDH DTRQRRCI PAAVQPPHPLGRNRH	490	500	510	520	530 540
a509	HTLTARVPKCR LKLNAARRQRYNRPQLFXSEHHHDH DTRQRRCI PAAVQPPHPLGRNWH	480	490	500	510	520 530
m509.pep	RRAAETFRRAYFGRRLRRFGCRRTXPTLPLRV SARX	550	560	570		
a509	RRAAETFRRAYFGRRLRRFGCRXPCFISP LPASARX	540	550	560	570	

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g510.seq
1  atgccttcgc ggacaccgca gggaaaaaagg ggttattcct gccccaagcg
51  ggatagtgcc ttttggcagg cgttgtccat atcggttatt ttacgcgcaa
101 aatcgccygt tgccaaatcg cgcgcgttca gggagggttt caataggctc
151 tggacgcagt tgagcgcggc cataatgacy attttttcgc tgcocgcgac
201 gcggccgect tcgcggatgg cttcggcttt gccgttgagc attccgactg
251 cctgcaacag tgtgtctttt tcttctgcgc gcgtgttgac agtcagccgg
301 ggcgtgcagt acctcgatgt agacttggtc gatgttcate ctttaatect
351 tattcgtcgc tttctctgcc ttggagagag cgcgcctgca atcgcgttaa

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g510.pep
1 MPSRTPOGKR GYSCPKRDSA FWQALSISVI LRAKSPIAKS PPFREVFNRS
51 WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTCSR
101 GVHDFDVDLF DVHPLILIAA FPAVGGGALP VR*

```
m510.seq
1  ATGCCTTCGC GGACACCGCA GGGnAAAAGG GGTATTCTCT GCGCCAAGCG
51  GGATAGTGGT TTTTGGCAGG CCGTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CGGTGGCTTA CGAGAGCTTT CAACAGGTGC
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTTCGC TGTCCGCGAC
201 GCGTCCGCCT TCGCGGATGG CTTCGGCTTT GCCGTTGAGC ATTCGGACTG
251 CCTGCAACAG TGTGTCTTTT TCTTCTGCCG GCGTGTTCAC GGTGACGCGG
301 GGCSTGCaWg ACTTCSAtGT GGACTTGTTC GATGTTGCAT CTTTAATCCG
351 TATTGCTGCG TTTCTTGCCA TTGGGGGAGG CGCGCTGCCA GTGCGCTGTA
```

m510.pep

1	MPSRTPQGR	GYSCAKRDSA	FWQALSISAI	LRAKSPIAKS	PPFREVENRS
51	WTTLSAAIMT	IFSLSATRPP	SRMASALPLS	IPTACNSVSF	SSAGVLTVSR
101	GVXDFXVDLF	DVHPLILIAA	FPAIGGGALP	VR*	

Computer analysis of this amino acid sequence gave the following results:

761

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 510 shows 96.2% identity over a 132 aa overlap with a predicted ORF (ORF 510.ng) from *N. gonorrhoeae*:

m510/g510

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSA	FWQALSISAILRAKSPIAKS	PPFREVFNRSWTTLSAAIMT			
g510	MPSRTPQGKRGYSCPKRDSA	FWQALSISVILRAKSPIAKS	PPFREVFNRSWTTLSAAIMT			
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLS	IPTACNSVSFSSAGVLT	VS	SRGVXDFXVDLFDVHPLILIAA		
g510	IFSLSATRPPSRMASALPLS	IPTACNSVSFSSAGVLT	VS	SRGVHDFDVLFDVHPLILIAA		
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
g510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1403>:

a510.seq

```

1  ATGCCTTCGC GGACACCGCA GGGAAAAAGG GGTATTTCCT GCGCCAAGCG
51  GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCCGTTCA GGGAGGTTT CAACAGGTCG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTTCGC TGCCCGCGAC
201 GCGTCCGCCT TCGCGGATGG CTTGGGCTTT GCCGTTGAGC ATTCCGACTG
251 CCTGCAACAG TGTGTCTTT TCTTCTGCCG GCGTGTGAC GGTGAGCCGG
301 G.CGTGCATG ACTTCGATGT GGACTTGTTT GATGTTTCATC CTTAATCCT
351 TATTGCTGCG TTTCTGCGG TTGGGGGAGG CCGCTGCCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1404; ORF 510.a>:

a510.pep

```

1  MPSRTPQGKR GYSCAKRDSA FWQALSISAI LRAKSPIAKS PPFREVFNR
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 XVHDFDVLDF DVHPLILIAA FPAVGGGALP VR*

```

m510/a510 97.0% identity in 132 aa overlap

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSA	FWQALSISAILRAKSPIAKS	PPFREVFNRSWTTLSAAIMT			
a510	MPSRTPQGKRGYSCAKRDSA	FWQALSISAILRAKSPIAKS	PPFREVFNRSWTTLSAAIMT			
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLS	IPTACNSVSFSSAGVLT	VS	SRGVXDFXVDLFDVHPLILIAA		
a510	IFSLSATRPPSRMASALPLS	IPTACNSVSFSSAGVLT	VS	SRXVHDFDVLFDVHPLILIAA		
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
a510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1405>:

g512.seq

```

1  atgaaagtgc ttgttttagg tgcgggtgtt gccggcgat cctccgtgtg

```

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```

51  gtatctggca gaggccggac atgaagtaac ggtcatcgac cgcaccgagg
101  gtgtggcgat ggaaaccagt tttgccaatg caggccagct ttcttacggc
151  tataccacgc cttgggcgc acccggtatt ccgaccaaag cactgaaacg
201  gctgtttaaag agccatccgc ctttactgtt ccgccctgac ggcggcctgt
251  atcaaatcga atggtctgtg cggtatgctgc aaaactgcac ggcaacgcgc
301  tatcaaatca ataaagagcg catggtcagg atttccgaat acagccgtga
351  aatgttccgc cgttttgaag cgcaaaccga catgaatttt gagggacgca
401  aaaaaggac gttgcagatt ttccgccaaa ccgaagaagt cgaagcggca
451  aaacaagaca ttgccgtttt ggaacgctac ggcggtgccg accgccgtct
501  gaagcccgaa gaatgcgcag aattcgagcc tgcgtggca cgcgttaccg
551  ccaaaattgt cggcggtctg cacctgcctg cggatgcgac cggcgactgc
601  cgcctcttca ccgaaaacct gtacaaattg tgtcaagaga agggggtacg
651  gttctacttc aaccaaacca tcagccgcat cgaccacaac gggtgcgca
701  tcaaagccgt tgaacgaaa caggcggtt tgaacagat gccgttgtct
751  gcgcgctcgg ctgcttcagc aggactgtgt tggcgagtt ggatctcaat
801  ctgcccattt atcccgtaa aggtattcc ttga

```

This corresponds to the amino acid sequence <SEQ ID 1406; ORF 512.ng>:

g512.pep

```

1  MKVLVLGAGV AGVSSVWYLA EAGHEVTVID RTEGVAMETS FANAGQLSYG
51  YTPWAAPGI PTKALKRLFK SHPPLLFRPD GGLYQIEWLW RMLQNCTATR
101  YQINKERMVR ISEYSREMFR RFEAQDTDMNF EGRKKGTLLQI FRQTEEEVAAA
151  KQDIAVLERY GVPYRRLKPE ECAEFEPALA RVTAKIVGGL HLPADATGDC
201  RLFTENLYKL CQEKGVRFYF NQTISRIDHN GLRIKAVETK QGGLKQMPLS
251  ARSAASAGLC WRSWISICPF IPSKAIP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1407>:

m512.seq (partial)

```

1  ..GTTTGGAAAC GCTACGGCGT GCCGTACCGC CGTCTGAAAC CCGAAGAATG
51  TGCAGAAATT GAGCCTGCGC TGGCACGCGT TACCGCCAAA ATTGCCGGCG
101  GCCTGCACCT GCCTGCAGAT GCGACCGCG ACTggCGCCT CTTCACTGAA
151  AACCTATACA AATTGTGTCA GGAAAAGGGC GTACGGTTTC ATTTCAACCA
201  AAACATCAGC CGCATCGACC ACAACGGGCT GCGCATCAAA ACCGTTGAAA
251  CCAAACAGGG CGGTTTGAAG CAGATGCCGT TGTCTGCGCG CTCGGTTGCT
301  TCAGCAGGAC GGTTTTGGCG CAGTTGGATC TCAATCTGCC CATTATCCC
351  GTCAAAGGCT ATTCCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1408; ORF 512>:

m512.pep (partial)

```

1  ..VLERYGVYR RLKPEECAEF EPALARVTAK IAGGLHLPAD ATGDWRLFTE
51  NLYKLCQKEG VRFHFQNQIS RIDHNGRLIK TVETKQGLK QMPLSARVA
101  SAGRFWRWI SICPFIPSKA IP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 512 shows 93.4% identity over a 122 aa overlap with a predicted ORF (ORF 512.ng) from *N. gonorrhoeae*:

m512/g512

m512.pep				10	20	30
				VLERYGVYRRLKPEECAEFEPALARVTAK		
g512						
	130	140	150	160	170	180
m512.pep	40	50	60	70	80	90
	IAGGLHLPADATGDWRLFTENLYKLCQEKGVRFHFQNQISRIDHNGRLIKTVETKQGLK					
g512	: : : : : : : : : :					
	190	200	210	220	230	240
m512.pep	100	110	120			
	QMPLSARSVASAGRFWRWISICPFIPSKAIP					
g512	:			QMPLSARSAASAGLCWRSWISICPFIPSKAIP		

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250 260 270

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1409>:

```
a512.seq
1  ATGAAAGTGC TTGTTTTAGG TGCTGGTGT GCCGGCGTAT CTTCCGCGTG
51  GTATCTGGCA GAGGCAGGAC ATGAAGTAAC GGTCATCGAC CGCGCCGAGG
101 GCGTGGCGAT GGAAACCACT TTTGCCAACG CAGGCCAGCT TTCTTACGGC
151 TATACCACGC CTTGGGCTGC ACCCGGTATT CCGACCAAAG CACTGAAATG
201 GCTGTTTAAA AGCCATCCGC CTTTGCTGTT TCGCCCCGAC GGCAGCCTGT
251 ATCAAATCGA ATGGCTGTGG CAGATGCTGC AACACTGCAC GGCAGCGCGC
301 TATCAAATCA ATAAAGAGCG CATGGTCAGG ATGTCCGAAT ACAGCCGTGA
351 AATGTTCCGC CGTTTGAAG CGCAAACCGG CATGAATTTT GAGGGACGCA
401 AAAAAGGGAC GTTGCAGATT TTCCGCCAAA CCAAAGAAGT CGAAGCGGCA
451 AAACAAGACA TTGCCGTTTT GGAACGCTAC GGCGTGCCGT ACCGCCGTCT
501 GAAGCCCGAA GAATGCGCAG AATTGAGCC TGCCTGGCA CGCGTTACCG
551 CCAAATTCG CGGCGGCCTG CACCTGCCC GAGACGCGAC CGGCGACTGC
601 CGCTCTTCA CTGAAAACCT GTACAAATG TGTCAGGAAA AGGGCGTACG
651 GTTTCATTTC AACCAAACCA TCAGCCGCAT CGACCACAAC GGGCTGCGCA
701 TCAAAACCGT TGAAACGAAA CAGGGCGGTT TGAAGCAGAT GCCGTTGTCT
751 GCGCGCTCGG CTGCTTCAGC AGGACGGTTT TGGCGCAAGT GGATCTCAAT
801 CTGCCGATTT ATCCCGTCAA AGGCTATTCC TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1410; ORF 512.a>:

```
a512.pep
1  MKVLVLGAGV AGVSSAWYLA EAGHEVTVID RAEGVAMETS FANAGQLSYG
51  YTFPWAAPGI PTKALKWLFK SHPPLLFRPD GSLYQIEWLW QMLQHCTAAR
101 YQNKERMVR MSEYSREMER RFEAQTGMNF EGRKKGLQI FRQTKVEEAA
151 KQDIAVLERY GVPYRRLKPE ECAEFEPALA RVTAKIAGGL HLPADATGDC
201 RLFTENLYKL COEKGVRHFH NQTISRIDHN GLRIKTVETK QGGLKQMPLS
251 ARSAASAGRF WRKWISICRF IPSKAIP*
```

m512/a512 95.9% identity in 122 aa overlap

m512.pep					10	20	30
					VLERYGVPYRRLKPEECAEFEPALARVTAK		
a512	TGMNFEGRKKGLQIFRQTKVEEAAKQDIAVLERYGVPYRRLKPEECAEFEPALARVTAK						
	130	140	150	160	170	180	
m512.pep		40	50	60	70	80	90
		IAGGLHLPADATGDWRLFTENLYKLCQEKGVRFHFNQNISRIDHNLRIKTVETKQGGLK					
a512	IAGGLHLPADATGDCRLFTENLYKLCQEKGVRFHFNQISRIDHNLRIKTVETKQGGLK						
	190	200	210	220	230	240	
m512.pep		100	110	120			
		QMPLSARSVASAGRFWRWSWISICPFIPSKAIPX					
a512	QMPLSARSAASAGRFWRKWISICRFIPSKAIPX						
	250	260	270				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1411>:

```
g513.seq
1  ATGGGTTCCG CGCCGAACGC CGCCGCGGCC GCCGAAGTGA AACACCCTGT
51  TTCGCAAGGT ATGATTCAAA TGCTGGGCGT GTTGTGCGAT ACCATCATCG
101 TTGTTCTTGG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
151 GATTTGAGCG GTGCGGCGCT GACGcAGGCG GCGATTGTCA GCCAAGTGGG
201 GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCITTT
251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
301 AAAAGCCATT GGCTGATTAC CGCCGTTTTT CGTATGCTGG TTTGGCGGTG
351 GGTCTATTTT GGC CGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
401 ATATGGCGAT GGGCATCATG GCGTGATCA ACCTCGTCGC CATCCTGCTG
451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
```

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501 AATGGGCAAA GACCCCGAGT TCAAACCTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1412; ORF 513.ng>:

g513.pep

1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
 51 DLGGAALTQA AIVSQVGQWG AGFLAVILEM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLKMKG DPEFKLSEHP GLKRRIKSDV W*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1413>:

m513.seq

1 ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCCTGT
 51 TTCGAAGGT ATGATTCAAA TGCTGGGCGT GTTTGTCGAT ACCATCATCG
 101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
 151 GATTTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
 201 GCAATGGGGC GCGGCTTTC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT
 251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
 301 AAAAGCCATT GGCTGATTAC CGCCGTTTTT CGTATGCTGG TTTTGGCGTG
 351 GGTCTATTTT GGCGCGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
 401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCCTGCTG
 451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
 501 AATGGGCAAA GACCCCGAGT TCAAACCTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1414; ORF 513>:

m513.pep

1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
 51 DLGGAALTQA AIVSQVGQWG AGFLAVILEM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLKMKG DPEFKLSEHP GLKRRIKSDV W*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 513 shows 99.5% identity over a 191 aa overlap with a predicted ORF (ORF 513.ng) from *N. gonorrhoeae*:

m513/g513

m513.pep	10	20	30	40	50	60
	MGSAPNAAAAAEVKHPVSQGMQMLGVFVDTIIVCSCTAFIILIYQQPYGDLGGAALTQA					
g513						
	10	20	30	40	50	60
	MGSAPNAAAAAEVKHPVSQGMQMLGVFVDTIIVCSCTAFIILIYQQPYGDLGGAALTQA					
	10	20	30	40	50	60
m513.pep	70	80	90	100	110	120
	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
g513						
	70	80	90	100	110	120
	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
	70	80	90	100	110	120
m513.pep	130	140	150	160	170	180
	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMXLRDYTAKLKMKGKDPEFKLSEHP					
g513						
	130	140	150	160	170	180
	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHP					
	130	140	150	160	170	180
m513.pep	190					
	GLKRRIKSDVW					
g513						
	GLKRRIKSDVW					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1415>:

a513.seq

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```
1 ATGAACGAGA ACCTTACCGA ATGGCTGCAC GGCTGGGTCG GCGCCATCAA
51 CGATCCGATG TGGTCATACT TGGTTTATNT GCTTTTGGGT ACGGGGCTTT
101 TCTTCACCGT AACCAACGGGC TTTGTCCAAT TCCGCCTGTT CGGGCGCAGC
151 ATCAAAGAAA TGCTCGGGCG CCGCAAACAG GGGGACGACC CTCACGGCAT
201 CACGCCGTTT CAGGCATTTG TAACCGGCCT TGCCAGCCGC ETGGGCGTGG
251 GCAATATCGC GGGCGTGGCC ATCGCCATCA AAGTCGGCGG ACCGGGCGCG
301 GTGTTTGGGA TGTGGGTAAC CGCCTTAATC GGTATGAGTT CGGCGTTTGT
351 CGAATCTTCG CTGGCGCAGC TCTTTAAAGT CCGCGACTAC GACAACCACC
401 ATTTCCGGGG CGGCCCTGCC TACTACATCA CTCAAGGCT GGGCAGAAA
451 TGGCTGGGCG TGTTGTTTCG CCTGAGCCTG ATTTTCTGTT TCGGCTTTGT
501 GTTTGAAGCG GTTCAGACCA ATACCATTGC CGATACCGTC AAAGCGGCGT
551 GGGGTGTTGA GCCTCATTAT GTCGGCGTCG CCCTGGTGAT TTTAACCCTG
601 CGATATATCT TCGGCGGCAT CAGGCGCATA TCTAAAGCGG CGGAAATCGT
651 CGTCCCCCTG ATGGCGGTTT TGTACCTCTT TATCGCGCTT TTCATCATTT
701 TGACCAATAT TCCGATGATT CCGGACGTGT TCGGTCAGAT TTTTTCGGGC
751 GCGTTCAAAT TCGACGCGGC AGCAGGCGGC TTAACGCGG GTCTGATTTC
801 GCAAACGATG ATGATGGGCA TCAAACGCGG CCTGTATTCC AACGAGGCGG
851 GTATGGGTTT CGCGCCGAAC GCCGCCGCCG CCGCCGAAGT GAAACACCCT
901 GTTTCCCAAG GTATGATTCA AATGCTGGGC CTGTTTGTCT ATACCATCAT
951 CGTTTGTCTT TGCACCGCCT TCATCATCTT GATTTACCAA CAGCCTTACG
1001 GCGATTTGAG CGGTGCGGCG CTGACGCAGG CGGCGATTGT CAGCCAAGTG
1051 GGGCAATGGG GCGCGGGCTT CCTCGCGTC ATCCTGTTTA TGTTTGCCTT
1101 TTCCACCGTT ATCGGCAACT ATGCCTATGC CGAGTCCAAC GTCCAATTCA
1151 TCAAAGCCA TTGGCTGATT ACCGCCGTTT TCCGTATGCT GGTTTTGGCG
1201 TGGGTCTATT TCGGCGCGGT TGCCAATGTG CCTTTGGTCT GGGATATGGC
1251 GGATATGGCG ATGGGCATTA TGGCGTGGAT CAACCTTGTG GCCATCTGCG
1301 TGCTCTCGCC CTTGGCGTTT AIGCTGCTGC GCGATTACAC CGCCAAGCTG
1351 AAAATGGGCA AAGACCCCGA GTTCAAACCT TCCGAACATC CGGGCTGAA
1401 ACGCGGTATC AAATCCGACG TTTGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1416; ORF 513.a>:

a513.pep

```
1 MNENFTEWLH GWVGAINDPM WSYLVYXLLG TGLEFTVTTG FVQFRLFGRS
51 IKEMLGGRKQ GDDPHGI*PF QAFVTGLASR VGVGNIAGVA IAIKVGPGPA
101 VFWMWVTALI GMSSAFVESS LAQLFKVRDY DNHHFRGGPA YYITQGLGQK
151 WLGVLFALSL IFCFGVFEEA VQNTIADTV KAAWGWEPHY VGVALVILTA
201 PIIFGGIRRI SKAAEIVVPL MAVLYLFIAL FIILTNIIPMI PDVFGQIFSG
251 AFKFDAAAGG LLGLISQTM MMGIKRLYS NEAGMGSAPN AAAAAEVKHP
301 VSQGMIOMLG VFVDIIIVCS CTAFIILIYQ OPYGDLGAA LTQAAIVSQV
351 GQWGAGFLAV ILFMFAFSTV IGNYAYAESN VQFIKSHWLI TAVFRMLVLA
401 WVYFGAVANV PLVWDMADMA MGIMAWINLV AILLLSPLAF MLLRDYTAKL
451 KMGKDPEFKL SEHPGLKRRRI KSDVW*
```

m513/a513 100.0% identity in 191 aa overlap

```
10 20 30
m513.pep MGSAPNAAAAAEVKHPVSQGMIOMLGVFVD
|||||
a513 DAAAGLLGLISQTM MMGIKRLYSNEAGMGSAPNAAAAAEVKHPVSQGMIOMLGVFVD
260 270 280 290 300 310

40 50 60 70 80 90
m513.pep TIIIVCSCTAFIILIYQQPYGDLGSAALTQAAIVSQVGWAGFLAVILFMFAFSTVIGNY
|||||
a513 TIIIVCSCTAFIILIYQQPYGDLGSAALTQAAIVSQVGWAGFLAVILFMFAFSTVIGNY
320 330 340 350 360 370

100 110 120 130 140 150
m513.pep AYAESNVQFIKSHWLI TAVFRMLVLAVVYFGAVANV PLVWDMADMA MGIMAWINLVAILL
|||||
a513 AYAESNVQFIKSHWLI TAVFRMLVLAVVYFGAVANV PLVWDMADMA MGIMAWINLVAILL
380 390 400 410 420 430

160 170 180 190
m513.pep LSPLAFMLLRDYTAKL KMGKDPEFKL SEHPGLKRRRI KSDVWX
|||||
```

766

a513 LSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVWX
440 450 460 470

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1417>:

g515.seq
1 atggttcaaa tacaggttgt gcgcgcgcgc gccgttgccc gtggtctgca
51 ttccgagttt gcgcgcgcgc taactgccga ggaaatagcc ttcgacaatg
101 ccgttttgaa tcacgaagcg cggcgcgcgc gcaacacctt ccgcatcaaa
151 atagctgctg cggaagagcg ggggatgtg cggttcttcg cgcaggttga
201 ggaaatcggg caggactttt ttgccgatgc tgcgatcag gaaactgctt
251 tggcggtaga gcgcgcgcgc ggagagtgtg ccgacgaggt gtccgatcag
301 cccgcccgaa acggtggtat cgaagaggac ggggtagctg cctgtcggga
351 tgctgcggct gccgagtcgg cgcaaagtgc ggcgggcgcg cgtttgaccg
401 atgggttcgg ggcgtgccat atccgcatgg cggcaggcgg aatcgtacca
451 gtagtcgcgc tgcattccgt ttctgtcggc ggcgacgacg ctgcaggaaa
501 tgctgtggtg cgtgctttgc cgggtgtcgg caaaaccgtg ggtgttgccg
551 taaacgtatt ggtactgtcc ggtttgcacc gccgcgcctt cggagttttc
601 gatgcggctg tccgtgtcca acgctgcctg ttccgattgt tttgccaaagc
651 cgacggcggc ttccgtatcc aaatccatt cgtggttaaag gtcggggtcg
701 ccgatgtgtt gcgccatcaa ctccgggtcg gcaagtcggc cgcaaccgtc
751 ttcggcggcg tggcgggcga tgcgcgcgcg ggcgcggacg gtgtcgcgca
801 gggcttgctt ggagaagtcg gcggtgcccg ccgcgccttt gcgtttgccg
851 acgtaaacgg taatgtccag cgatttgtcc tgcgtggaact cgatttgttc
901 gatttcgccc aagcgcacgc tgacgctttg tccgagcgat tcgctgaagt
951 cggcttcggc ggcggtcgcg cccgctgctt ttgccaagtc gagcgtgcgg
1001 cggcagaggt cgaggagttc ggaagcggcg tgggtgaaca gcataacaat
1051 ctttcttggt ggagcgttgt ggcattttaa

This corresponds to the amino acid sequence <SEQ ID 1418; ORF 515.ng>:

g515.pep
1 MVQIQVVRAA GVARGLHSEF ARAVTAEIEA FDNVLNHEA RRGNTFRIK
51 IAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADEVSDQ
101 PARNGGIEED GVAACRDAAG AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSVFFVG GDDAAGNAV V RALPVCCKTV GVAVNVLVLS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVKSGATV
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFVLELDLF
301 DFAQAHADAL SERFAEVGFG GGRARCFCQV ERAAAVEVEF GSGVVEQHNN
351 LSWSVVAF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1419>:

m515.seq (partial)
1 ..GGAAAGAGCG GGGGATGTGC GTTCTTCGCG CAGGTTGAGG AAATCGGGCA
51 GGACTTTTCT GCCGATGCTG TCGATCAGGA AACTGCTTTG GCGGTAGAGC
101 GCGCCGCCCG AGAGTGCGCC GACGAGGTGT CCGATAAGAC CGCCCGAAAC
151 GGTGGTATCG AAGAGGACCG GGTAGCTGCC TGTCCGGATG CTGCGGCTGC
201 CGAGTCGGCG CAAAGTGCGG CCGGCGGCGG TTTGACCGAT GGTTCGGGG
251 CTGTCCATAT CCGGATGGCG GCAGGCGGAA TCGTACCAGT AGTCGCGCTG
301 CATGCCGTTT TCGTCGGCGG CAACGACGCT GCAGGAAATG CTGTGGTGCG
351 TGCCTTGCCG GTGTGCGGCA AAACCGTGGG TGTGCCGTA AACGTATTGG
401 TAATGGCCCG TTGACCCGCG CGCGCCTTCG GAGTTTTCGA TCGCTCATC
451 CTCGTTGAGG GCGGCTTGTT CGCATTGTTT TGCCAAGCCG ACGGCGGCTK
501 CCGTATCCAA ATCCCATTCG TGGTAAAGGT CCGGGTCGCC GATGTGTTTT
551 GCCATCAGAC AGGCATCGGC AAGTCCGGCG CAACCGTCTT CCGCGGTGTG
601 GCGGCGGATG TCGATGGCGG CTTGACGGT GTCTTGCAAG GCTTTTTCGG
651 AGAAGTCGCG AGTACTGGCG CGGCCTTTCG GTTTGCCGAC GTAAACGGTA
701 ATGTCCAGCG ACTTGTCTTG CTGGAACGCG ATTTGTTsGA TTTsGCCCAG
751 CCGCACGCTG ACGCTTTGTC CCAATGATTC GCTGAAATCG GCTTCGGCGG
801 CGGTTGCGCC CGTCGCTTTT GCCAAGTCGA CGGTGCGGCG GCAGAGGTGCG
851 AGGAGTTCGG AAGCGGTGTG GTTgAACAGC ATAGAAATCT TTCTTGATGA
901 TGCTTTGCGG CATTTTAA

This corresponds to the amino acid sequence <SEQ ID 1420; ORF 515>:

m515.pep (partial)

767

```

1  ..GKSGGCAFFA QVEEIGQDFS ADAVDQETAL AVERAAGECA DEVSDKTARN
51  GGIEEDGVAA CRDAAAESA QSAAGGGLTD GFGAVHIRMA AGGIVPVVAL
101 HAVFVGGNDA AGNAVVRALP VCGKTVGVAV NVLVMAGLHR RAFGVFDALI
151 LVQGGFLFALF CQADGGXRIQ IPFVVKVGVA DVFCHQTGIG KSGATVFGGV
201 AGDVGDFGDLG VLQGFGEVGT STGAFAFAD VNGNVQRLVL LELDLXDXAQ
251 PHADALSQXF AEIGFGGGCA RRFCOVERAA AEVEEFGSGV VEQHRNLSXX
301 CFAAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 515 shows 85.9% identity over a 304 aa overlap with a predicted ORF (ORF 515.ng) from *N. gonorrhoeae*:

m515/g515

```

m515.pep          10      20      30
                  GKSGGCAFFAQVEEIGQDFSADAVDQETALA
g515              30      40      50      60      70      80
AEEIAFDNAVLNHEARRGGNTFRIKIAAAERAGDVRFFAQVEEIGQDFFADAVDQETALA

m515.pep          40      50      60      70      80      90
VERAAGECADEVSDKTARNGGIEEDGVAAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
g515              90     100     110     120     130     140
VERAAGECADEVSDQPARNGGIEEDGVAAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA

m515.pep          100     110     120     130     140     150
GGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTVGVAVNVLMAGLHRRRAFGVFDALIL
g515              150     160     170     180     190     200
GGIVPVVALHSVFVGGDDAAGNAVVRALPVCCKTVGVAVNVLSGLHRRRAFGVFDAAVR

m515.pep          160     170     180     190     200     210
VOGGLFALFCQADGGXRIQIPFVVKVGADVDFCHQTGIGKSGATVFGGVAGDVGDFG
g515              210     220     230     240     250     260
VQRCLFALFCQADGGFRIQIPFVVKVGADVLRHLGVGKSGATVFGGVAGDVGGGADGV

m515.pep          220     230     240     250     260     270
LQGFGEVGVSTGAFAFADVNGNVQRLVLELDLXDXAQPHADALSQXFAEIGFGGGCR
g515              270     280     290     300     310     320
AQGLFGEVGGAGAAFAFADVNGNVQRFVLELDLDFDAQAHADALSERFAEVFGGGRAR

m515.pep          280     290     300
RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAF
g515              330     340     350
CFCQVERAAAEVEEFGSGVVEQHNNLSWWSVVAF

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1421>:

a515.seq

```

1  ATGGTTCAAA TAAAGGTGTT GCGCGCCGCC GCGTTGCCCC GTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GGAATAGCC TTCGACAATG
101 CCGTTTGTAA TCACGAAGCG CGGTGCGGTG GCAACGCTT CCGCATCAAA
151 ATAGCTGCTG CCGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTGCG CCGACGAGGT GTCCGATAAG
301 ACCGCCCCGA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTCCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGGCGGC GGTTCGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCAATGCCG TTTCTGTCGG GCGAACGACG CTCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAACCGTA GGTGTTGCCG

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551 TAAACGTATT GGTAATGGCC GGTTCGCACC GCCGCGCCTT CGGAGTTTTC
601 CATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCTGATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGCGCGTG TGGCGGGCGA TGTCNNNNGC GCGCGGACG GTGTCGCGCA
801 GGGCTTGTTT GGAGAAATCG GCGGTGCCGG CGCGGCCTTT GCGTTGCGG
851 ACGTAAACGG TAATGTCCAG CCACTGTGCC TGCTGAAACT CGATTGTGTC
901 GATTTGCGCC AGCCGCACGC TGACGCTTTG TCCCAATGAT TCGCTGAAAT
951 CGGCTTCGGC GCGGTTGCG CCCGTCGCTT TTGCCAAGTC GAGCGTGCGG
1001 CGGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGGTTGAACA GCATAGAAAT
1051 CTTTCTTGAT GATGCTTTCG GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1422; ORF 515.a>:

```

a515.pep
1  MVQIKVVRAA  GVARGLHSEF  ARAVTAEEIA  FDNAVLNHEA  RCGGNAFRIK
51  IAAAERAGDV  RFFAQVEEIG  QDFFADAVDQ  ETALAVERSA  GECADSVSDK
101  TARNGGIEED  GVVACRDAAA  AESAQAAGG  GLTDGFGAVH  IRMAAGGIVP
151  VVALHAVFVG  GNDAGNAVAV  RALPVCCKTV  GVAVNVLMVA  GLHRRAFGVF
201  DALILVQGG  FALFCQADGG  FRIQIPFVVK  VGVADVLRHQ  LGVGKSGATV
251  FGGVAGDVXX  GADGVAQGLF  GEIGGAGAAF  AFADVNGNVQ  RLVLKLDLF
301  DFAQPHADAL  SQ*FAEIGFG  GGCARRFCQV  ERAAAEVEEF  GSGVVEQHRN
351  LS**CFAAF*

```

m515/a515 92.1% identity in 304 aa overlap

```

m515.pep                                10      20      30
                                GKSGGCAFFAQVEEIGQDFSADAVDQETALA
                                ::|  |||||  |||||  |||||  |||||
a515      AEEIAFDNAVLNHEARCGGNAFRIKIAAAERAGDVRFQVEEIGQDFFADAVDQETALA
              30      40      50      60      70      80

m515.pep              40      50      60      70      80      90
VERAAGECADEVSDKTARNGGIEEDGVAAACRDAAAESAQAAGGGLTDGFGAVHIRMAA
||:|||||  |||||  |||||  |||||  |||||  |||||
a515      VERSAGECADEVSDKTARNGGIEEDGVVACRDAAAESAQAAGGGLTDGFGAVHIRMAA
              90      100     110     120     130     140

m515.pep              100     110     120     130     140     150
GGIVPVVALHAVFVGNDAGNAVVRALPVCCKTVGVAVNVLMAGLHRRAFGVFDALIL
|||||  |||||  |||||  |||||  |||||  |||||
a515      GGIVPVVALHAVFVGNDAGNAVVRALPVCCKTVGVAVNVLMAGLHRRAFGVFDALIL
              150     160     170     180     190     200

m515.pep              160     170     180     190     200     210
VQGGFLFALFCQADGGXRIQIPFVVKVGADVLFCHQTGIGKSGATVFGGVAGDVGGFDGV
|||||  |||||  |||||  |||||  |||||  |||||
a515      VQGGFLFALFCQADGGFRIQIPFVVKVGADVLRHQLGVGKSGATVFGGVAGDVXXGADGV
              210     220     230     240     250     260

m515.pep              220     230     240     250     260     270
LQGGFFGEVGSTGAFAFADVNGNVQRLVLELDLXDQAQPHADALSQXFAEIGFGGGCAR
||:||||  |||||  |||||  |||||  |||||  |||||
a515      AQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLFDFAQPHADALSQXFAEIGFGGGCAR
              270     280     290     300     310     320

m515.pep              280     290     300
RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX
|||||  |||||  |||||
a515      RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX
              330     340     350     360

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1423>:

```

g515-1.seq
1  ATGTTTCAAA  TACAGTTTGT  GCGCGCCGCC  GCGGTTGCCC  GTGGTCTGCA

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51  TTCCGAGTTT GCGCGCGCTG TAACTGCCGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGCGCGGTG GCAACACCTT CCGCATCAAA
151 ATAGCTGCTG CCGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCGGCC GGAGAGTGTG CCGACGAGGT GTCCGATCAG
301 CCCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTGCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGCGGCG GGTTCGACCG
401 ATGTTTTCGG GGCTGTCCAT ATCCGATGCG CCGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATTCCGT TTTCGTGCGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTG GGTGTGCGCG
551 TAAACGTATT GGTAGTGTCC GGTTCGACC GCCGCGCCTT CGGAGTTTTT
601 GATGCGGCTG TCCGTGTCCA ACGCTGCCTG TTCGATTGT TTTGCCAAGC
651 CGACGGCGCG TTCCGTATCC AAATCCCAT CTGTTGTAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTGCGCGGTG TGGCGGGCGA TGTGCGGCGC GCGCGGACG GTGTGCGCGA
801 GGGCTTTGTT GGAGAAGTCG GCGGTGCGCG CCGCGCCTT CGGTTGCGCG
851 ACGTAAACGG TAATGTCCAG CGATTGTGCC TGCTGGAACG CGATTGTGTT
901 GATTTGCGCC AAGCGCACGC TGACGCTTTG TCCGAGCGAT TCGCTGAAAT
951 CGGCTTGGCG GCGGGTCGCG CCCGCTGCTT TTGCCAAGTC GAGCGTGCAG
1001 CCGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGGTTGAACA GCATAACAAT
1051 CTTCTTGGT GGAGCGTGT GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1424; ORF 515-1.ng>:

g515-1.pep

```

1  MVQIQVVRAA GVARGLHSEF ARAVTAEEIA FDNVLNHEA RRGNTFRK
51  IAAERAGDV RFFAQVEEIG QDFFAVDQ ETALAVERAA GECADSVSDQ
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIYP
151 VVALHSEFVG GNDAAAGNAV RALPVCCKTV GVAVNLVVS GLHRRAFGVF
201 DAAVRVORCL FALFCQADGG FRIQIPFVK VGVADVLRH LGVKGSGATV
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAA AFADVNGNVQ RVLLELDLF
301 DFAQAHADAL SERFAEVGFG GGRARCFCQV ERAAAEVEEF GSGVVEQHNN
351 LSWNSVVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1425>:

m515-1.seq

```

1  ATGGTTCAAA TACAGGTTGT GCGCGCGGCC GCGGTTGCCC GTGGTCTGCA
51  TACCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCTT CCGCATCAAA
151 ATAGCTGCTG CCGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCGGCC GGAGAGTGTG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTGCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGCGGCG GGTTCGACCG
401 ATGTTTTCGG GGCTGTCCAT ATCCGATGCG CCGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTGCGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTG GGTGTGCGCG
551 TAAACGTATT GGTAAATGGCC GGTTCGACC GCCGCGCCTT CGGAGTTTTT
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGATTGT TTTGCCAAGC
651 CGACGGCGCG TTCCGTATCC AAATCCCAT CTGTTGTAAG GTCGGGGTCG
701 CCGATGTGTT TTGCCATCAG ACAGGCATCG GCAAGTCCGG CGCAACCGTC
751 TTGCGCGGTG TGGCGGGCGA TGTGATGGC GGCTTTGACG GTGCTTGCA
801 GCGCTTTTTC GGAGAAGTCG CCACTACTGG CGCGGCTTT CGGTTGCGCG
851 ACGTAAACGG TAATGTCCAG CGACTGTGCC TGCTGGAACG CGATTGTGTT
901 GATTTGCGCC AGCCGCACGC TGACGCTTTG TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1426; ORF 515-1>:

m515-1.pep

```

1  MVQIQVVRAA GVARGLHTEF ARAVTAEEIA FDNVLNHEA RCGGNAFRK
51  IAAERAGDV RFFAQVEEIG QDFFAVDQ ETALAVERAA GECADSVSDK
101 TARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIYP
151 VVALHSEFVG GNDAAAGNAV RALPVCCKTV GVAVNLVMA GLHRRAFGVF
201 DALILVQGLL FALFCQADGG FRIQIPFVK VGVADVFCQG TGIGKSGATV
251 FGGVAGDVGG GFDGVLQGF GEVGTGAAG AFADVNGNVQ RVLLELDLF
301 DFAQPHADAL SQ*

```

m515-1/g515-1 91.7% identity in 312 aa overlap

	10	20	30	40	50	60
g515-1.pep	MVQIQVVRAAGVARGLHSEFARAVTAEEIAFDNVLNHEARRGGNTFRIKIAAAERAGDV					
m515-1	MVQIQVVRAAGVARGLHTEFARAVTAEEIAFDNVLNHEARRCGGNAFRIKIAAAERAGDV					

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	70	80	90	100	110	120
g515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDQPARNGGIEEDGVAACRDAAA					
m515-1	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA					
	70	80	90	100	110	120
g515-1.pep	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHSVFVGGNDAAGNAVVRALPVCCKTV					
m515-1	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAFVGGNDAAGNAVVRALPVCCKTV					
	130	140	150	160	170	180
g515-1.pep	GVAVNVLVVSGLHRRAFGVFDAAVRVORCLFALFCQADGGFRIQIPFVVKVGVADVLRHQ					
m515-1	GVAVNVLMAGLHRRAFGVFDALILVQGGFLALFCQADGGFRIQIPFVVKVGVADVLFCHQ					
	190	200	210	220	230	240
g515-1.pep	LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEVGGAGAAFAFADVNGNVORFVLELDLF					
m515-1	TGIGKSGATVFGGVAGDVGGGADGVLQGFGEVGGAGAAFAFADVNGNVORFVLELDLF					
	250	260	270	280	290	300
g515-1.pep	DFAQAHADALSERFAEVFGGGRARCFCQVERAAAEVEEFGSGVVEQHNNLSWWSVVAFX					
m515-1	DFAQPHADALSQX					
	310	320	330	340	350	360

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1427>:

a515-1.seq

```

1  ATGGTTCAAA TAAAGGTTGT GCGCGCCGCC GCGCTTGCCC GTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTGTAA TCACGAAGCG CGGTGCGGTG GCAACGCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CCGTCTTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTCCG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCCG CGCAAAGTGC GCGCGGCGCG GGTTTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGATGCG GCGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTCGCC GCGAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CCGTGTGCGG CAAACCCGTA GGTGTGCGCG
551 TAAACGTATT GGTAATGGCC GGTTCGACC GCCGCGCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCAATTG TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCAT CGTGTAAG GTCCGGGTGC
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGCGGGGCGA TGTGCGCGC GCGCGGACG GTGTGCGCGA
801 GGGCTTGTTC GGAGAAATCG GCGGTGCGG CCGCGCCTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTGTGCC TGCTGAACT CGATTGTGTC
901 GATTTGCGCC AGCCGCACGC TGACGCTTG TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1428; ORF 515-1.a>:

a515-1.pep

```

1  MVQIKVVRAA GVARGLHSEF ARAVTAEIEA FDNVNLNHEA RCGGNAFRIK
51  IAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERSA GECADDEVSDK
101 TARNGGIEED GVVACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHAFVVG GNDAAAGNAV RALPVCCKTV GVAVNVLVMA GLHRRAFGVF
201 DALILVQGGI FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEIGGAGAAF AFADVNGNVQ RLVLKLDLF
301 DFAQPHADAL SQ*

```

m515-1/a515-1 94.9% identity in 312 aa overlap

	10	20	30	40	50	60
a515-1.pep	MVQIKVVRAAGVARGLHSEFARAVTAEIEAFDNVNLNHEARCGGNAFRIKIAAERAGDV					
m515-1	MVQIQVVRAAGVARGLHTEFARAVTAEIEAFDNVNLNHEARCGGNAFRIKIAAERAGDV					
	10	20	30	40	50	60
a515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERSAGECADEVSDKTARNGGIEEDGVVACRDAAA					

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m515-1	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA
	70 80 90 100 110 120
a515-1.pep	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
m515-1	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
	130 140 150 160 170 180
a515-1.pep	GVAVNVLMAGLHRRAFGVFDALILVQGGFLALFCQADGGFRIQIPFVVKVGVADVLRHQ
m515-1	GVAVNVLMAGLHRRAFGVFDALILVQGGFLALFCQADGGFRIQIPFVVKVGVADVLRHQ
	190 200 210 220 230 240
a515-1.pep	LGVGKSGATVFGGVAGDVGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKDLF
m515-1	TGIGKSGATVFGGVAGDVGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKDLF
	250 260 270 280 290 300
a515-1.pep	DFAQPHADALSQX
m515-1	DFAQPHADALSQX
	310

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1429>:

g516.seq

```

1  atgttggttcc gtaaaacgac cgccgccgtt ttggcggcaa ccttgatact
51  gaacggctgt acgatgatgt tgcgggggat gaacaacccg gtcagccaaa
101 caatcacccg caaacacgtt gacaaagacc aaatccgcgc cttcgggtgtg
151 gttgccgaag acaatgccca attggaaaag ggcagcctgg tgatgatggg
201 cgggaaatac tggttcgccg tcaatcccca agattcggcg aagctgacgg
251 gccttttgaa ggcggggttg gacaagccct tccaaatagt tgaggatacc
301 ccgagctatg ccgcccacca agccctgccg gtcaaattcg aagcgcccg
351 cagccagaat ttcagtaccg gaggtctttg cctgcgctat gataccggca
401 gacctgacga catcgccaag ctgaaacagc ttgagtttaa agcggtcaaa
451 ctcgacaatc ggaccattta cagcgctgct gtatccgccg aaggcaataa
501 ctacgccacg ccgcaaaaac tgaacgccga ttatcatttt gagcaaatgt
551 tgcccgcgca tatttattat acggttactg aaaaacatac cgacaaatcc
601 aagctggttg gaaatatctt atatacgccc cccttggtga tattggatgc
651 ggcggccgcg gtgctggtct tgcctatggc tctgattgca gccgcgaatt
701 cctcagacaa atga

```

This corresponds to the amino acid sequence <SEQ ID 1430; ORF 516.ng>:

g516.pep

```

1  MLFRKTTAAV LAATLILNGC TMMLRGMNPN VSQTITRKHV DKDQIRAFGV
51  VAEDNAQLEK GSLVMMGGKY WFAVNPEDSA KLTGLLKAGL DKPFQIVEDT
101 PSYARHQALP VKFEAPGSQN FSTGGLCLRY DTGRPDIAK LKQLEFKAVK
151 LDNRTIYTRC VSAKGYYAT PQLNADYHF EQSVPADIYY TVTEKHTDKS
201 KLFGNILYTP PLLILDAAA VLVLPALIA AANSSDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1431>:

m516.seq

```

1  ATGTTGTTCC GTAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGCT
51  GAACGGCTGT ACGTTGATGT TGTGGGAAT GAACAACCCG GTCAGCGAAA
101 CAATCACCCG CAAACACGTT GACAAAGACC AAATCCGC GCCTTCGGTGTG
151 GTTGCCGAAG ACAATGCCCA ATTGAAAAG GGCAGCCTGG TGATGATGGC
201 CGGAAAATAC TGGTTCGTCG TCAATCCCGA AGATTCGCGC AAGCTGACGG
251 GCATTTTGAA GGCAGGGCTG GACAAACCCT TCCAAATAGT TGAGGATACC
301 CCGAGCTATG CTCGCCACCA AGCCCTGCCG GTCAAACCTG AATCGCCTGG
351 CAGCCAGAAT TTCAGTACCG AAGGCCTTTG CCTGCGCTAC GATACCGACA
401 AGCCTGCCGA CATCGCCAAG CTGAAACAGC TCGGGTTTGA AGCGGTCAAA
451 CTCGACAATC GGACCATT TA CACGCGCTGC GTATCCGCCA AAGGCAAATA

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501 CTACGCCACA CCGCAAAAAC TGAACGCCGA TTACCATTTT GAGCAAAGTG
 551 TGCCTGCCGA TATTTATTAC ACGGTTACTG AAGAACATAC CGACAAATCC
 601 AAGCTGTTTG CAAATATCTT ATATACGCCC CCCTTTTGA TACTGGATGC
 651 GGCGGGCGCG GTACTGGCCT TGCCTGCGGC GGCTCTGGGT GCGTCTGTGC
 701 ATGCCGCCCG CAAATGA

This corresponds to the amino acid sequence <SEQ ID 1432; ORF 516>:

m516.pep
 1 MLFRKTTAAV LAATLMLNGC TLMLWGMNPN VSETITRKHV DKDQIRAFGV
 51 VAEDNAQLEK GSLVMMGGKY WVVNPEDSA KLTGILKAGL DKPFQIVEDT
 101 PSYARHQALP VKLESPGSON FSTGLCLRY DTDKPADIAK LKQLGFEAVK
 151 LDNRTIYTRC VSAKGKYYAT PQKLNADYHF EQSVPADIYY TVTEEHTDKS
 201 KLFANILYTP PFLILDAAGA VLALPAAALG AVVDAARK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 516 shows 90.0% identity over a 231 aa overlap with a predicted ORF (ORF 516.ng) from *N. gonorrhoeae*:

m516/g516

	10	20	30	40	50	60
m516.pep	MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDKDQIRAFGVVAEDNAQLEK					
g516	MLFRKTTAAVLAATLILNGCTMMLRGMNPNVSQTITRKHVDKDQIRAFGVVAEDNAQLEK					
	10	20	30	40	50	60
m516.pep	GSLVMMGGKYWVVNPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSON					
g516	GSLVMMGGKYWFAVNPEDSAKLTGLLKAGLDKPFQIVEDTPSYARHQALPVKFEAPGSON					
	70	80	90	100	110	120
m516.pep	FSTGLCLRYDTDKPADIAKLKQLGFEAVKLDNRTIYTRCVSAKGKYYATPQKLNADYHF					
g516	FSTGGLCLRYDTGRPDDIAKLKQLEFKA VKLDNRTIYTRCVSAKGKYYATPQKLNADYHF					
	130	140	150	160	170	180
m516.pep	EQSVPADIYYTVTEEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARK					
g516	EQSVPADIYYTVTEKHTDKSKLFGNIIYTPPLILDAAGAVLALPAAALGAVVDAARK					
	190	200	210	220	230	239
m516.pep	EQSVPADIYYTVTEEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARK					
g516	EQSVPADIYYTVTEKHTDKSKLFGNIIYTPPLILDAAGAVLALPAAALGAVVDAARK					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1433>:

a516.seq
 1 ATGTTGTTCC GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGTT
 51 GAACGGCTGT ACAGTAATGA TGTGGGGTAT GAACAGCCCG TTCAGCGAAA
 101 CGACCGCCCG CAAACACGTT GACAAGGACC AAATCCGCGC CTTCGGTGTG
 151 GTTGCCGAAG ACAATGCCCA ATTGGAAGG GGCAGCCTGG TGATGATGGG
 201 CGGGAAATAC TGGTTCGTCT TCAATCCTGA AGATTGCGCG AAGCTGACGG
 251 GCATTTTGAA GGCCGGGTTG GACAAGCAGT TTCAAATGGT TGAGCCCAAC
 301 CCGCGCTTTG CCTACCAAGC CCTGCGGTC AACTCGAAT CGCCCGCCAG
 351 CCAGAATTTC AGTACCGAAG GCCTTGCCT GCGCTACGAT ACCGACAGAC
 401 CTGCCGACAT CGCCAAGCTG AACAGCTTG AGTTTGAAAG GGTGGAATC
 451 GACAATCGGA CCATTTACAC GCGCTGCGTC TCCGCCAAG GCAAATACTA
 501 CGCCACACCG CAAAAACTGA ACGCCGATTA TCATTTGAG CAAAGTGTGC
 551 CTGCCGATAT TTATTACAG GTTACGAAA AACATACCGA CAAATCCAAG
 601 TTGTTTGAAA ATATTGCATA TACGCCACC ACGTTGATAC TGGATGCGGT
 651 GGGCGCGGTG CTGCCCTTGC CTGTCGCGGC GTTGATTGCA GCCACGAATT
 701 CCTCAGACAA ATGA

This corresponds to the amino acid sequence <SEQ ID 1434; ORF 516.a>:

a516.pep

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```

1  MLFRKTTAAV LAATLMLNGC TVMMWGMNSP FSETTARKHV DKDQIRAFGV
51  VAEDNAQLEK GSVLMMGGKY WVVNPEDSA KLTGILKAGL DKQFQMVPEPN
101 FRFAYQALPV KLESPASQNF STEGLCLRYD TDRPADIAKL KQLEFEAVEL
151 DNRTIYTRCV SAKGKYATP QKLNADYHFE QSVPADIIYYT VTKKHTDKSK
201 LFENIAYTPT TLILDAVGAV LALPVAALIA ATNSSDK*

```

m516/a516 86.1% identity in 238 aa overlap

	10	20	30	40	50	60
m516.pep	MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHV	DKDQIRAFGVVAEDNAQLEK				
a516	MLFRKTTAAVLAATLMLNGCTVMMWGMNSPFSETTARKHV	DKDQIRAFGVVAEDNAQLEK				
	10	20	30	40	50	60
m516.pep	GSVLMGGKYWVVNPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQA	LPVKLESPGSQN				
a516	GSVLMGGKYWVVNPEDSAKLTGILKAGLDKQFQMVPEPNRFA-YQALP	VKLESPASQN				
	70	80	90	100	110	120
m516.pep	GSVLMGGKYWVVNPEDSAKLTGILKAGLDKQFQMVPEPNRFA-YQALP	VKLESPASQN				
a516	GSVLMGGKYWVVNPEDSAKLTGILKAGLDKQFQMVPEPNRFA-YQALP	VKLESPASQN				
	70	80	90	100	110	
m516.pep	FSTEGCLCLRYDTPKPADIAKLKQLGFQAVKLDNRTIYTRCVSAKGKYATP	QKLNADYHFE				
a516	FSTEGCLCLRYDTPKPADIAKLKQLEFEAVELDNRTIYTRCVSAKGKYATP	QKLNADYHFE				
	130	140	150	160	170	180
m516.pep	FSTEGCLCLRYDTPKPADIAKLKQLGFQAVKLDNRTIYTRCVSAKGKYATP	QKLNADYHFE				
a516	FSTEGCLCLRYDTPKPADIAKLKQLEFEAVELDNRTIYTRCVSAKGKYATP	QKLNADYHFE				
	120	130	140	150	160	170
m516.pep	EQSVPADIIYYTVTEEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAV	VDAARKX				
a516	EQSVPADIIYYTVTKKHTDKSKLFENIAYTPTTLILDAVGAVLALPVAALIA	ATNSSDKX				
	180	190	200	210	220	230

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1435>:

```

g517.seq
1  atgcatcggg tttcagacgg cattggagtg tcagtcgtgt tctgccgatt
51  cgtaggcttc gacgattttt tgcaccagag gatgccggac aacgtcttcg
101 ccggtgaagg tatggaaata cagtcctgcc acgccgtgca gttcttcacg
151 tgcgtctttc aatcccgaatt tgatgttttt gggcaggctg atttggtctg
201 tgcgcgggtt aatgacggct ttcgcgccga agccgatgag ggtcaggaac
251 attttcattt gttcgggctt ggtgttttgc gcttcgtcga ggatgatgta
301 tgcgcgggtt agcgtcttgc cgcgcataata ggcgagcggg gcgatttcaa
351 tcaggccttt ttcaatcagc ttggttacac ggtcaaagcc catcagggtca
401 tagaggcat cataaagcgg acggaggtag gggtcgactt tttgggtcag
451 gtctccgggc aggaagccca gtttctcacc ggcttcgacg gcaggccgaa
501 ctaa

```

This corresponds to the amino acid sequence <SEQ ID 1436; ORF 517.ng>:

```

g517.pep
1  MHRVSDGIGV SVVFCRFVGF DDFLHQMPD NVFAGEGMEI QSCHAVQFLT
51  CVFQSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGFNQAF FNQLGYTVKA HQVIEGIIKR TEVGVDFLGQ
151 VSGQEAQFLT GFDGRPN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1437>:

```

m517.seq
1  ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51  CGTAGGCTTC GACGATTTTT TGCACCAAAG GATGCCGGAC AACGTCTTCG
101 CCGGTAAAGG TGTGGAAATA CAGCCCTTCC ACGTTGTGCA GTTCTCACG
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG
201 TTTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAGGAAC
251 ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTGCA GGATGATGTA
301 TGCGCGGTTG AGCGTCCTGC CGCGCATATA GGCAGCGGG GCgatttcaa
351 TCAGGCCTTT TTCAATCAGC TTGTTACAC GGTCAAAGCC CATCAGGTCA
401 TAGAGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG

```

```
m517.pep
  1  MHRVSDGIGM SVVFCRFVGF DDFLHQRMPP NVFAGKGVEI QPFHVVQFLT
51  RIFXSRFDVF QQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVDDV
101 CAVERPAANI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TKVGIDFLGQ
151 VSGOEAOFLA GFDGWAH*
```

m517/q517

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQRPMDNVFAGKGVEIQPFHVVQFLTRIFXSRFDVF					
	: : : : :					
g517	MHRVSDGIGIVSVVFCRFVGFDDFLHQRPMDNVFAGEGMEIQSCHAVQFLTCVFQSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	: : : : :					
g517	GQVDLAGVAGNDGFRAEADAGQEHFLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	70	80	90	100	110	120
	130	140	150	160		
m517.pep	FNQLGYTVKAHQVIEGIIKR TKVGIDFLGQVSGQEAQFLAGFDGWAH					
	: : : :					
g517	FNQLGYTVKAHQVIEGIIKRTEVGVDFLGQVSGQEAQFLTGFGRPN					
	130	140	150	160		

```
a517.seq
1  ATGCATCGGG TTTCCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
5  CGTAGGCTTC GACGATTTTT TGCACCAAAG GATGCCGGAC AACGCTTCGG
101 CCGGTAAAGG TGTGGAATAA CAGCCCTTCC ACGCCGTGCA GTTTCCTCAG
151 CGCATTTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG
201 TGTCCGCGGT AATCAGGCGT TTCGCCGCGA AGCCGATGCG GCTCAGGAGG
251 ATTTTCATTT GTTCGGGCGT GSTGTTTTGC GCTTCGTGCA GGATGATGTA
301 TGCGCGCTTG AGCGTCTGCG CGCGCATATA GCGCAGCGGG GCAATTCTAA
351 TCACAGCTTT TCCAATCAGC TTGGTGACAC GGTCGAGGCC CATCAGGTCA
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG
451 GTCACCGGGC AGAAAACCCA GTTTCCTGCC GGCTTCGACG GCAGGCCGCA
501 CTAAG
```

```
a517.pep
1  MHRVSDGIGM  SVVFCRFVGF  DDFLHQMPD  NVFAGKGEI  QPFHAVQFLT
51  RIF+SRFDVF  GQVDLAGVAG  NDGFRAEADA  GQEHFHLFGR  GVLRFVEDDV
101  CAVERPAAAH  GERGNLNOTF  FNQLGDTVEA  HQVIEGI+IKR  TKVGIDFLGQ
151  VTGOKTOFLA  GF+DGRPH*
```

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQRMPDNV	FAGKGEIQPFHV	QQLTRIFXSR	FDV		
a517	MHRVSDGIGMSVVFCRFVGFDDFLHQRMPDNV	FAGKGEIQPFH	AVQQLTRIFXSR	FDV		
	10	20	30	40	50	60
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRG	VLRFVEDD	VC	AV	PA	AHIGERGD
a517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRG	VLRFVEDD	VC	AV	PA	AHIGERGNL
	70	80	90	100	110	120
m517.pep	QF					
a517	QF					

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	70	80	90	100	110	120
m517.pep	130	140	150	160		
	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAHX					
a517	130	140	150	160		
	FNQLGDTVEAHQVIEGIIKRTKVGIDFLGQVTGQKQFLAGFDGRPHX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1441>:

```

g518.seq
1  atgacgtttt  cggcggcaaa  gctcaacatt  tgggcactga  tgttgtgtct
51  ttccggcagga  atgaccgttt  tactttccgc  ttttttactg  ctccgaccgg
101 aaggcagcat  cttattcaac  cattttttca  gcataaatat  tctgacccca
151 agagcggcat  ctccacgggc  aaccgtgttc  agactgcata  aggcgggtacg
201 attccacaag  atgccgaaaa  ccataagcaa  aatgcgtaga  aactacgccg
251 tccgaatcac  gccgcctcct  cgggcggcaa  cgcttcatta  taacagattg
301 ccccttaaaa  aatcagaccc  tgcttttgtg  gcggagtctg  aaatttga

```

This corresponds to the amino acid sequence <SEQ ID 1442; ORF 518.ng>:

```

g518.pep
1  MTFSAAKLNI  SALMLCLSAG  MTVLLSAFLL  LRPEGSILFN  HFFSINILTR
51  RAASPRATVF  RLHQAVRFHK  MKPTISKMR  NYAVRITPPP  RAATLHYNRI
101 PLKKSDFAFV  AESEI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1443>:

```

m518.seq
1  ATGACGTTTT  CGGCGGCAAA  GCTCAACATT  TCGGCACGGA  TGTGTGTCT
51  TTCGGCAGGA  ATGACCGTTT  TACTTTCGCG  TTTTCTACTG  CTCCGACCGG
101 AAGGCAGCAT  CTTATTCAAC  CATTTTTTC  GCATAAATAT  TCTGACCCGA
151 AGAGCGGCAT  CTCCACAGGC  AACCCTGTT  AGACGGCATC  AGGCGCGGTT
201 TGCAAGATGC  CGTACCATAA  ACAAAGGCG  TAGAACTAC  GCCGTCCGAA
251 TCACGCGGCC  CTCGCG.GCG  GCAACGCGTC  ATTATAACAG  ATTGCCCTCC
301 GCGGCAGGCT  TAGTGCGGCG  GGAGCGCGC  CGTTGCGCAG  TAATATTGTC
351 TAACGGGAGG  AAAAAATCAG  ACCCTGCTT  TGTGGCAGAG  TCTGAAATT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 1444; ORF 518>:

```

m518.pep
1  MTFSAAKLNI  SARMLCLSAG  MTVLLSAFLL  LRPEGSILFN  HFFSINILTR
51  RAASPRATVF  RRHQARFARC  RTINKRRRNY  AVRITPPSXA  ATRHYNRLPS
101 AAGLVRERR  RCAVILSNR  KKSDFAFVAE  SEI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 518 shows 74.1% identity over a 135 aa overlap with a predicted ORF (ORF 518.ng) from *N. gonorrhoeae*:

```

m518/g518

m518.pep  MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF
g518      MTFSAAKLNISALMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF
              10      20      30      40      50      60

              70      80      90      100     110
m518.pep  RRHQA-RFARC-RTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRERRRCAVILSN
g518      RLHQAVRFHKMPKTISKMRNYAVRITPPRAATLHYNRLPL-----
              70      80      90      100

m518.pep  120      130
g518      GRKKSDFAFVAESEI
              |||||
g518      --KKSDFAFVAESEI
              110

```


The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1445>:

```
a518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTGTGTCT
51  TTCGCGAGGA ATGACCGTTT TACTTTCCGC TTTTCTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTCAT GCATAAATAT TCTAACCCGA
151 AGASCGGCAT CTCCACGGGC AACCCTGTTC AGACGGCATC AGGCGGTACG
201 ATTCCGCAAG ATGCCGACCA TAAACAAAAG GCGTAGAAAC TACGCCGTCC
251 GAATCAGGCC GTCCTCG.CG GCGGCAACGC GTCATTATAA CAGATTGCCC
301 TCC.....
351 .....AAAAAAT CAGACCCTGC TTTGTGGCA GAGCTGAAA
401 TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1446; ORF 518.a>:

```
a518.pep
1  MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RRHQAVRFRK MPTINKRRRN YAVRITPSSX AATRHYNRLP
101 S..... .KKSDPAFVA ESEI*

m518/a518 79.9% identity in 134 aa overlap

          10      20      30      40      50      60
m518.pep  MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPOATVF
          |||
a518      MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF
          10      20      30      40      50      60

          70      80      90      100     110     119
m518.pep  RRHQA-RFARCTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRERRRRCVILSNG
          |||
a518      RRHQAVRFRKMPTINKRRRNYAVRITPPSXAATRHYNRLPS-----
          70      80      90      100

m518.pep  120      130
          RKKSDPAFVAESEIX
          |||
a518      -KKSDPAFVAESEIX
          110
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1447>:

```
g519.seq
1  atggaatttt tcattatctt gttggcagcc gtcgcccgtt tcggcttcaa
51  atccctttgtc gtcaccccc agcaggaagt ccacgttgtc gaaaggctcg
101 ggcgtttcca tcgcgccctg acggccggtt tgaatatttt gattcccttt
151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc ctttagacgt
201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actgttgacg
251 gcatcatcta tttccaagta accgatccca aactcgcttc atacggttcg
301 agcaactaca ttatggcaat taccagctt gcccaaacga cgctgcgttc
351 cgttatcggg cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
401 tcaacagtac cgtcgtctcc gccctcgatg aagccgcccg ggcttggggt
451 gtgaaagtcc tccgttacga aatcaaggat ttggttcgcg cgcaagaaat
501 ccttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
551 gtattgccga atccgaaggc cgtaaaatcg aacaaatcaa cttgccagt
601 ggtcagcgtg aagccgaaat ccaacaatcc gaaggcgagg ctcaggctgc
651 ggtcaatgcg tccaatgccg agaaaatcgc ccgcatcaac cgcgccaaag
701 gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
751 cgtcaaattg ccgcccgcct tcaaaccгаа agcggggcgg atgcggtcaa
801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
851 aagacaatac gcgattaag ccgcgcaaag ttgccgaaat cgggaaccct
901 aattttcggc ggcatgaaaa attttcgcca gaagcaaaaa cggccaataa
951 a
```

This corresponds to the amino acid sequence <SEQ ID 1448; ORF 519.ng>:

```
g519.pep
1  MEFFIILLAA VAVFGFKSFV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
```

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```

101 SNYIMAITQL AQTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEEAQAANA SNAEKIARIN RAKGEAESLR LVAEANAEN
251 RQIAAALQTO SGADAVNLKI AGQYVTAFKN LAKEDNTRIK PAKVAEIGNP
301 NFRRHEKFSP EAKTAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1449>:

```

m519.seq (partial)
1  ..TCCGTTATCG GCGGTATGGA GTTGGACAAA ACGTTTGAAG AACGCGACGA
51  AATCAACAGT ACTGTTGTTG CCGCTTTGGA CGAGGCGGCC GGGgCTTgGG
101 GTGTGAAGGT TTTGCGTTAT GAGATTAAAG ACTTGGTTCC GCCGCAAGAA
151 ATCCTTCGCT CAATCGAGGC GCAAATTACT GCCGAACGCG AAAAACGCGC
201 CCGTATCGCC GAATCCGAAG GTCGTAAAT CGAACAAATC AACCTTGCCA
251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT
301 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCCGCATCA ACCGCGCCAA
351 AGGTGAAGCG GAATCCTTGC GCCTTGTTGC CGAAGCCAAT GCCGAAGCCA
401 TCCGTCAAAT TGCCGCCGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC
451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA
501 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTGCGCGAC ATCGGCAGCC
551 TGATTTCTGC CGGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAaTAA

```

This corresponds to the amino acid sequence <SEQ ID 1450; ORF 519>:

```

m519.pep (partial)
1  ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
51  ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLAGQREAE IQQSEGEAQA
101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV
151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLISAGMK IIDSSKTAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

m519/g519

m519.pep				10	20	30
				SVIGRMELDKTFEERDEINSTVVAALDEAA		
g519	YFQVTDPKLASYGSSNYIMAITQLAQTLRSVIGRMELDKTFEERDEINSTVVSALDEAA					
	90	100	110	120	130	140
m519.pep		40	50	60	70	80
		GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLAGQREAE				
g519		GAWGVKVLRYEIKDLVPPQEILRAMQAQITAEREKRARIAESEGRKIEQINLAGQREAE				
		150	160	170	180	190
m519.pep		100	110	120	130	140
		IQQSEGEAQAANASNAEKIARINRAKGEAESLRLVAEANAENRQIAAALQTQGGADAV				
g519		IQQSEGEAQAANASNAEKIARINRAKGEAESLRLVAEANAENRQIAAALQTQSGADAV				
		210	220	230	240	250
m519.pep		160	170	180	190	200
		NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL-ISAGMKIIDSSKTAK				
g519		NLKIAGQYVTAFKNLAKEDNTRIKPAKVAEIGNPNFRRHEKFSP EAKTAK				
		270	280	290	300	310

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1451>:

```

a519.seq
1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GGCCTTTCCA TCGCGCCCTG ACGGCCGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCTACCG CCATTGCTG AAAGAAATCC CTTAGACGT

```

```

201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCC
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGGGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTTCAGCGC AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCRAATGCCG AGAAAATCGC CCGCATCAAC CGCGCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GCGCGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGCGAGCCTG
901 ATTCTCGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAATAAT

```

This corresponds to the amino acid sequence <SEQ ID 1452; ORF 519.a>:

```

a519.pep
1  MEFFIILLAA VVVFGEKSEV VIPQOEHVHV ERLGRFHRAL TAGLNILIPF
51  IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESG RKTEQINLAS
201 GQREAEIQQS EGEAQAQVNA SNAEKIARIN RAKGEAESLR LVAEANAELAI
251 RQIAAALQTO GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

m519/a519 99.5% identity in 199 aa overlap

m519.pep
10 20 30
SVIGRMELDKTFEERDEINSTVVAALDEAA
|||||
a519 YFQVTDPKLASYGSSNYIMAITQLAQTTLRVIGRMELDKTFEERDEINSTVVSALDEAA
90 100 110 120 130 140

m519.pep
40 50 60 70 80 90
GAWGVKVLRYEIKDLVPPQEILRSMAQITAEREKRARIAESEGRKIEQINLASGQREAE
|||||
a519 GAWGVKVLRYEIKDLVPPQEILRSMAQITAEREKRARIAESEGRKIEQINLASGQREAE
150 160 170 180 190 200

m519.pep
100 110 120 130 140 150
IQQSEGEAQAQVNASNAEKIARINRAKGEAESLRLVAEANAELAIQIAAALQTGGADAV
|||||
a519 IQQSEGEAQAQVNASNAEKIARINRAKGEAESLRLVAEANAELAIQIAAALQTGGADAV
210 220 230 240 250 260

m519.pep
160 170 180 190 200
NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
|||||
a519 NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
270 280 290 300 310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1453>:

```

g519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51  ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCTTTT
151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTCC
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAAGTCC TCCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACCGC CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAATCGC AACAAATCAA CCTTGCCAGT
601 GGTTCAGCGT AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCRAATGCCG AGAAAATCGC CCGCATCAAC CGCGCAAAG
701 CGAAGCGGA ATCCCTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GCGGGGCGG ATGCGGTCAA

```

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801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GCATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1454; ORF 519-1.ng>:

g519-1.pep

1 MEFFIILLAA VAVFGPKSFV VIPQQEVHV ERLGRFHRAL TAGLNILIPF
 51 IDRVAVRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAENAEAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1455>:

m519-1.seq

1 ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA
 51 ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTGTC GAAAGGCTGG
 101 GCGGTTTCCA TCGCGCCCTG ACGGcCGGTT TGAATATTTT GATTCCCTTT
 151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
 201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
 251 GCATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCTG
 301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
 351 CGTTATCGGG CGFATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
 401 TCACAGTAC TGTGTGTCG GCTTTGACG AGGCGGCCGG GGCTTGGGGT
 451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGTTTCCGC CGCAAGAAAT
 501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAACGCGAA AAACGCGCCC
 551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
 601 GGTCAAGCGG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
 651 GGTCAATGCG TCAATGCGG AGAAATCGC CGCATCAAC CGCGCCAAAG
 701 GTGAAGCGGA ATCCTTGCGC CTGTTGCGG AAGCCAATGC CGAAGCCATC
 751 CGTCAATGCG CCGCGCCCT TCAAAACCAA GCGGTGCGG ATGCGGTCAA
 801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1456; ORF 519-1>:

m519-1.

1 MEFFIILLVA VAVFGPKSFV VIPQQEVHV ERLGRFHRAL TAGLNILIPF
 51 IDRVAVRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAENAEAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

m519-1/g519-1 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFIILLAAVAVFGPKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSI					
m519-1	MEFFIILLVAVAVFGPKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSI					
	10	20	30	40	50	60
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMAQITAERE					
	130	140	150	160	170	180
g519-1.pep	KRARIAESEG RKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEG RKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep	KRARIAESEG RKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEG RKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					

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m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
g519-1.pep  LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLINPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLINPANVADIGSL
              250      260      270      280      290      300

              310
g519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1457>:

```

a519-1.seq
1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTGTGTT TCGGCTTCAA
51 ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GCTGTCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAA GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCGGG AGCTTGGGGT
451 GTGAAGGTTT TCGGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTACGCGCG AAGCCGAAAT CCAACAATCC CAAGCGGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATCCCG AGAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCGG AAGCCAATGC CGAAGCCATC
751 CGTCAAATG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCGCG GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCGGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAAA TATCGACAGC AGCAAAACCG CCAATAAA

```

This corresponds to the amino acid sequence <SEQ ID 1458; ORF 519-1.a>:

```

a519-1.pep.
1  MEFFIILLAA VVVFGRKSFV VIPQEVHV VRLGRFHRAL TAGLNILIPF
51 IDRVA YRHS L KEIPLDVPSQ VCITRDNTQL TVDGIYFQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 QREAEIQQS EGEEAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN IAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 99.0% identity in 315 aa overlap

```

              10      20      30      40      50      60
a519-1.pep  MEFFIILLAAVVVFGRKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
              |||||
m519-1      MEFFIILLVAVVFGFKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
              10      20      30      40      50      60

              70      80      90      100     110     120
a519-1.pep  KEIPLDVPSQVCITRDNTQLTVDGIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
              |||||
m519-1      KEIPLDVPSQVCITRDNTQLTVDGIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
              70      80      90      100     110     120

              130     140     150     160     170     180
a519-1.pep  RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
              |||||
m519-1      RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
              130     140     150     160     170     180

              190     200     210     220     230     240
a519-1.pep  KRARIAESEGRKIEQINLASGQREAEIQQSEGEAAVNASNAEKIARINRAKGEAESLR
              |||||

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m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
a519-1.pep  LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
|||||
m519-1      LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
a519-1.pep  ISAGMKIIDSSKTAKX
|||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

Expression of ORF 519

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. ORF 519 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 4A shows the results of affinity purification, and Figure 4B shows the expression in E.coli. Purified Nis-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 4C), western blot (Figure 1E), and a bactericidal assay (Figure 4D). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 519 are provided in Figure 8. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby as provided herein.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1459>:

```

g520.seq
1  atgcctgcgc ttctttcaat acgtcgggca aacgcgctgc ctttttcgcg
51  catttcggaa aggatgaagt tgctgggtgcc gttaataatg ccggcgatgg
101 atttaatcct gtttgccgcc aaaccttcgc gcacggcttt gatgattggg
151 ataccgcccg ctactgccgc ttcaaattgg acgatgacgt tttgtttttc
201 cgccagcggg aagatttcgt tgccgtattc ggcgagcagt ttttggttg
251 cggtaacgat gtgtttgccg ttttcaatgg ctttcaacac cgcttctttg
301 gcaatgcccg tgccgccgaa caattcgacc aagacatcga cgtctttacg
351 cgcgaacagt tcgaacggat cttttgacaa gggcgggcga cgggccgatt
401 ttggcgggct ttttcttcgc ttaagtcgca catggcagaa atacggattt
451 cgcgcccacg gcggcgggaa atttcctctg cgttgctccc caacacggca
501 gccgcaccgc cgccgacgct acctaagcct aaaagaccga tgtttactgg
551 cttcattgtg tctccttgta agccgactga aatgtaaata ttga

```

This corresponds to the amino acid sequence <SEQ ID 1460; ORF 520.ng>:

```

g520.pep
1  MPALLSIRRA NALPFSRISE RMKLLVPLIM PAMDILIFAA KPSRTALMIG
51  IFPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST KTSTSLRANS SNGSFDKGGG RADFGGLFLR LSRTWQKYGF
151 RAPSGGKFPL RCPATRQPHR RRPYLSLKDR CLLASLCLLV SRLKCKY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1461>:

```

m520.seq
1  ATGCCTGCGC TTCTTTCAGT ACATCG.GCA AACGCGCTGC CTTTTTCGCG
51  CATTTCGGrk AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCCG CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGGG AAGATTTCGT TGCCGTATTC GCGAGCAGT TTTTGTGTGG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG

```

m520.ppt

m520/g520

a520.seq

a520.pep

1 MPALLSVHRX NALPFSRISE RMKLLVPLIM PAMDILFAA KPSRRALMIG
51 IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCPL FSMAFNTASL
101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLELH SNRTQKYGF

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151 RAPSDGKFPP RCPATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

m520/a520 98.0% identity in 197 aa overlap

	10	20	30	40	50	60
m520.pep	MPALLSVHXANALPFSRISXRMKLLVPLIMPANDLILFAAKPSRRALMIGIPPATAASNW					
a520	MPALLSVHRXNALPFSRISERMKLLVPLIMPANDLILFAAKPSRRALMIGIPPATAASNW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m520.pep	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNNTASLAMPVPPNNSTTTSTSSRATS					
a520	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNNTASLAMPVPPNNSTTTSTSSRATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m520.pep	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGERAPSDGKFPPRCXATRQPYRRRPYPNLKDR					
a520	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGERAPSDGKFPPRCPATRQPYRRRPYPNLKDR					
	130	140	150	160	170	180
	190					
m520.pep	CLLASLCLLVSRKCKYX					
a520	CLLASLCLLVSRKCKYX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1465>:

g520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTCGTTGCG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC TTCTTTGGCA ATGCCCGTGC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTTACGCGC GACCAGTTCG
301 AACGGATCTT TGACAAAGGC GCGGACGGG CAGATTGGC GGGCTTTTTC
351 TTCGCTTAAG TCGCACATGG CAGAAATACG GATTTCGCGC CCCAAGCGGC
401 GGGAAATTTT CTCTGCGTTG TCCCGCAACA CGGCAGCCGC ACCGCCGCCG
451 ACCGTACCTA AGCCTAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1466; ORF 520-1.ng>:

g520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51  ISLPYSASSF LLAVTMCLPF SMAFNNTASLA MPVPPNNSTT TSTSLRATSS
101 NGSLLKAADG QIWRAFSSLK SHMAEIRISR PKRREISSAL SRNTAAAPP
151 TVPKPRPMF TGFIVSPCKP TEM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1467>:

m520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTCGTTGCG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCCGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACAGTGC GACCAGTTCG
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGTTTGTG GGGCTTTTTC
351 TTTACTCAAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTTT CTCTGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG
451 ACCGTACCCA AACCTAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1468; ORF 520-1>:

m520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51  ISLPYSASSF LLAVTMCLPF SMAFNNTASLA MPVPPNNSTT TSTSSRATSS

```


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101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

g520-1/m520-1 97.1% identity in 173 aa overlap

	10	20	30	40	50	60
g520-1.pep	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASG	KISLPYSASSF	
m520-1	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASG	KISLPYSASSF	
	10	20	30	40	50	60
	70	80	90	100	110	120
g520-1.pep	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSLR	ATSSNGSLTKA	ADGQIWRAFSSLK	
m520-1	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSSLK	
	70	80	90	100	110	120
	130	140	150	160	170	
g520-1.pep	SHMAEIRISRPKR	REISSALSRNTAA	PPPTVPKPKRPM	FTGFIVSPCKP	TEMX	
m520-1	SHTAEIRISRPKR	REISSALSRNTAA	VPPTVPKPKRPM	FTGFIVSPCKP	TEMX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1469>:

a520-1.seq
1 ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51 TGCCGCCAAA CCTTCGCGCA GGGCTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTCGTTGCG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTGGCA ATGCCGGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACGTGC GACCAGTTG
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGGTTTGTG GGGCTTTTTC
351 TTCACTCAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTC CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTCA TTGTGCTCC
501 TTGTAAGCCG ACTGAAATGT AA

This corresponds to the amino acid sequence <SEQ ID 1470; ORF 520-1.a>:

a520-1.pep
1 MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51 ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS
101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

m520-1/a520-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
a520-1.pep	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASG	KISLPYSASSF	
m520-1	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASG	KISLPYSASSF	
	10	20	30	40	50	60
	70	80	90	100	110	120
a520-1.pep	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSSLK	
m520-1	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSSLK	
	70	80	90	100	110	120
	130	140	150	160	170	
a520-1.pep	SHTAEIRISRPKR	REISSALSRNTAA	VPPTVPKPKRPM	FTGFIVSPCKP	TEMX	
m520-1	SHTAEIRISRPKR	REISSALSRNTAA	VPPTVPKPKRPM	FTGFIVSPCKP	TEMX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1471>:

g521.seq
1 ATGAAATCAA AACTCCCTT AATCCTAATC AACCTTTCCC TGATTCAAG
51 CCCATTGGGT GCGAATGCGG CCAAATCTA TACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCACCAAG CCGTCTAAAA GCTGCCACTC AACCGATTG

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151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCTGC CCCAACTCC
201 CGAACCGGCA CCATCACCGT CAAACGGCGG ACAGGCTGTC AAATATAAAG
251 CCCCAGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCTCAA
301 CAAGCACCTG TAAATAACAG CAGACGCTCC ATTCTcgaag caGaattaa
351 cAatgaacgc aaagccctGa ctGaAGCCCA AAAAATGTTA TCACAagcac
401 gtCtGGCAAA AGGCGGcaAC AtcaaCCatc aaaAaatcaa cgcattgtaa
451 AGCAATGTTt tggacAGACA GCAAAATaTC Caagcactgc aaaGAgAATt
501 GGGACGTATG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1472; ORF 521.ng>:

```

g521n.pep
1 MKSKLPLILI NLSLISSPLG ANAAKIYTCT INGETVYTTK PSKSCHSTD
51 PPIGNYSSER YILPQTPEPA PPSNGGQAV KYKAPVKTVS KPAKSNTTPQ
101 QAPVNNRRS ILEAELSNER KALTEAQKML SQARLAKGN INHQKINAL*
151 SNVLDROQNI QALQRELGRM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1473>:

```

m521.seq
1 ATGAAATCAA AACTCCTCTT AATCCTAATC AACTTTTCCC TGATTTCAG
51 CCCATTGGGT GCGAATGCGG CCAAAATCTA sACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCAaCAAG CCGTCCAAAA GCTGCCACTC AACCGATTG
151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAAACGCC
201 CGAACCGGTA TCATCACCGT CAAACGGCGG ACwGGTTGTC AAATATAAAG
251 CCCCAGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCTCAA
301 CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AAACAGAATT
351 GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CCAAAAAATG TTATACAAG
401 CACGTCTGGC AAAGGGCGGC AACATCAACC ATCAAGAAAT AAATGCATTA
451 CAAAGCAATG TATTGGACAG GCAGCAAAT ATTCAAGCCC TGCAAAGGGA
501 ACTGGGGCGT ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1474; ORF 521>:

```

m521.pep
1 MKSKLLLLILI NFSLISSPLG ANAAKIXTCT INGETVYTXK PSKSCHSTD
51 PPIGNYSSER YIPPQTPEPV SPSNGGXV KYKAPVKTVS KPAKSXTPPP
101 QQAPSNNRRS SILETELSNE RKALVEAQKM LSQARLAKGG NINHQBINAL
151 QSNVLDROQN IQALQRELGR M*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 521 shows 90.6% identity over a 171 aa overlap with a predicted ORF (ORF 521.ng) from *N. gonorrhoeae*:

m521/g521

	10	20	30	40	50	60
m521.pep	MKSKLLLLILINFSLISSPLGANAAKIXTCTINGETVYTXKPSKSCHSTDLPPIGNYSSER					
	: : : : : : : : :					
g521	MKSKLPLILINLSLISSPLGANAAKIYTCTINGETVYTTKPSKSCHSTDLPPIGNYSSER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	YILPQTPEPVSSPSNGGXVVKYKAPVKTVSKPAKSXTPPPQQAPSNNRRSILETELSNE					
	: : : : : : : :					
g521	YILPQTPEPAPSPSNGGQAVKYKAPVKTVSKPAKSNTTPP-QQAPVNNRRSILEAELSNE					
	70	80	90	100	110	
	130	140	150	160	170	
m521.pep	RKALVEAQKMLSQARLAKGGINHQBINALQSNVLDROQNIQALQRELGRMX					
	: : : : : : : :					
g521	RKALTEAQKMLSQARLAKGGINHQBINALXSNVLDROQNIQALQRELGRMX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1475>:

```

a521.seq
1 ATGAAATCAA AACTCCCTT AATCCTAATC AACTTTTCCC TGATTTCAG

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```

51  CCCATTGGGT GCGAATGCGG CCAAAATCTA CACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCACCAAG CCGTCCAAAA GCTGCCTCTC AACCGATTTG
151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAACATC
201 CGAACCGACA CCATCACCGT CAAACGGCGG ACAGGCTGTC AAATATAAAG
251 CCCCGGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCGCCG
301 CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AAACAGAATT
351 GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CCAAAAAATG TTATCACAAG
401 CACGCTGGC AAAAGGCGGC AACATCAACC ATCAAGAAAT CAACGCATTG
451 CAAAGCAATG TATTGGACAG GCAGCAAAAT ATCCAAGCAC TGCAAAGAGA
501 ATGGGACGT ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1476; ORF 521.a>:

```

a521.pep
1  MKSKLPLILI NFSLISSPLG ANAAKIYTCT INGETVYTTK PSKSLSTDL
51  PPIGNYSSER YIPPQTSEPT PSPSNGGQAV KYKAPVKTVS KPAKSNTPPP
101 QQAPSNNRRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSVLDRQQN IQALQRELGR M*

```

m521/a521 94.2% identity in 171 aa overlap

	10	20	30	40	50	60
m521.pep	MKSLLLLILINFSLISSPLGANAAKIXTCTINGETVYTXKPSKXSCHSTDLPPIGNYSSER					
a521	MKSKLPLILINFSLISSPLGANAAKIYTCTINGETVYTTKPSKSLSTDLPPIGNYSSER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	YIPPQTPEPVSSPSNGGXVVVKYKAPVKTVSKPAKSXTPPPQQAPSNNRRRSILETELSNE					
a521	YIPPQTSEPTSPSNGGQAVKYKAPVKTVSKPAKSNTPPPQQAPSNNRRRSILETELSNE					
	70	80	90	100	110	120
	130	140	150	160	170	
m521.pep	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
a521	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1477>:

```

g522.seq
1  atgactgagc cgaaacacga aacgccgacg gaagagcagg ttgccgcgcg
51  caaaaaagca aaagccaaaa tccgcaccat ccgcatttgg gcgtgggtca
101 ttttgcggtt gctcgcttca accgccctgc tctcccaatg cgcgatgtcc
151 aaaccgcagg caaaacagaa aattgtcgag tcttgcataa aaaatattcc
201 gtttgctgaa aaatggcaga acgatttgaa agcgcgcggc ttggatgcgg
251 acaatacccg tctcgccgct gactactgca aatgtatgtg ggagcagcct
301 ttggacggat tgagcgagaa acagatcagc tccttcggca aactcggtgc
351 acaagaacag cttgacctgc tcggcgcgcc aaacgcgttt gaaactcgag
401 acaacaatg tgtcgcggat ttgaaagccg attga

```

This corresponds to the amino acid sequence <SEQ ID 1478; ORF 522.ng>:

```

g522.pep
1  MTEPKHETPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMs
51  KPQAKQKIVE SCMKNIPFAE KWQNDLKARG LDADNTRLAV DYCKCMWEQP
101 LDGLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKAD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1479>:

```

m522.seq
1  ATGACTGAGC CGAAACACGA AATGCTGACG AAAGAGCAGG TTGCCGCGCG
51  CAAAAAAGCA AAAGCCAAAA TCCGCACCAT CCGCATTGCG GCGTGGGTCA
101 TTTTGGCGTT GCTCGCTTTA ACCGCCCTGC TCTCCCAATG CGCGATGTCC
151 AAACCGCAGG CAAAACAGAA AATTGTCGAG TCTTGCGTGA AGAATATTCC
201 GTTTGCCGAA AAATGGCAAA ACGATTGCGG GGCCCGCGGT TTAGATTCAA
251 ACAATACCCG CCTCGCCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT

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301 TTGGACAGAT TGAGCGAGAA ACAGATTAGA TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAGCACGTG
 401 ACAAGCAGTG TGTGCGCAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1480; ORF 522>:

m522.pep

1 MTEPKHEMLT KEQVAARKKA KAKIRTIRIW AWVILALLAL TALLSQCAMS
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLAV DYCKCMWEQP
 101 LDRLSEKQIR SFGKLGAQEQ LDLLGGANAF EARDKQCVAD LKSE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 522 shows 91.0% identity over a 144 aa overlap with a predicted ORF (ORF 522.ng)
 from *N. gonorrhoeae*:

m522/g522

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
g522	MTEPKHETPTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSNNTRLAVDYCKCMWEQPLDRLSEKQIRSFGLGAQEQ					
	: : :					
g522	SCMKNIPFAEKWQNDLKARGLDADNTRLAVDYCKCMWEQPLDGLSEKQISSFGLGAQEQ					
	70	80	90	100	110	120
	130	140				
m522.pep	LDLLGGANAFEARDKQCVADLKSEX					
	: : :					
g522	LDLLGGANAFETRDKQCVADLKAD					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1481>:

a522.seq

1 ATGACTGAGC CGAAACACGA AATGCCGACG GAAGAGCAGG TTGCCGCGCG
 51 CAAAAAAGCA AAAGCCAAAA TCCGCACCAT CCGCATTTGG GCATGGGTCA
 101 TTTTGGCGTT GCTCGCTTCA ACCGCCCTGC TCTCCCAATG CGCGATGTCC
 151 AAACCGCAGG CAAAACAGAA AATTGTCGAG TCTTGCCTGA AGAATATTCC
 201 GTTTGCCGAA AAATGGCAAA ACGATTGCG GGCCCGCGGT TTAGATTCAA
 251 ACAATACCG CTTACCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT
 301 TTGGACAGAT TGAGCGAGAA ACAGATTAGT TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAACGCGAG
 401 ACAAGCAGTG TGTGCGCAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1482; ORF 522.a>:

a522.pep

1 MTEPKHEMPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMS
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLTV DYCKCMWEQP
 101 LDRLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKSE*

m522/a522 95.8% identity in 144 aa overlap

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
a522	MTEPKHEMPTTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSNNTRLAVDYCKCMWEQPLDRLSEKQIRSFGLGAQEQ					
a522	SCVKNIPFAEKWQNDLRARGLDSNNTRLTVDYCKCMWEQPLDRLSEKQISSFGLGAQEQ					
	70	80	90	100	110	120

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	130	140
m522 . pep	LDLLGGANAFEARDKQCVADLKSEX	
a522	LDLLGGANAFETRDKQCVADLKSEX	
	130	140

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1483>:

g523 . seq

```

1  atgactgtat ggtttgttgc cgctgttgcc gtcttaatca tcgaattatt
51  gacgggaacg gtttatcttt tggttgtag cgcggtttg gcgggttcgg
101 gcatctgcta cgggctgact ggcagcacgc ctgccgccgt cttgaccgcc
151 ggcactgctt cgcgcgtggg catttggtc gtacatgcca aaaccgccgt
201 gggaaaagtt gaaacggatt catatcagga ttggatacc ggaaaatatg
251 ccgaaatcct ccgatacaca ggcggcaacc gttacgaagt tttttatcgc
301 ggtacgcact ggcaggcgca aaatacggg caggaagtgt ttgaaccggg
351 aacgcgcgcc ctcatcgcc gcaaagaagg taaccttctt atcatcgcaa
401 acccttaa

```

This corresponds to the amino acid sequence <SEQ ID 1484; ORF 523.ng>:

g523 . pep

```

1  MTVWFVAAVA VLIIELLTGT VYLLVVSAA AGSGIAYGLT GSTPAAVLTA
51  ALLSALGIWF VHAKTAVGKV ETDSYQDLDT GKYAEILRYT GGNRYEVFYR
101 GTHWQAQNTG QEVFEPGTRA LIVRKEGNLL IIANP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1485>:

m523 . seq (partial)

```

1  ..GCCGTCTTAA TCATCGAATT ATTGACGGGA ACGGTTTATC TTTTGGTTGT
51  nAGCGCGGCT TTGGCGGGTT CGGGCATTGC TTACGGGCTG ACCGGCAGTA
101 CGCCTGCCGC CGTCTTGACC GnCGCTCTGC TTTCCGCGCT GGGTATTTnG
151 TTCGTACACG CCAAAACCGC CGTTAGAAAA GTTGAAACGG ATTCATATCA
201 GGATTTGGAT GCCGACAAT ATGTCGAAAT CCTCCGACAC ACAGGCGGCA
251 ACCGTTACGA AGTTTTLTAT CGCGGTACGc ACTGGCAGGC TCAAAATACG
301 GGGCAAGAAG AGCTTGAACC AGGAACCTCG GCCCTCATTG TCCGCAAGGA
351 AGGCAACCTT CTTATTATCA CACACCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1486; ORF 523>:

m523 . pep (partial)

```

1  ..AVLIIELLTG TVYLLVVSAA LAGSGIAYGL TGSTPAAVLT XALLSALGIX
51  FVHAKTAVRK VETDSYQDLDT AGQYVEILRH TGGNRYEVFY RGTWQAQNT
101 GQEELEPGTR ALIVRKEGNL LIITHP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF523 shows 91.3% identity over a 126 aa overlap with a predicted ORF (ORF 523.ng) from *N. gonorrhoeae*:

m523/g523

	10	20	30	40	50
m523 . pep	AVLIIELLTGTVYLLVVSAA LAGSGIAYGLTGSTPAAVLT XALLSALGIXF				
g523	MTVWFVAAVAVLIIELLTGTVYLLVVSAA LAGSGIAYGLTGSTPAAVLTAALLSALGIWF				
	10	20	30	40	50
	60	70	80	90	100
m523 . pep	VHAKTAVRKVETDSYQDLDTAGQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA				
g523	VHAKTAVGKVETDSYQDLDTGKYAEILRYTGGNRYEVFYRGTHWQAQNTGQEVFEPGTRA				
	70	80	90	100	110
	120				
m523 . pep	LIVRKEGNLLIITHP				

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g523 LIVRKEGNLLIIANPX
130

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1487>:

a523.seq
1 ATGACTGTAT GGTTTGTGTC CGCTGTTGCC GTCTTAATCA TCGAATTATT
51 GACGGGAACG GTTTATCTTT TGGTTGTCAG CGCGGCTTTG GCGGGTTTCGG
101 GCATTGCTTA CGGGCTGACC GGCAGCACGC CTGCCGCCGT CTGACCGCC
151 GCTCTGCTTT CCGCGCTGGG TATTGTTGTC GTACACGCCA AAACCGCCGT
201 GGGAAAAGTT GAAACGGATT CATATCAGGA TTTGGATGCC GSGCAATATG
251 CCGAAATCCT CCGGCACGCA GCGGCAACC GTTACGAAGT TTTTATCGC
301 GGTACGCACT GGCAGGCTCA AAATACGGGG CAAGAAGAGC TTGAACCAGG
351 AACGCGCGCC CTAATCGTCC GCAAGGAAGG CAACCTTCTT ATCATCGCAA
401 AACCTTAA

This corresponds to the amino acid sequence <SEQ ID 1488; ORF 523.a>:

a523.pep
1 MTVWFVAAVA VLIIELLTGT VYLLVVSAAAL AGSGIAYGLT GSTPAAVLTA
51 ALLSALGIWF VHAKTAVGKV ETDSYQDLDA GQYAEILRHA GGNRYEVFYR
101 GTHWQAQNTG QEELFPGTRA LIVRKEGNLL IIAKP*

m523/a523 94.4% identity in 126 aa overlap

	10	20	30	40	50
m523.pep	AVLIIELLTGT VYLLVVSAAALAGSGIAYGLTGSTPAAVLTXALLSALGIXF				
a523	MTVWFVAAVAVLIIELLTGT VYLLVVSAAALAGSGIAYGLTGSTPAAVLTAALLSALGIWF				
	10	20	30	40	50
	60	70	80	90	100
m523.pep	VHAKTAVRKVETDSYQDLDAQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELFPGTRA				
a523	VHAKTAVGKVETDSYQDLDAQYAEILRHAGGNRYEVFYRGTHWQAQNTGQEELFPGTRA				
	70	80	90	100	110
	120				
m523.pep	LIVRKEGNLLIITHPX				
a523	LIVRKEGNLLIIAKPX				
	130				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1489>:

g525.seq
1 atgaagtacg tccggttatt tttcctcggc acggcactcg ccggcactca
51 agcggcggct gccgaaatgg ttcaaatcga aggcggcagc taccgcccgc
101 tttatctgaa aaaagatacc gccctgatta aagtcaaacc gttcaaactg
151 gataaatatc ccgttaccaa tgccgagttt gccgaatttg tcaacagcca
201 cccccaatgg caaaaaggca ggatcggttc caaacaggca gaaccgctt
251 acctgaagca ttggatgaaa aacggcagcc gcagctatgc gccgaaggcg
301 ggccaattga aacagccggt taccaatatt tcttggtttg ccgccaacgc
351 ctattgcccgc gcacaaggca aacgcctgcc gaccatcgac gaatgggaat
401 ttgcccggact tgcttccgcc acgcagaaaa aacggctcaa acgaaccggg
451 ctacaaccgc actattctcg attggtatgc cgacggcgga cggaaaaggcc
501 tgcacgatgt cggcaagca ccgcccgaac tactgggggtg tttatgatat
551 gcacgggctg a

This corresponds to the amino acid sequence <SEQ ID 1490; ORF 525.ng>:

g525.pep
1 MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
101 GELKQPVNTI SWFAANAYCA AQKRLPTID EWEFAGLASA TQKKRLKRTR
151 LQPHYSRLVC RRRTERPARC RQSTARTGV FMICTG *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1491>:

This corresponds to the amino acid sequence <SEQ ID 1492; ORF 525>:

m525 . pep

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 525 shows 94.1% identity over a 186 aa overlap with a predicted ORF (ORF 525.ng) from *N. gonorrhoeae*:

m525/q525

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1493>:

a525.seq

1	ATGAAGTTTA	CCCGGTTACT	CTTCTCTGT	GCGGCACTCG	CCGGCACTCA
51	AGCGGCAGCT	GCCGAAATGG	TTCAAATCGA	AGCGGGCAGC	TACCGCCCGC
101	TTTATCTGAA	AAAAGATACC	GGCTCTGATTA	AAGTCAAAAC	GTTCAAAGTC
151	GATAAATATC	CCGT1TACCAA	TGCGCAGGTTT	CCGGAATTTG	TCAACAGCCA
201	CCCCCAATGG	CAAAAAGGCA	GGATCGGTTT	CAAAACAGGCA	GAACCCGCTT
251	ACCTTGAGCA	TGTGATGAAA	AACGGCAGCG	GCAGCTATGC	GCCGAAGGCG
301	GGCGATTTAA	AACAACCGGT	AACCAATGTT	TCTTGGTTTC	CCGCCAACGC
351	CTATTGCGCC	GCACAAGGCA	AACGCTGCC	GACCATTGAC	GAATGGGAAT
401	TTGCCGGAAT	TGCTCCGCTC	ACGCAG.AAA	AACGGCTCAA	AGCAACCCGG
451	CTACAAACCG	ACTATTCTCG	ACTGGTATGC	GGATGGCGAC	CGGAAAGACC
501	TGACACGATG	CGGCAAAG.G	TCGCCGAAC	TACTGGGGCG	TTTATGATAT
551	GCACGGTCTG	A			

This corresponds to the amino acid sequence <SEQ ID 1494; ORF 525.a>:

```
a525.pep
  1 MKFTRLLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
101 GDLKQPVTNV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQXKRLKRTR
151 LQPHYSRLVC GWRPERPARC RQXVARTTGA FMICTV*
```

m525/a525 90.8% identity in 185 aa overlap

```

      10      20      30      40      50      60
m525.pep  MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
a525      MKFTRLLFLCAALAGTQAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
      10      20      30      40      50      60

      70      80      90      100     110     120
m525.pep  AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVTNVSWXAANAYCA
a525      AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGDLKQPVTNVSWFAANAYCA
      70      80      90      100     110     120

      130     140     150     160     170     180
m525.pep  AQGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCRRRTERPARCRXKAARTTGA
a525      AQGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCGWRPERPARCRQXVARTTGA
      130     140     150     160     170     180

m525.pep  FMICTGX
          |||||
a525      FMICTVX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1495>:

```
g525-1.seq
  1 ATGAAGTACG TCCGGTTATT TTTCCTCGGC ACGGCACTCG CCGGCACCTCA
 51 AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TSCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAGGCA GATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGAATTGA AACAGCCGGT TACCAATATT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCGCGC GACCATCGAC GAATGGGAAT
401 TTGCGCGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAGGCCCT
501 GCACGATGTC GGCAAAGACC GCCCGAATA CTGGGGTGT TATGATATGC
551 ACGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTGC AGCGCGGCAT CTGTCGGGGC
651 GAGCGACTCG TCCAACTATG CCGCCTTCCT CCGCTACGGC ATCGGCACCA
701 GCCTGCAATC CAAATACGTC CTGCACAAC TGGGCTTCCG CTGCGCAAGC
751 CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1496; ORF 525-1.ng>:

```
g525-1.pep
  1 MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
101 GELKQPVTNI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGRRKGLHDV GKDRPNYWGV YDMHGLIEWE TEFNSLSLLS
201 SGNANAQMFC SGASVGSASD SNYAAFLRYG IRTSLQSKYV LHNLFRCAS
251 R*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1497>:

```
m525-1.seq
  1 ATGAAGTATG TCCGGTTATT TTTCCTCGGC GCGGCACTCG CCGGCACTCA
 51 AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
```


m525-1.pep

m525-1/q525-1 97.6% identity in 251 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1499>:

a525-1.seq

1	ATGAAGTTTA	CCCGGTTACT	CTTTCTCTGT	GCGGCACTCG	CCGGCACTCA
51	AGCGCGAGCT	GCCGAATGCG	TTCAAATCGA	AGGCGCGAGC	TACCGCCCGC
101	TTTATCTGAA	AAAAGATACC	GGCCTGATTA	AAGTCAAACG	TTGCAAACGT
151	GATAAATATC	CCGTTACCAA	TGCCGAGTTT	GCGGAATTGT	TCAACAGCCA
201	CCCCCAATGG	CAAAAAGGCA	GGATCGGTTT	CAAAACGGCA	GAACCCCGTT
251	ACCTGAAGCA	TTGATGTAAA	ACCGCGAGCC	GCAGCTATGC	CCCGAAGCGC
301	GGCGATTTTA	AACAACCGGT	AACCAATGTT	TCCTTGGTTG	CCGCGCAACG
351	CTATTGCGCG	GCAACAAGCA	AACGCGTGCC	GACCATTTGAC	GAATGGGAAT
401	TTGCCGGACT	TGCTCTCGCC	ACGCAGAAAA	ACGGCTCAAA	CGAACCCGGC
451	TACAACCGCA	CTATTCTCGA	CTGGTATGCG	GATGGCGACC	GGAAGAGACT
501	GCACGATATG	GGCAAAGGTC	CGCGGAATGC	CTGGGGCGTT	TATGATATGC
551	ACGGTCTGAT	TTGGGAATGG	ACGGAAGATT	TCAACAGCAG	CCTGCTTTCT
601	TCCGGCAATG	CCAACGCGCA	AATGTTTTGC	AGCGCGCGGT	CTATCGGGTC
651	GAGCGACTCG	TCCAACATG	CGCCTTTCC	TCGCTACGGC	ATCCGACCA
701	CGCTGCAATC	CAAATATGTC	TTGCACAAC	TGGGCTTCCG	TTGCACAAGC
751	CGATAA				

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This corresponds to the amino acid sequence <SEQ ID 1500; ORF 525-1.a>:

a525-1.pep

```

1  MKFTRLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKDT GLIKVKPFL
51  DKY?VTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GDLKOPVTNV SWFAANAYCA AOGKRLPTID EWEFAGLASA TOKNGSNEPG
151 YNRTILDWYA DGDRLDHDV GKGRPNYWG VYDMHGLIEWE TEDFNSLLS
201 SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLFGRCTS
251 R*
```

m525-1/a525-1 97.2% identity in 251 aa overlap

	10	20	30	40	50	60
m525-1.pep	MKYVRLFFLGAALACTQAAA	AEMVQIEGGSYRPLYLKDTGLIKVKPFLDKYPVTNAEF				
a525-1						
	10	20	30	40	50	60
	70	80	90	100	110	120
m525-1.pep	AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVTNVSWFAANAYCA					
a525-1						
	70	80	90	100	110	120
	130	140	150	160	170	180
m525-1.pep	AQGKRLPTIDWEFAGLASATQKNGSNEPGYNRTILDWYADGGRKGLHDVGKGRPNYWG					
a525-1						
	130	140	150	160	170	180
	190	200	210	220	230	240
m525-1.pep	YDMHGLIEWETEDFNSLLSSGNANAQMFCSGASIGSSDSSNYAAFLRYGIRTSLSQSKYV					
a525-1						
	190	200	210	220	230	240
	250					
m525-1.pep	LHNLFGRCTSRX					
a525-1						
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1501>:

g527.seq

```

1  atgggttttac cagtctcctt ttttcagcct gtccagttgg cggcgggtcgc
51  gcttggtcgg tctgcccgtcg ggatgggccc aagtgatgcg gctgaattgg
101 tcgagctggt tgcactcttc cctcaatgct gccgttttcg cgtcttcttc
151 atacagaagc cgcgcctcgg gtgcccggcg gcgttggtgg ttcaaacctt
201 taaccttgat tttatgggga agggaattga gcgtcaggtc gataatatcg
251 ccgatgtcta tgggttttact gtttttgact ttcgagccgt ttacttgaac
301 cctaccagcgt tcgatatgct tttgcgcaag ggaacgggtc ttgaaaaaac
351 gtgccgcccc aagccatttg tccagccgca tggcgggaaga atcgtgcttg
401 tctttcatatc gatatttgtt gaaataattg aatttgtttc gagtttagca
451 taa
```

This corresponds to the amino acid sequence <SEQ ID 1502; ORF 527.ng>:

g527.pep

```

1  MVLPVSFQFP VLAAVALGR SAVGMGSSDA AELVELFALF PQCCRFRVFF
51  IQKPRLGCRALVVQTFNLD FMGKGIERQV DNIADVYGFT VDFRAVYLN
101 PTQFDMLLRK GTGLEKTRCP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1503>:

m527.seq

```

1  ATGGTITTTAC CAGTCTCCIT TTTTCAGCCT GTCCAGTTGG CGGCGGTTCGC
51  GCTTGGTTCG TCTGCCGTCTG GCATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TGCGCTCTTC CCTCAATGTT GCCGTWTCG CGTCTCTTC
151 ATACAGAAGC CGGCYTCGG ATGCCGGCG CCGTTGGTGG TTCAAACCTT
```

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```

201 TAACCKTGAT TTTATAGGGA AGGG.AATTk AgCkTCaGty GrTwATaTCG
251 CsGATGTmTA TGGTTTTACT GTTTTIGACC TTCGAGCCGT TTACTTGAAC
301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
351 GTGCCGCCCA AAGCCATTTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
401 TCTTTCATAC GATTTTGTTC GAAATAATTG AATTTGTTTC CAGTTTAGCA
451 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1504; ORF 527>:

m527.pep

```

1 MVLPSVFFQP VLAAVALGR SAVGIGGSDA AELVELFALF PQCCRVRVLF
51 IQKPRXGCRA ALVVQTFNND FIGKXNXASV XXIADVYGFT VFDLRAVYLN
101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 527 shows 90.0% identity over a 150 aa overlap with a predicted ORF (ORF 527.ng) from *N. gonorrhoeae*:

m527/g527

	10	20	30	40	50	60
m527.pep	MVLPSVFFQPVLAAVALGRSAVGIGGSDAAELVELFALFPQCCRVRVLFIQKPRXGCRA					
	: : : : :					
g527	MVLPSVFFQPVLAAVALGRSAVGMGGSDAAELVELFALFPQCCRFRVFFIIQKPRLGCR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m527.pep	ALVVQTFNNDFIGKXNXASVXXIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
	: : : : :					
g527	ALVVQTFNLDPMGKIERQVDNIADVYGFTVFDLRAVYLNPTQFDMLLRKGTGLEKTCRP					
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHGGRIVLVFHTILFEIIEFVSSLA					
	: : : : :					
g527	KPFVQPHGGRIVLVFHTILFEIIEFVSSLA					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1505>:

a527.seq

```

1 ATGTTTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTGCG
51 GCTTGGTCGG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TCGCTCTTTC CCTCAATGTT GCCGTTTTCG CGTCCTCTTC
151 ATACAGAAGC CGCGCCTCGG ATGCCGGGCG CGCTTGGTGG TTCAAACCTT
201 TAACCTTGAT TTTATAGGGA AGGGAATTGA GCGTCAGGTC GATAATATCG
251 CCGATGTCTA TGGTTTTACT GTTTTIGACC TTCGAGCCGT TTACTTGAAC
301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
351 GTGCCGCCCA AAGCCATTTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
401 TCTTTCATAC GATTTTGTTC GAAATAATTG AATTTGTTTC GAGTTTAGCA
451 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1506; ORF 527.a>:

a527.pep

```

1 MVLPSVFFQP VLAAVALGR SAVGIGGSDA AELVELFALF PQCCRFRVLF
51 IQKPRLGCRALVVQTFNLD FIGKIERQV DNIADVYGFT VFDLRAVYLN
101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

m527/a527 93.3% identity in 150 aa overlap

	10	20	30	40	50	60
m527.pep	MVLPSVFFQPVLAAVALGRSAVGIGGSDAAELVELFALFPQCCRVRVLFIQKPRXGCRA					
	: : : : :					
a527	MVLPSVFFQPVLAAVALGRSAVGIGGSDAAELVELFALFPQCCRFRVLFIIQKPRLGCR					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m527.pep	ALVVQTFN	XDFIGKXN	XASVXXI	ADVYGFTV	FDLRAVYL	NPTQFDVLLR
			:			
a527	ALVVQTFN	LDFIGKGI	ERQVDNI	ADVYGFTV	FDLRAVYL	NPTQFDVLLR
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHG	GRIVLVFH	TILFEIIE	FVSSLAX		
a527	KPFVQPHG	GRIVLVFH	TILFEIIE	FVSSLAX		
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1507>:

```

g528.seq
1  atggaattc gggtaataaa atatacggca acggtcgcgt tgtttgcatt
51  tacggttgca ggctgccggc tggcggggtg gtatgagtgt ttgtccttgt
101 ccggtctggtg taagccgaga aaacctgccg ccatacgattt ttgggatatt
151 ggccgagaga gtccgctgtc tttagaggac tacgagatac cgctttcaga
201 cggcaatcgt tccgtcaggg caaacgaata tgaatccgcg caaaaatctt
251 acttttatag gaaaataggg aagtttgaag cctgcgggtt ggattggcgt
301 acgcgtgacg gcaaaccttt gggtgagagg ttcaaacagg aaggtttcga
351 ctgtttgga aagcagggtt tgcggcgcaa cggcctgtcc gagcgcgtcc
401 gatggttaa

```

This corresponds to the amino acid sequence <SEQ ID 1508; ORF 528.ng>:

```

g528.pep
1  MEIRVIKYTA TAALFAFTVA GCRLAGWYEC LSLSGWCKPR KPAAIDFWDI
51  GGESPLSLED YEIPLSDGNR SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLVER FKQGGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1509>:

```

m528.seq (partial)
1  ATGGAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51  TACGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGTGTGTG TAAGCCGAGA AAACCGGCTG CCATCGATT TTTGGGATATT
151 GGCGGCGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATAGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG C.TGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTTGA
351 CTGCTTGGAA AAG....

```

This corresponds to the amino acid sequence <SEQ ID 1510; ORF 528>:

```

m528.pep (partial)
1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51  GGESPPSLGD YEIPLSDGNS SVRANEYESA QKSYFYRKIG KFEXCGLDWR
101 TRDGKPLIET FKQGGFDCLE K....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 528 shows 89.3% identity over a 121 aa overlap with a predicted ORF (ORF 528.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m528.pep	MEIRAIKYT	AMAALLAFT	VAGCRLAG	WYECSSLT	GWCKPRKP	AAIDFWDIG
g528	MEIRVIKYT	AATAALFA	FTVAGCRL	AGWYEC	LSL	SGWCKPRKP
	10	20	30	40	50	60
	70	80	90	100	110	120
m528.pep	YEIPLSDG	NSSVRANE	YESAQKSY	FYRKIGK	FEACGLD	WRTRDGKPL
g528	YEIPLSDG	NRSVRANE	YESAQKSY	FYRKIGK	FEACGLD	WRTRDGKPL
	70	80	90	100	110	120

a528.seq

```
1 ATGGAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51 TACGTTGCA GGCTGCCGGT TGGCAGGTG GTATAGTGT TCGTCCCTGT
101 CCGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATT TTGGGATATT
151 GCGCGCGAGA GTCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTTACA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTTGA
351 TTGTTTGAAA AAGCAGGGGT TCGCGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA
```

```
a528.pep
1  MEIRAIKYTA MAALLAFTVA GCLRGWYEC SLSGWCKPR KPAADFWDI
51  GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKOEGFDCLK KOGLERNGLS ERVRW*
```

	10	20	30	40	50	60
m528.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAIDFWDIGGESPPSLGD					
	:					
a528	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAIDFWDIGGESPPSLED					
	10	20	30	40	50	60
	70	80	90	100	110	120
m528.pep	YEIPLSDGNSSVRANEYESAQQSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE					
	:					
a528	YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLE					
	70	80	90	100	110	120

m528.pep K
 |
a528 KQGLRRNGLSERVRWX
 130

g528-1.seq

1	ATGGA AATTC	GGGTAATAAA	ATATACGGCA	ACGGCTGCGT	TGTTTGCAAT
51	TACGGTTCGA	TGGTGCCGGC	TGGCGGGGTG	GTATGAGTTT	TCGTCCTTGT
101	CCGGCTGGTG	TAGGCCGAGA	AAACCTGCCG	CCATCGATT	TGGGATATT
151	GGCGGCGAGA	GTCGCTGTCT	TTTAGAGATC	TACGAGATAC	CGCTTTCAGA
201	CGGCAATCGT	TCCGTCAGGG	CAACAGAATA	TGAATCCGCG	CAAAAATCTT
251	ACTTTTATAG	AAAAATAGGG	AAAGTTGAAG	CCTCGGGGTT	GGATTGGCGT
301	ACGCGTGACG	GCAACCTTTT	GTTGAGAGG	TTCAAACAGG	AAGGTTTCGA
351	CTGTTTGGA	AAGCAGGGGT	TGCGGCGCAA	CGGCCTGTCC	GAGCGCGTCC
401	GATGGTAA				

```
g528-1.pep
1  MEIRVIKYTA  TAALFAFTVA  GCRLAGWYEC  SSLSGWCKPR  KPAALDFWDI
51 GGESPLSLED  YEIPLSDGNR  SVRANEYESA  QKSIFYRKIG  KDFACGLDWR
101 TRDGKPLVER  FKQEGFDCL  KQGLRRNGLS  ERVRW*
```

m528-1.seq
1 ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT

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```

51  TACSGTGTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATTT TTGGGATATT
151 GGCSCGCGAGA GTCCGCCGTC TTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTTGA
351 CTGCTTGGAA AAGCAGGGGT TGCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1516; ORF 528-1>:

m528-1.pep..

```

1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51  GGESPPSLGD YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDNR
101 TRDGKPLIET FKQGGFDCLE KQGLRRNGLS ERVRW*

```

g528-1/m528-1 92.6% identity in 135 aa overlap

	10	20	30	40	50	60
g528-1.pep	MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPLSLED					
m528-1	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
g528-1.pep	YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE					
m528-1	YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE					
	70	80	90	100	110	120
	130					
g528-1.pep	KQGLRRNGLSERVRWX					
m528-1	KQGLRRNGLSERVRWX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1517>:

a528-1.seq

```

1  ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT
51  TACGGTGTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GGCSCGCGAGA GTCCGCCGTC TTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTGA
351 TTGTTTGAAG AAGCAGGGGT TGCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1518; ORF 528-1.a>:

a528-1.pep

```

1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51  GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDNR
101 TRDGKPLIET FKQEGFCLK KQGLRRNGLS ERVRW*

```

a528-1/m528-1 97.0% identity in 135 aa overlap

	10	20	30	40	50	60
a528-1.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPPSLED					
m528-1	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
a528-1.pep	YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFCLK					
m528-1	YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE					
	70	80	90	100	110	120
	130					
a528-1.pep	KQGLRRNGLSERVRWX					
m528-1	KQGLRRNGLSERVRWX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1519>:

```
g529.seq (partial)
1  atgacccata tcaaacccgt cattgccgcg ctgcactca tcgggcttgc
51  cgcctgctcc ggcagcaaaa ccgaacagcc caagctcgac taccaaagcc
101 ggtcgaccgg cctgatcaaa ctggaagtcc cgcctgattt gaacaacccc
151 gaccaaggca acctctaccg cctgcctgcc ggttcgggag ccgtccgcgc
201 cggggatttg gaaaaacgcc gcacaccgcg cgtccaacag ccagcggatg
251 ccggaagtat tgaaaagcgt caaaggcgct cgcttcgagc ggcgacggca
301 gccaacgcct ggcttgctgt tgacggcaaa tcccccgccg aaatctccgc
351 cgctttctg.
```

This corresponds to the amino acid sequence <SEQ ID 1520; ORF 529.ng>:

```
g529.pep (partial)
1  MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
51  DQGNLYRLPA GSGAVRAGDL EKRRTPAVQQ PADAGSIEKR QRRPLRAATA
101 ANAWLVVDGK SPAEISAAF.
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1521>:

```
m529.seq
1  ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGACTCA TCGGGCTTGC
51  CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTCGCACCG CCTGATCAAA CTTGAAGTCC CACCTGATTG GAACAACCCC
151 GACCAAGGCA ACCTCTACCG CCTGCCTGCC GGTTCGGGCG CCGTCCGCGC
201 CAGCGATTTC GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT GAAAAGCGTC AAAGGTGTCC GCCTCGAGCG CGACGGCAGC
301 CAACGCTGGC TCGTTGTCTGA CGGCAAGTCT CCTGCCGAAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAAA TCCGAAGAAC
401 CCGCCATCGG ACAAATGGAA ACCGAGTGGG CGGAAAACCG CGCCAAAATC
451 CCCCAGACA GCTTGCGCCG CCTCTTCGAC AAAGTCGGCT TGGGCGGCAT
501 CTACTCCACC GGCAGCGCGG ACAAATTCAT CGTCCGTATC GAACAGGGCA
551 AAAACGGCGT TTCGACATC TTCTTCGCCC ACAAAGCCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCCTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTATGCAA TATTGGGCG
701 TTGACGGACA GCAGGCGGAA AACGCATCGG CAAAAAACC TACCCTTCCC
751 GCCGCCAACG AATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
801 CGACTACGGC AGAAACTGCG GCGCACCGT GCTCGCCCTC GACCGCATCG
851 GGCTGACCGT CGTCGGTCAA AACACCGAAC GCCACGCCTT CCTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAATTACC GAACAAAAC CCGGCCTGTT
951 CAAACGCCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCAGAA CCTGTCGCCA ACGGCTCGCG CATCGTCCTG
1051 CTCAACAAAG ACGGCAGCGC ATATGCCGCG AAAGACGCAT CGCATTATT
1101 GGGCAAATC CATTCCGAAC TCGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1522; ORF 529>:

```
m529.pep
1  MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
51  DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PADAELVLSV KGVRLERDGS
101 QRWLVVDGKS PAEIWPLLKA FWQENGFDIK SEEPALGQME TEWAENRAKI
151 PQDSLRLRLFD KVLGGIYST GERDKFIVRI EQKNGVSDI PFAHKAMKEV
201 YGGKDKDTTV WQPSPSDPNL EAAFLTRFMQ YLGVDGQQAE NASAKKPTLP
251 AANEMARIEG KSLIVFGDYG RNWRRTVLAL DRIGLTVVGQ NTERHAFIVQ
301 KAPNESNAVT EQKPLFKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
351 LNKDGSAYAG KDASALLGKL HSELR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 529 shows 83.5% identity over a 115 aa overlap with a predicted ORF (ORF 529.ng) from *N. gonorrhoeae*:

g529/m529

```

          10      20      30      40      50      60
g529.pep  MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA
```

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```

|||||
m529      MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPDQGNLYRLPA
              10      20      30      40      50      60

              70      80      90      100     110     120
g529. pep  GSGAVRAGDLEKRRTPAVQQPADAGSIEKRQRRLRAATAANAWLVVDGKSPAEISAAFX
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m529      GSGAVRASDLEKRRTPAVQQPADA EVLKS VKGVRLER-DGSQRWLVDGKSPAEIWPLLK
              70      80      90      100     110

m529      AFWQENGFDIKSEEP AIGQMETEWAENRAKIPQDSLRLR LFDKVGLGGIYSTGERDKFIVR
120      130      140      150      160      170

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1523>:

```

a529. seq
1  ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
51  CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTTCGCACCG CCTGATCAAA CTCGAAGTCC CACCTGATT GAACAACCCC
151 GACCAAGGCA ACCTCTACCG CCTGCCTGCC GGTTCGGGCG CCGTCCGCGC
201 CAGCGATTTG GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT GAAAAGCGTC AAAGGTGTCC GCCTCGAGCG CGACGGCAGC
301 CAACGCTGGC TCGTTGTCGA CGGCAAGTCT CATGCCGAAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAAA TCCGAAGAAC
401 CCGCCATCGG ACAATGGAA ACCGAGTGGG CGGAAAACCG TGCCAAAATC
451 CCCCAGACA GCTTGCGCCG CCTATTCGAC ACAGTCGGTT TGGGCGGCAT
501 CTACTCCACC GGCAGCGCGG ACAATTTCAT CGTCGTATC GAACAGGGCA
551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAGGCCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCGTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTGGGCG
701 TTGACGACA GCAGCGGAA AACGCATCGG CAAAAAACC TACCCTTCCC
751 CCGCCCAACG AATGGCGCG TATCGAAGCG AAAAGCCTGA TTGTCTTTGG
801 CGACTACGGC AGAACTGGC GCGCACCGC GCTCGCCCTC GACCGCATCG
851 GGCTGACCGT CGTCGGTCAA AACACCGAAC GCCACGCTTT CTTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAGTTACC GAACAAAAAC CCGGCCTGTT
951 CAACGCCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCCGAG CCTGTCGCCA ACGGCTCGCG CATCGTCCTG
1051 CTCAACAAAG ACGGCAGCGC ATATGCCGGC AAAGACGCAT CCGCATTATT
1101 GGGCAAATC CATTCCGAAC TGC GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1524; ORF 529.a>:

```

a529. pep
1  MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNPN
51  DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PADA EVLKS VKGVRLERDGS
101 QRWLVVDGKS HAEIWPLLKA FWQENGFDIK SEEP AIGQME TEWAENRAKI
151 PQDSLRLRFD TVGLGGIYST GERDKFIVRI EQGKNGVSDI FFAHKAMKEV
201 YGGDKDQTTV WQPSDPNLE EAAFLTRFMQ YLGVDGQQA E NASAKKPTLP
251 AANEMARIEG KSLIVFGDYG RNWRRTALAL DRIGLTVVGQ NTERHAFIVQ
301 KAPNESNAVT EQKPLFKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
351 LNKDGSAYAG KDASALLGKL HSELRL*

```

m529/a529 99.2% identity in 375 aa overlap

```

              10      20      30      40      50      60
m529. pep  MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPDQGNLYRLPA
|||||
a529      MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPDQGNLYRLPA
              10      20      30      40      50      60

              70      80      90      100     110     120
m529. pep  GSGAVRASDLEKRRTPAVQQPADA EVLKS VKGVRLERDGSQRWLVDGKSPAEIWPLLKA
|||||
a529      GSGAVRASDLEKRRTPAVQQPADA EVLKS VKGVRLERDGSQRWLVDGKSHAEIWPLLKA
              70      80      90      100     110     120

              130     140     150     160     170     180

```


800

m529. pep	FWQENGFDIKSEEP	PAIGQMETEWAEN	RAKIPQDSLRR	LFDKVLGGIYST	GERDKFIVRI
a529	FWQENGFDIKSEEP	PAIGQMETEWAEN	RAKIPQDSLRR	LFDTVLGGIYST	GERDKFIVRI
	130	140	150	160	170 180
m529. pep	EQGKNGVSDIFFA	HKAMKEVYGGKDK	DTTVWQPS	SDPNLEAAFLTR	FMQYLGVDGQQA
a529	EQGKNGVSDIFFA	HKAMKEVYGGKDK	DTTVWQPS	SDPNLEAAFLTR	FMQYLGVDGQQA
	190	200	210	220	230 240
m529. pep	NASAKKPTLPAAN	MARIEGKSLIVFG	DYGRNWRRTV	LALDRIGLTVV	GQNTERRHAFVQ
a529	NASAKKPTLPAAN	MARIEGKSLIVFG	DYGRNWRRTA	LALDRIGLTVV	GQNTERRHAFVQ
	250	260	270	280	290 300
m529. pep	KAPNESNAVTEQK	PGLFKRLLGKGK	AEKPAEQPELIV	YAEPVANGSRIV	LLNKDGSAYAG
a529	KAPNESNAVTEQK	PGLFKRLLGKGK	AEKPAEQPELIV	YAEPVANGSRIV	LLNKDGSAYAG
	310	320	330	340	350 360
m529. pep	KDASALLGKLHSE	LRX			
a529	KDASALLGKLHSE	LRX			
	370				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1525>:

g530. seq
 1 atgagtgcga gcgcggcaat gacgggtttg atatgggtca tcgtgtcatc
 51 ctgtgtgatg gatattaaag tgtttgtcat gttatgccgt ccgaacgggt
 101 cagacggcat ggctatatatt aaagtgtgcc tgaggcttc agggcggcgc
 151 ggacttttgc ctgtccgcct tccgtcagcg gaacgagcgg caggcgacg
 201 tgcggtccgc atccgcccga ggcgataacc gccatttcg gtgcggcggg
 251 actgggttcg cagaacatgg tgcgtaaat cggaatcagc cggtcgttga

This corresponds to the amino acid sequence <SEQ ID 1526; ORF 530.ng>:

g530. pep
 1 MSASAAMTGL IWVIVSSCVM DIKVFVMLCR PNGSDGMAIF KVVLRRLSGRR
 51 GLLPVRLPSA ERAAGARAVR IRPRRIPPIS VRRDWVRRTW CRKSESAGR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1527>:

m530. seq
 1 WTGAGTGCGA GCGCGGCAAT GACGGGTyTG ATATGGGTCA TCGTGTATC
 51 STGTGTGATG GATATTAAAG TGTyTGTGTC GWTATGCCGT CCGAACGGTT
 101 CGGACGGCAT GGmTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
 151 GGACTkTTGC WTGTCCGTTT yCCGTCAGCG GAACGAGCGG CAGGCGGACG
 201 TGCGGTTTCG ATCTGCCCAg GCGGATACC GCCCATTTTCG STGCGGCGGG
 251 GCTGGGTTTCG CAGAACATGG TGTCTGTAAT CGGAATCAGT CGGTCTGTGA

This corresponds to the amino acid sequence <SEQ ID 1528; ORF 530>:

m530. pep
 1 XSASAAMTGL IWVIVSSCVM DIKVXVAXCR PNGSDGMXIF KVVLRRLSGRR
 51 GLLXVRFPSA ERAAGGRAVR ICPGRIPPIS VRRGWVRRTW CRKSESVGR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 530 shows 88.8% identity over a 98 aa overlap with a predicted ORF (ORF 530.ng) from *N. gonorrhoeae*:

m530/g530

m530. pep	XSASAAMTGLIWVIVSSCVM	DIKVXVAXCRPNGSDGMXIF	KVVLRRLSGRRGLLXVRFPSA	60

g530	MSASAAMTGLIWIVVSSCVMDIKVFVMLCRPNGSDGMAIFKVVLRLLSGRRGLLPVRLPSA	60
	10 20 30 40 50 60	
m530.pep	ERAAGGRAVRICPGRIPIISVRRGWVRTWCRKSESVGR	99
	: : :	
a530	ERAAGARAVRIRPRRIPIISVRRDWVRTWCRKSESAGR	99

```
a530.seq
1  ATGAGTGCGA GCGCGGCAAT GACGGGTTTG ATATGGGTCA TCGTGTCA TC
51  CTGTGTGATG GATATTAAAG TGTTTGTTCG GTTAGCCGT CCGAACGGTT
101 CCGACGGCAT GGCTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGACTTTTTC CTGTCCGCCT TCGGTCAGCG GAACGACGGC CAGGCGGAGG
201 TGCGGTTTCG ATCTGCCCAAT GTCGGATAAC GCCCATTCG GTGCGGCGGG
251 SCTGGGTTTC CAGAACATGG TGTCGTAAAT CGGAATCAGC CGGTGTTTGA
```

a530.pep
1. MSASAAMTGL IWVIVSSCVM DIKVFVALCR PNGSDGMAIF KVVLRLSGR
51. GLLPVRLPSA ERAAGGRAVR ICPGRIIPIS VRRGWVRRTW CRKSESAGR*

	10	20	30	40	50	60
m530.pep	XSASAAMTGLIWVIVSSCVM	DIKVXVAXCRPN	SGDMXIFKVVLRLSGRRGLL	XVRFPSA		
a530	MSASAAMTGLIWVIVSSCVM	DIKFVVALCRPN	SGDMAIFKVVLRLSGRRGLL	FPVRLPSA		
	10	20	30	40	50	60
	70	80	90	100		
m530.pep	ERAAGGRAVRI	CPGRIPPISVRRGW	VRRTWCRKSESVGRX			
a530	ERAAGGRAVRI	CPGRIPPISVRRGW	VRRTWCRKSESAGR			
	70	80	90	100		

```

g531.seq
1  ATGACCGCCC TACTCGTCAT CCTCGCCCTC GCCCTGATAG CCGTCGGCAC
51  GGCAGGCATC GTCTATCCCG CCCTGCCCGG CTTGGCATTG ATGTTTGCCG
101 GAACATGGCT GCTTGCTAT  GCGGGCGGCT ATCAAATCTA CGGCGCAGGC
151 ATCTTGTGGA CGGTCGGACT CATCAGCCTT GCGCGCATAC TGCGCGACTA
201 TATGGCAGGC ATGTTGGGGG TAAAAATACAC TGGGGCAGGC AAAACTGCCG
251 TCCGAGGTGC ATTGGCCGGC AGCATCATCG GCATATTTTT CTCCTTCCC
301 GGAATAATAC TCGGCCCTT TATCGGCGCG GCGCAGGCG AACTGATCGA
351 TCGGCACAAT AGCTTTCAGG CAGGTAAAGC GGGCTGGGCT ACGCTGTTGG
401 GGTATTGTCG TCAGCAGGCG TTCAAAATCG GTGTGCGCGT ATCCATCTTG
451 TTATCTCTGT TGGTGAATA CATGCATAC CTGTTTTAA

```

g531.ppe

1	MTALLVILAL	ALIAVGTAGI	VYPALPGLAL	MFAGTWLLAY	AGGYQIYGAG
51	ILWTVGLISL	GGILADYMag	MLGVKYTGAG	KLAVRGALAG	SIIGIFFSLP
101	<u>GLILGPFIGA</u>	AAGELIDRRN	MLQAGKAGLG	TLLGLVVGTA	<u>FKIGCAVSIL</u>
151	FILLVKYIAY	LF			

```
m531.seq
  1  ATGACCGTAC  TGACCGTCAT  CCTCGCCCTC  GCCCTGATAG  CCGTCGGCAC
51  GGCCGGGCAT  GTTTaCCCCG  CCTGCGCCGG  ATTGGCATTG  ATGCTTTGCCG
101 GAACATGGCT  GCTTGCCAT  CCGCGCGGCT  ACCAAATCTA  CGCGCGGGC
151 GTTTTGTTGA  CGGTCGGACT  CATCAGCCTT  GCCGGCATA  TGGCGGACTA
201 TGTGGCAGGC  ATATGGGGGA  CAAATATAC  CGGAGCGGGC  AAGCTCCGC
251 TTCCGCGCGC  ATTGGCCGCG  AGCATCATCG  GCATATTTT  CTCCCTTCCC
301 GGACTAATAC  TCGGTCCCTT  TATCGCGCG  CGGCGAGCG  AACTGATCGA
```

in531.pcp

1 MTVLTVILAL ALIavgTAGI VYPALPGLAL MfAGTWLLAY AGGYQIYGAG
51 VLWTVGLISL AGILADYVAG IWGTYKTGAG KLAVRGALAG SIIGIFFSLP
101 GLILGPFIGA AAGEI.TERRN MLQAGKAGLG TLGLLVGTA FKIGCAVSIL
151 FILLVKYIAY LF*

Homology with a predicted ORF from *N. gonorrhoeae*

from *N. gonorrhoeae*:

m531/q531

	10	20	30	40	50	60							
m531.pep	MTVLT	VILAL	ALIAV	GTAGI	VYPAL	PGLAL	MFAGT	WLLAY	AGGYQ	IYGAG	VLWTV	GLISL	
	:												
g531	MTALL	VILAL	ALIAV	GTAGI	VYPAL	PGLAL	MFAGT	WLLAY	AGGYQ	IYGAG	ILWTV	GLISL	
	10	20	30	40	50	60							
	70	80	90	100	110	120							
m531.pep	AGILAD	YVAGI	WGT	KYTG	AGKLA	VRGAL	AGSI	IIGIF	FSLP	GLIL	GPFIG	AAAGEL	IERN
	:	:	:	:	:	:	:	:	:	:	:	:	:
g531	GGILAD	YMGML	GVKYT	GAGKL	AVRGAL	AGSI	IIGIF	FSLP	GLIL	GPFIG	AAAGEL	IDRRN	
	:	:	:	:	:	:	:	:	:	:	:	:	:
	70	80	90	100	110	120							
	130	140	150	160									
m531.pep	MLQAG	KAGL	GTL	LLGL	VVGTA	FKIG	CAV	SILF	ILLV	KYI	AYLF		
	:	:	:	:	:	:	:	:	:	:	:		
g531	MLQAG	KAGL	GTL	LLGL	VVGTA	FKIG	CAV	SILF	ILLV	KYI	AYLF		
	:	:	:	:	:	:	:	:	:	:	:		
	130	140	150	160									

a531.seq

1	ATGACCGCCT	TGCTCGTCAT	CCTCGCCCTC	GCCTGATAG	CCGCCGGTAC
51	GGCGGGCATC	GTTTACCCCG	CCCTGCCCCG	ATTGGCATTG	ATGTTTGCCG
101	GAACCTGGCT	GCTCGCCTAC	TCCGGCGAGT	ACCAATCTA	CGCGCGGGGC
151	GTTTGTGTGA	CGGTGGACT	CATCAGCCCT	CGCGGCATA	TGGCGGACTA
201	TGTGGCAGCG	ATATGGGGGA	CAAAATATAC	CGGAGCGGAG	CGGCTCGCCG
251	TTCGCGGCGC	ATTGGCGGGC	AGCATCATCG	GCATATTTTT	CTCCCTTCCC
301	GGACTAATAC	TCGGTCCCTT	TATCGGCGCG	CGGCAGGCG	AACTGATCGA
351	ACGGCGCAAT	ATGCTTCAGG	CAGTAAAGC	GGGCTTGGGT	ACGCTGTTGG
401	GGCTTATCGT	CGGTACGGCG	TTCAAATACG	GCTGCGCCGT	ATCCATCTTG
451	TTTATCCCTGT	TGGTGAAATA	CATCGCCTAC	CTGTTTTTAA	

a531.pep

1 MTALLVILAL ALIAAGTAGI VYPALPGLAL MFA GTWLLAY SGGYQIYGAG
51 VLWTVGLISL AGILADYVAG IWGTKYTGA G KLAVRGALAG SIIGIFFSLP
101 GLILGPFFIGA AGELIERN MLQAGKAGLG TLLGLIVGTA FKIGCAVSIL
151 FILLVKYIAY LF*

	10	20	30	40	50	60
m531.pep	MTVLT	VILALALIA	AVGTAGIV	YPALPGLALM	FAGTWLLAY	AGGYQIYGAGVLWTVGLISL
	:		:			
a531	MTALLV	LALALIA	AAGTAGIV	YPALPGLALM	FAGTWLLAY	SGGYQIYGAGVLWTVGLISL
	10	20	30	40	50	60
	70	80	90	100	110	120
m531.pep	AGILADY	VAGI	WGTKYT	GACKLAV	RGA	LAGSIIGIFFSLPGLILGPF
						IGAAAGELIERRR

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|||||
a531  AGILADYVAGIWGTYKGTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIERN
      70      80      90      100     110     120

      130     140     150     160
m531.p  MLQAGKAGLGTLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
      |||||
a531    MLQAGKAGLGTLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
      130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1537>:

g532.seq (partial)

```

1  atggctgaaa caatgaaaa acagggcgat tcgcctgatt tgggtgtacgg
51  ttgggaagac aggcgcgctg tcggtaatgc gctcttgagc gcggttaccc
101 atcttttggc gattttcgtg ccgatgatta cgcccgcgct gattgtgggc
151 ggcgcgctgg aattgccggt ggagatgacg gcgtatctgg tgatcgatggc
201 gatggttgctg tcgggtgctg gcacttattt gcaggtaaac cgcttcgggt
251 cggtcggtgc ggggatgctg tccatccagc gttaccgtca tgattgcgct
301 cggcgcgggg atgaaagagg gcggtttgag ...

```

This corresponds to the amino acid sequence <SEQ ID 1538; ORF 532.ng>:

g532.pep (partial)

```

1  MAETMKKQAD SPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMMVA SGVGTYLQVN RFGSVGSGML SIQYRHDCA
101  RRGDERGRFE ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1539>:

m532.seq

```

1  ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTTGGAAGAC AGGCCGCGGT TCGGTAATGC GCTCTTGAGC GCGGTACCC
101  ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151  GCGCGCGCTG AATTGCCGCT GGAGATGACG GCGTATCTCG TGTCGATGGC
201  GATGGTTGCG TCGGGTGTG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251  CGGTCGGTTC GGGGATGCTG TCCATCCAGT CCGTGAATTT TTCGTTCTGTT
301  ACCGTGATGA TTGCGCTGGG CGCGGGGATG AAAGAGGCGG GTTTGACTAA
351  GGATGCGATG ATTTGACGCG TCTTGGGCGT ATCGTTTGTC GGCGCGTTTT
401  TGGTGTGTTT CTCGGCGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
451  CCGACGCTCA GCGGCGTGGT CGTGATGCTC ATTGGTTTGA GTTTGGTACA
501  CGTCGGCATT ACCGATTTCG GCGGCGGCTT CCGCGCGAAG GCGGACGGCA
551  CGTTCGGCTC GATGGAACAC TTGGGGCTGG CATCGCTGGT GTTGCTGATT
601  GTGTTGTTGT TCAACTGCAT GAAAAACCCG CTGTTGCGCA TGAGCGGCAT
651  TGCGGTCGGG CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701  TGGATTTTTC CGCGCTGCAA AACCTGCCGC TGGTTACGCT GCCCGTACCG
751  TTAAATACG GTTTTGCTTT CGACTGGCAC GCGTTTATTG TGGCGGGCGC
801  GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CCGCGATTTA ACCGCGACGG
851  CAATGGTGTC CGACCAGCCG ATTGAAGGCG AGGAATACAC CAAACGCCTG
901  CGCGGCGGCG TGTGCTGTA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
951  GGGTTCGCTG CCGCTGACGA CGTTTGCACA AAACAACGGC GTGATTCAGA
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCT CGTTGTGCGT CGCGCGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGTTTTT GATGTTGCGC TTAATGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGTCACG GCATCCGAG GCGCGAAGCG
1201 GTGATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTCG CGTTTGAGCC
1251 GGAAGTGTTC AAAAACTGC CCGTCTTGTT CCAAACTCT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTGTT TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1540; ORF 532>:

m532.pep

```

1  MSGQLKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSFV
101  TVMIALGAGM KEGGLTKDAM ISTLLGVSPV GAFLVCFSAW LLPYLKKVIT
151  PTVSGVVVML IGLSLVHVG I TDFGGGFGAK ADGTFGSMEN IGLASLVLLI

```

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201 VLVFNCKMNP LLRMSGIAVG LIAGYIVALEF LGKVDFSALQ NLPLVTLVPV
 251 FKYGFAPDWH AFIVAGAIFL LSVFEAVGDL TATAMVSDQP IEGEYTKRL
 301 RGGLADGLV SVIATAGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
 351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRREA
 401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNI.VI.PEDKT
 451 EAAVKFDTDH LEH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF532 shows 91.4% identity over a 93 aa overlap with a predicted ORF (ORF 532.ng) from *N. gonorrhoeae*:

g532/m532

	10	20	30	40	50	60
g532 . pep	MAETMKKQADSPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVGGALELPVEMT					
	: :					
m532	MSGQLGKGADAPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVGGALELPVEMT					
	10	20	30	40	50	60
	70	80	90	100	110	
g532 . pep	AYLVSMAMVASGVGTYLQVNRFGSVGSGMLS IQRYRHDCARRGDERGRFEX					
m532	AYLVSMAMVASGVGTYLQVNRFGVPVSGSGMLS IQSVNFSFVTVMIALGAGMKEGGLTKDAM					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1541>:

a532 . seq

```

1   ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTTGGAGGAT AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GGCGCGCTGG AATTGCCGGT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGTGTCG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CGGTCGGTTC GGGGATGCTG TCCATCCAGT CCGTGAATTT CTCGTTTCGT
301 ACCGTCATGA TTGCGCTCGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTTCGACG TCTTGGGCGT ATCGTTTGTC GGCGCGTTT
401 TGGTGTGTTT TTCGGCGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGTGTGGT GGTGATGCTG ATCGGCTTGA GTTTGGTACA
501 CGTCGGTATT ACCGATTTCG GCGGCGGCTT CGGCGCAAAG GCGGACGGCA
551 CGTTCGGCTC GATGGAACAC TTGGGGCTGG CATCGCTGGT GCTGCTGATT
601 GTGCTGGTGT TCAATTGCAT GAAAAACCCG CTGCTGCGGA TGAGCGGCAT
651 TCGGGTCGGT CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC GGCAC TGCAA AACCTGCCGC TGGTTACGCT GCCCGTACCG
751 TTAAATATG GTTTTGCTTT TGA CTGGCAC GCATTATTG TGGCGGGTGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATT TG ACGGCGACGG
851 CAATGGTGTC CGACCAGCCG ATTGAAGGCG AGGAATACAC CAAACGCTTG
901 CGCGGCGGCG TGTGGCGGGA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTTCGCTG CCGCTGACGA CGTTTGACA AAACAACGGC GTGATT CAGA
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATA TTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCT CGTTGTGCGA CGCGCGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTTT GATGTTCCGC TTGATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGCCACG GCATCCGCAG GCGCGAAGCG
1201 GTAATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTCG CGTTTGAGCC
1251 GGAAGTGTTT AAAAACC TGC CCGTCTTGTT CAAAAC TCT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTGG TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1542; ORF 532.a>:

a532 . pep

```

1   MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMAMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSFV

```

```

101 TVMIALGAGM KEGGLTKDAM ISTLLGVSVFV GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVMI IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI
201 VLVFNCKMNP LLRMSGIavg LIAGYIVALF LGKVDFSALQ NLPLVTLVPV
251 FKYGFADFVH AFIVAGAIFL LSVFEAVGDL TATAMVSDQP IEGEEYTKRL
301 RGGVLADGLV SVIATAGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRREA
401 VIAATSVGLG LGVAFEPFV KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
451 EAAVKFDTDH LEH*

```

m532/a532 100.0% identity in 463 aa overlap

	10	20	30	40	50	60
m532.pep	MSGQLGKGADAPDLVYGLEDPRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
a532	MSGQLGKGADAPDLVYGLEDPRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m532.pep	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM					
a532	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m532.pep	ISTLLGVSVFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMIIGLSLVHVGITDFGGGFGAK					
a532	ISTLLGVSVFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMIIGLSLVHVGITDFGGGFGAK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m532.pep	ADGTFGSMENLGLASLVLLIVLVFNCKMNP LLRMSGIavg LIAGYIVALFLGKVDFSALQ					
a532	ADGTFGSMENLGLASLVLLIVLVFNCKMNP LLRMSGIavg LIAGYIVALFLGKVDFSALQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
m532.pep	NLPLVTLVPVPFKYGFADFVHAFIVAGAI FLLSVFEAVGDLTATAMVSDQPIEGEEYTKRL					
a532	NLPLVTLVPVPFKYGFADFVHAFIVAGAI FLLSVFEAVGDLTATAMVSDQPIEGEEYTKRL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m532.pep	RGGVLADGLSVIATAGSLPLTTFAQNNGVIQMTGVASRHHVGKYIAVILVLLGLFPVVG					
a532	RGGVLADGLSVIATAGSLPLTTFAQNNGVIQMTGVASRHHVGKYIAVILVLLGLFPVVG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m532.pep	RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRREAVIAATSVGLGLGVAFEPFV					
a532	RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRREAVIAATSVGLGLGVAFEPFV					
	370	380	390	400	410	420
	430	440	450	460		
m532.pep	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX					
a532	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1543>:

g535.seq

```

1 atgccctttc ccggttttcag acaantattt gcttngtcct tgctacggtt
51 ttttgccgta ggtcggattc tcgaatccga catttccaac agcgggtttt
101 cggaaacgat aaacgcgtca aatgtttttt ttgtcggata cgaatatccg
151 gcctgcattt caaatttaca tcgcttccaa ttctgcaaac ttggtatcca
201 gttctttcac gccctgtttg ccgaagtga tggtcagtcg ggcggattcg
251 cctttgtctg cggcatcgat aatcacgccg gtgccgaatt tggcgtgacg
301 gacgttttgt ccgatgcgga agcctgcgta gggttcggc tgtttgaagt

```

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```

351 ccatgatgat tttgtcccggt tgtacgggtgg tttggcgcggt gttgcccgtag
401 ctgtcgaagg cgggttttttt gacggacagg tagtgcaata cttctggcgg
451 gatttcttcg acgaagcggg atgcgatgcc gaattgggtt tgtccgtgca
501 gcatgcgttg ctgtgccatg gtgatgtaga ggcgtttgctg ggcgcgggtg
551 atggcgacgt acatgaggcg gcgttcttct tcgagggcgc cgcgctcggc
601 aaggetcatt tcgctgggga aacgcccctc ttccataccg gtgaggaaga
651 cggcggtgaa ttccaagcct ttggcgcggt ggacgggtcat cagttggacg
701 gctttttcgc ctgcccctgc ttggttttcg ccggattcga gggcggcgtt
751 gctcaagaag gcgaggatgg ggaaggcggg atcgtctga

```

This corresponds to the amino acid sequence <SEQ ID 1544; ORF 535.ng>:

g535.pep

```

1 MPFPVFRQXF AXSLLRFFAV GRILESDISN SGFSETINAS NVFVGYEYEP
51 ACISNLHFRFQ FRKLGIQFFH ALFAEVDGQS GGFAFVCGID NHAGAEFGVT
101 DVLSDAEACV GLRLFEVIDD FVPLYGGLAR VAVAVEGGFF DGQVVQYFWR
151 DFFDEAGCDA ELGLSVQHALL LCHGDVEAFA GAGDGDVHEA AFFFEAAALG
201 KAHFAGETPL FHTGEEDGVE FQAFGGVDGH QLDGFFACPC LVFAGFEGGV
251 AQEGEDGEGG IV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1545>:

m535.seq

```

1 aTGCCCTTtC CCGTTTTcAG ACGGCCTTTT GCTTTGTCCT TACTtACGTT
51 TTTTGCCGTA AGTCAGATTC TTGTATCCGA CATTTCCAAC AGCGGTGTTT
101 CGGAAACAAT AGACGCGTCA AATGTTTTTG TCGGATACGA ATATCCGACC
151 TACATTTCAA ATTTACATCT CTTCCAATTT CGCAAACCTG GTGTCCAAC
201 CTTTCACGCC CTGTTTGCCG AAATTGATGG TCAGTCGGGC GGATTGCGCT
251 TTATCTGCGG CATCGATAAT CACGCCCGTG CCGAATTGG CGTGGCGGAC
301 GTTTTGTCGG ATACGGAAAC CTGCGTAGGT TTGGGGCTGT TTGTAGTCGT
351 CGATGATTTT ATCTTTGGAT GCGGCGGTTT GCGCGGTGTT GCCGTAACTG
401 TCGTAGGCAG GCTTTTTGAC GGACAGGTAG TGCAATACTT CGGGTGGGAT
451 CTCTTCGACG AAGCGGGAGA CGATGCCGAA TTGGGTTTGT CCGTGCAGCA
501 TCGCTTGTG CGCCATGGTG ATGTAGAGGC GTTTGCGGGC GCGGGTGATG
551 GCGACGTACA TGAGGCGGCG TTCTTCTTCG AGGCCCGCGC GTTCGGCAAG
601 GCTCATTTTC CTGGGGGAAGC GGCCTTCTTC CATGCGGGTG AGGAAGACGG
651 CGTTAAATTC CAAGCCTTTG GCGGCGTGGA CGGTCATGAG TTGGACGGCC
701 TTTTCGCCCTG CGCTGCCTG GTTTTCACCG GATTGAGGG CGGCATTGCT
751 TAGGAAGGCG AGAATGGGGA AGGCGGGGTC GTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1546; ORF 535>:

m535.pep

```

1 MPFPVFRFPF ALSLLTFFAV SQILVSDISN SGVSETIDAS NVFVGYEYPT
51 YISNLHLFQF RKLGVQLFHA LFAEIDGQS GFAFICGIDN HAGAEFGVAD
101 VLSDTETCVG LGLFVVDDF IFGCGGLARV AVTVVCRFLD GQVVQYFGWD
151 LFDEAGDDAE LGLSVQHALL RHGDVEAFAG AGDGDVHEAA FFFEAAAFGK
201 AHFAGEAAFF HAGEEDGVKF QAFGGVDGHE LDGLFACACL VFTGFEGGIA
251 XEGENEGGV V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 535 shows 80.9% identity over a 262 aa overlap with a predicted ORF (ORF 535.ng) from *N. gonorrhoeae*:

m535/g535

```

          10      20      30      40      50      59
m535.pep  MPFPVFRFPFALSLLTFFAVSQILVSDISNSGVSETIDASNVF-VGYEYPTYISNLHLFQ
          |||||: || ||| ||||: || ||||| ||||: ||||| |||||: ||||| ||
g535      MPFPVFRQXFAXSLLRFFAVGRILESDISNSGFSETINASNVFVGYEYPACISNLHFRFQ
          10      20      30      40      50      60

          60      70      80      90      100     110     119
m535.pep  FRKLGVLFLHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVDD
          |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: ||
g535      FRKLGIQFFHALFAEVDGQSGGFAFVCGIDNHAGAEFGVTDVLSDAEACVGLRLFEVIDD
          70      80      90      100     110     120

```

	120	130	140	150	160	170	179
m535.pep	FIFGCGGLARVAVTVVGRFLFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRRHGDVEAFA						
	: : : :						
g535	FVPLYGGLARVAVAVEGGFFDGQVVQYFWRDFFDEAGCDAELGLSVQHALLCHGDVEAFA						
	130	140	150	160	170	180	
	180	190	200	210	220	230	239
m535.pep	GAGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGHELDGLFACAC						
	: : : : :						
g535	GAGDGDVHEAAFFFEAAALGKAHFAGETPLFHTGEEDGVVEFQAFGGVDGHHQLDGGFACPC						
	190	200	210	220	230	240	
	240	250	260				
m535.pep	LVFTGFEGGIAXEGENGE			GGGVV			
	: :			: :			
g535	LVFAGFEGGVAQEGEDG			EGGIV			
	250	260					

a535.seq (partial)

```
1   TTCAGACGGC CTTTTCGCTT GTCCTTGCTA CAGTTTTTTG CCATAGGTCG
51  GATTTCGCAA TCCGACATTG CCAACAGCGG TTTTTCGSGA ACGATAGACG
101 CGTCAAATAT TTTTTCGCGA TACGAGTATC CAGCCTGCAT TTCAAATTTA
151 CATCGCTTCC AATTTCGCAA ACTTGGTGTC CAACTCTTTC AGCCCGTGTT
201 TGCCGAAATT GATGGTCAGT CGGGCGGATT CGCCTTTATC TCGCGCATCG
251 ATAATCAGCG CGGTGCCGAA TTTGGCGTGG CGGACGTTT GTCCGATACG
301 GAAACCTCGC TAGGTTTGGG GCTGTTTGTA GTCGTCGATG ATTTTGTCTT
351 TGGGCGCGCG GGTTTGGCGC GTGTGGCCAT AGCGGTCGTA GCGGGGTTTT
401 TTGACGGACA GGTAGTGCAA TACTTCGGGC GGGATTTCCT CGACGAAGCG
451 GGAGACGATG CCGAATTGGG TTTGTCGCTG CAGCATTCGT TGTTTGGCCA
501 TGGTGATGTA GAGGCGTTTG CGGGCGCGGG TGATGGCGAC GTACATCAGG
551 CGCGCTTCTT CTTCCAGGCC CGCGCGTTCG GCAAGGCTTA TTTCGTGGG
601 GAAGCGGCCT TCTTCCATGC CCGTGAGGAA TACGGCGTTA AATTCCAAGC
651 CTTTGGCGGG GTGCACGGTC ATAGATTGTA CGGCTTTTTC GCCCGGCGCT
701 GCTTGGTTTT CGCCGGATTG GAGAGCAGCA TTGCTTAGGA AAGCGAGGAT
751 GGGGAAGCGC GGGTCGTCTG A
```

a535.pep (partial)

1	FRRPFALSL	QFFAIGRL	LE	SDISNSGFSE	TIDASNI	FVG	YEYPACISNL
51	HRFQFRKLGV	QLFHAF	FAEI	DGQSGGFAFI	CGIDNHAGAE	FVGVADVLSDT	
101	ETCVGLGLFV	VVDVDFV	FGRG	GLARVAIVV	GGFFDGQVVQ	FVGRDFVFEA	
151	GDDAELGLSV	QHALLRHGDV	EAFAGAGDGD	VHQAAFFFEA	AAFGKAHFAG		
201	EAAFFHAGEE	YGVKQFAFGG	VHGHELYGFF	ARACLVFAGF	ESSIA*ESED		
251	EGGVV*						

	10	20	30	40	50	60
m535.pep	MPFPVFRPPFALSLLTFFAVSQILVSDISNSGVSETIDASNVFVGYEPTYIISNLHLRFQF					
	: : : :					
a535	FRPPFALSLLQFFAIGRILESDISNSGFSETIDASNI FVGYEYPACISNLHRFQF					
	10	20	30	40	50	
	70	80	90	100	110	120
m535.pep	RKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF					
	: : : :					
a535	RKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF					
	60	70	80	90	100	110
	130	140	150	160	170	180
m535.pep	IFGCGGLARVAVTVVGRFLFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	: : : : : :					
a535	VFGRGGLARVAIVGGFFDGQVVQYFGRDFFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	120	130	140	150	160	170

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	190	200	210	220	230	240
m535.pep	AGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGHELDGLFACACL					
a535	AGDGDVHQAAFFFEAAAFGKAHFAGEAAFFHAGEEYGVKFQAFGGVHGHELYGFFARACL					
	180	190	200	210	220	230
	250	260				
m535.pep	VFTGFEGGIAXEGENGEGGVVX					
a535	VFAGFESSIAXESEDGEGGVVX					
	240	250				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1549>:

g537.seq

```

1 atgaaatccc tttttatttg gctgcttcta ttgggctcgg cggcaggcgt
51 tttctaccat acccaaaacc aatccctgcc cgcgggcgaa cttgtctatc
101 cgtccgcacc gcaaatcagg gacggcgcg atgcgctgca ctacctcaac
151 cgcacccgca cacaatcgg ttgacacg cgccacacg cgccggtttt
201 ggaaaattcc gccgcagc acgcacgcta tctcacgctc aatcccgaag
251 acggacacgg cgaacaccat cccgacaatc cgcactacac cgcacaaaag
301 ctgaccgaac gcacacgcct tgccgggtat ctctacaacg gcgtgcatga
351 aaacatcagc acggaagagg aagccgcgga atcgccgac agcgacatcc
401 gcacgcagca acgccaagtg gacgcttga tgagcgcaat ctaccaccgc
451 ctttcgctgc ttgaccgcca taccgacgaa gcaggtgcgg cattttgtcg
501 cgaaaacggc aaaaccgtcc tcgtattcaa tcaggcgcaac ggcagcttcg
551 agcgcgcctg tgcaaaagga aggcggcagc cggaagcagg acggaatat
601 taccgcaacg cttgccacaa cggcgcgcc gtttatgctg acgaagccat
651 gcccgtaacg gaattgcttt ataccgccta tccggttggc ggcggcgcg
701 tgccttattt ttacggggaa cgtcccgacc ccgtgccgga atatgaaatc
751 acaggcaatc ctgccagcat tgatttttcc gagggcgag gcaaaattgc
801 gatgaaaagt ttcaagctgt atcagggtaa aaacgaaatc cgcccgtca
851 gggttttaac cgcggcaac gaccctaacg gcaggctgac cgcgcacca
901 ttgcgccctt tcccgtcaa acctttggaa tacggcacgc tttatacggc
951 ggtattcgac tatgtccgca acggacggca cgcgcaggcg aaatggcagt
1001 ttagaaccg aaaaccgat tacccttatt ttgaggtaaa cggcgcgag
1051 acacttgagg ttagaaaagg gaaaaatat ttcattccact ggcgcggag
1101 ctggtgtctg gaagcgtgta cccgttatac ctaccggcgg cagttcggca
1151 acagcctgtc cactactcgg cacgaagcgg gcggcattgt cttcagcgtc
1201 agcggaatgg cgggaagccg catcaggctt actccggaag acagcccgga
1251 acgcggtgta accctttatt tgcaggattg a

```

This corresponds to the amino acid sequence <SEQ ID 1550; ORF 537.ng>:

g537.pep

```

1 MKSLFIWLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
51 RIRTQIGLHA LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
101 LTERTRLAGY LYNGVHENIS TEEAAESSD SDIRTQQRQV DALMSAIYHR
151 LSLDRHTDE AGAFAVRENG KTVLVFNQGN GSFERACAKG RROPEAGRKY
201 YRNACHNGAA VYADEAMPVT ELLYTAYPVG GGALPYFYGE RPDVPPEYEI
251 TGNPASIDFS EAAGKIAMKS FKLYQGKNEI RPVRVLTAGN DPNGRHTAHQ
301 FALFPLKPLE YGTLYTAVFD YVRNGRHAQA KWQFRTRKPD YPYFEVNGGE
351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRR QFGNSLSILR HEAGGIVFSV
401 SGMAGSRIRL TPEDSPERGV TLYLQD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1551>:

m537.seq (partial)

```

1 ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCGG CGGCAGGCGT
51 TTTCTACCAT ACCCAAAmCC AATCCCTGCC CGCGGGCGAA CTGTCTATC
101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
151 CGCATCCGAG CCCAAATCGG TTGACACAAG CTGGCACACG CGCCGGTTTT
201 GGAATACTCC GCCCGCAGGC ACGCAAGCTA CCTCACGCTC AATCCGAAG
251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG

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301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
 351 AAACATCAGC ACGGAAGAAG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
 451 CTTTCCCTAC TTGACCGCCA TACGGATGAG TCAGGAGCGG CATT...

This corresponds to the amino acid sequence <SEQ ID 1552; ORF 537>:

m537.pep (partial)
 1 MKSLFIRLLL LGSAGVFYH TOXQSLPAGE LVYPSAPOIR DGGDALHYLN
 51 RIRAQIGLHK LAHAPVLENS ARRHASYLTL NPEDGHGEHH PDNPHYTAQK
 101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
 151 LSLDRHTDE SGAA...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 537 shows 95.7% identity over a 164 aa overlap with a predicted ORF (ORF 537.ng) from *N. gonorrhoeae*:

m537/g537

	10	20	30	40	50	60
m537.pep	MKSLFIRLLL LGSAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLN RIRAQIGLHK					
g537	MKSLFIWLLL LGSAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLN RIRAQIGLHA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m537.pep	LAHAPVLENSARRHASYLTLNPEDGHGEHHPDNPHYTAQK LTERTRLAGYLYNGVHENIS					
g537	LAHAPVLENSARRHARYLTLPEDGHGEHHPDNPHYTAQK LTERTRLAGYLYNGVHENIS					
	70	80	90	100	110	120
	130	140	150	160		
m537.pep	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA					
g537	TEEEAESSDSDIRTQQRQVDALMSAIYHRLSLDRHTDEAGAAFVRENGKTVLVFNQGN					
	130	140	150	160	170	180
	190	200	210	220	230	240
g537	GSFERACAKGRRQPEAGRKYRNACHNGAAVYADEAMPVTELLYTAYPVGGGALPYFYGE					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1553>:

a537.seq
 1 * ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCGG CGGCCGGCGT
 51 TTTCTATCAT ACCCAAACCC AATCCCTGCC CGCGGGCGAA CTTGTCTATC
 101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
 151 CGCATCCGCG CCCAAATCGG TTGACACAAG CTGGCACACG CGCCGGTTTT
 201 GGAAAATTCC GCCCGCAGGC ACGCACGCTA TCTCACGCTC AATCCCGAAG
 251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG
 301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
 351 AAACATCAGC ACGGAAGAGG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
 451 CTTTCCCTAC TTGACCGCCA TACGGATGAG GCAGGAGCGG CATTGTGCGG
 501 CGAAAACGGT AAAACCGTTC TCGTATTCAA TCAGGGCAAC GGCAGGTTTG
 551 AGCGGCATTG CGCCCAAGGC AGAAATCAGC CGGAAGCAGG ACGGAAATAT
 601 TACCGCAACG CCTGCCATAA CCGTGCGGTC GTGTACACCG ACGAAGCCAT
 651 GCGCGCACAG GAGCTGCTCT ATACAGCCTA TCCCGTCGGC AACGGCGCAC
 701 TGCCTTATTT CCACGGCGAG CGTCCAGACC CCGTGCCGGA ATATGAAATC
 751 ACGGGAATC CTGCCAGCAT TGATTTTTCG GAGGCGGCAG GCAAAATTAC
 801 GATGAAAAGT TTCAAGCTGT ATCAGGGTAA AAACGAAATC CGCCCGTCA
 851 GGGTTTAAAC CGCCGGCAAC GACCCCAACG GCAGGCTGAC CGCGTACCAA
 901 TTCGCGCTTT TCCCGCTCAA GCCTTTGGAA TACGGTACGC TTTATACGGC
 951 GGTATTCGAC TATGTCCGCA ACGGACGGCG CGCGCAGGCG AAATGGCAGT
 1001 TTAGAACCAG AAAACCCGAT TACCCTTATT TTGAGGTAAA CGGCGGCGAG
 1051 AACTTTGCGG TTAGAAAAGG CGAAAAATAT TTCATCCACT GCGCGGAGCG
 1101 CTGGTGTGTTG GAAGCGTGTA CCCGTTATAC CTACCGGCAG CGACCCGGCA

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1151 GCCGCCTGTC CATAGGAAGG CACAAGGCGG GCGGCATCGT CTTACAGCGTT
 1201 GACGGAATGG CGGGCAGCCG CATCACGCTT GCACCGGAAG GAGAAACGGA
 1251 ACGAGGCGTA ACCCTTTATT TACAGGATTG A

This corresponds to the amino acid sequence <SEQ ID 1554; ORF 537.a>:

a537.pep
 1 MKSLFIRLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAQIGLHK LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
 101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
 151 LSLDRHTDE AGAAVRENG KTVLVFNQGN GRFERHCAQG RNOPEAGRKY
 201 YRNACHNGAV VYTDEAMPAQ ELLYTAYPVG NGALPYFHGE RPDVPYEYEI
 251 TGNPASIDFS EAAGKITMKS FKLYQGKNEI RPVRVLTAGN DPNGRLTAYQ
 301 FALFPLKPLE YGTLYTAVFD YVRNGRRAQA KWQFRTRKPD YPYFEVNGGE
 351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRQ RFGSRLSISR HKAGGIVFSV
 401 DGMAGSRITL APEGETERGV TLYLQD*

m537/a537 98.2% identity in 164 aa overlap

	10	20	30	40	50	60
m537.pep	MKSLFIRLLL	LGSAAGVFYHTQXQSLPAGE	LVYPSAPQIR	IRDGGDALHYLN	RIRAQIGLHK	
a537	MKSLFIRLLL	LGSAAGVFYHTQXQSLPAGE	LVYPSAPQIR	IRDGGDALHYLN	RIRAQIGLHK	
	70	80	90	100	110	120
m537.pep	LAHAPVLENS	ARRHASYLTLNPEDGHGEHH	PDNPHYTAQK	LTERTRLAGY	LYNGVHENIS	
a537	LAHAPVLENS	ARRHARYLTLNPEDGHGEHH	PDNPHYTAQK	LTERTRLAGY	LYNGVHENIS	
	130	140	150	160		
m537.pep	TEEEAESSD	SDIRTQQRQVDGLMSAIYHRL	SLDRHTDE	SGAA		
a537	TEEEAESSD	SDIRTQQRQVDGLMSAIYHRL	SLDRHTDE	AGAAVRENGKTVLVFNQGN		
	170	180				
a537	GRFERHCAQ	GRNPEAGRKYR	NACHNGAVVYTDEAMPAQ	ELLYTAYPVG	NGALPYFHGE	
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1555>:

g538.seq
 1 atgtcaggta gaacaggacg gaacagtgcc actcaggcgc aaccggaacg
 51 cgtcatgctg gtgggcgtaa tgttgataa agatgatac ggcagcaatg
 101 ccgcccgctc gaacggtttt cagacggcat tggcggaagc cgtcgagctg
 151 gtcaaagcgg cgggcggcga ttccgtacgc gtggagactg ccaaacgcga
 201 ccgccgcac actgcgctgt ttgtcggcac gggcaaggcg gcggagctgt
 251 cggaagcagt tgcgcagac ggcattgatt tggctgtatt caaccacgaa
 301 cttactccca cgcaggaacg caatttggaa aaaatctcc aatgccgcgt
 351 attggacaga gtggggctga ttctggcgat ttccgccgc cgcgcccgca
 401 cgcaggaagg caggctgcaa gtcgagttgg cgcaattgag ccatttggcg
 451 ggacgcttga tacgcggtta cggacattg caaagccagc gcggcggtat
 501 cggcatgaaa gggccggcg aaaccaaact ggaaaccgac cgccgattaa
 551 ccgcccatcg gatcaacgcc ttgaaaaaac agcttgccaa cctcaaaaaa
 601 cagcgcgccc tgcgcgcaa gtcccgcgag tcgggcagaa tcaaacgtt
 651 tgcgctggtc ggctatacca atgtcggcaa atccagcctg ttcaaccggc
 701 tgaccaagtc gggcatatat gcgaaagacc agcttttcgc cactctcgac
 751 acgacggcgc ggcggctgta catcagtcgc gcatcgagca ttatcctgac
 801 cgataccgtc ggattcgtca gcgatctgcc gcacaaactg atttccgcct
 851 tttccgccac cttggaagaa accgtgcaag ccgatgtgct gctgcacgtc
 901 gtcgatgctg ccgccgggaa cagcgggcag cagattgaag acgtggaaaa
 951 cgtactgcaa gaaatccatg cccacgatat tccgtgcac aaggtgtaca
 1001 acaaaaccga cctgctgccg tctgaagaac aaaacacggg catatggcgc
 1051 gacgctgcgg gaaaaattgc cgccgtccgc atttccgttg ctgaaaaatac

1	MSGRTGRNSA	TQAQPERVML	VGVMLDKDDT	GSNAARLNGF	OTALAEAVEL
51	VKAAGGDSVR	VETAKRDRPH	TALFVGTGKA	AELSEAVAAD	GIDLVPVFHNE
101	LTPTQERNLE	KILQCRVLDR	VGFLIAIFAR	RARTQEGRLQ	VELAQOLSHLA
151	GLRLIRGYHL	QSORGGIGMK	GPGETKLETD	RLRLTAHRINA	LKKQALANLKK
201	QRALRRKSRE	SGRIKTFALV	GYTNVGKSSL	FNRLTKSGIY	AKDOLFATLD
251	TTARRLYISP	ACSIIILDTV	GFVSDLPHLK	ISAFSATLEE	TVQADVLLHV
301	VDAAARNSSQ	QIEDVENVLQ	EIHANDIPCI	KVYNKTDLLE	SEQQNTGIWR
351	DAAGKIAAIV	ISVAENTGID	ALREAIAYEC	AAAPNTDETE	MP*

m538.seq

1	ATGACAGGCA	GAACAGGCGG	CAACGGCAGT	ACCCAAGCGC	AACCCGAACG
51	CGTCATGCTG	GTGGGCGTAA	TGTTGGACAA	AGATGGTACG	GGCAGTACTG
101	CCGCCAGCTG	GAACGGT'TTT	CAGACGGCAT	TGGCGGAAGC	TGTCGAGCTG
151	GTCAAAGCGT	CGGGCGGCCA	TTCCGTGCGC	TGGGAGACTG	CCAAACCGCA
201	CCGTCCGCAC	ACCGCGCTGT	TGTGCGGCAC	GGGCAAGGCG	CGGGAGCTGT
251	CAGAAGCAGT	TGCCCGCAGC	GGCATCGATT	TGGTCGTATT	CAACCACGAA
301	CTCAGCGCCA	CGCAGGAACG	CAACCTTGAA	AAAGAACTGA	AATGCCGCGT
351	ATTGGACAGG	GTAGGGGTGA	TTCTTGGCAT	TTTCGCTCGC	CGCGCCCGCA
401	CGCGGAAGG	CAGGCTGCAA	TCGAGTTTGG	CGCAATTGAG	CCATT'TGGCG
451	GGACGCTTGA	TACGCGGTTA	CGGCCATCTG	CAGAGCCAGC	CGCGGCGTAT
501	CGGCATGAAA	GGCCCCGGCG	AAACCAAAC	GGAACCGAC	CGCCGATTGA
551	TCGCCCATCG	GATCAATTGCC	TTGATAAAC	AGCTTGCCAA	CCTCAAAAAA
601	CAGCGCGCCG	TGCGCGCAA	GTChCGCGAA	TCGGGCACAA	TCAAAACGTT
651	TGCGCTGGTC	GGCTATACAA	ATGTCGCAAA	ATCCAGCCTG	T'TCAACCGCG
701	TGACAAAGTC	GGGCATATAT	GCAAAGGACA	AGCTTAGTCC	CGAATGCAGC
751	ATTATCCTGA	CCGATACCGT	CGGATTTCGTn	AGCGATCTGC	CGCAcAAACT
801	GATTTCGCGC	TTTTGcCC .	CGCTGGGAAG	AACCGCGCAA	GCCGATGTGC
851	TGCTGACAGT	CGTCGATACG	GCGCTCCGA	ACAGCGGACA	GCAGATTGAA
901	GACGTGGAAA	ACGTACTGCA	GAAATCCAT	CGCGGCGATA	T'TCCGTGCAT
951	cAAGGTGTAC	AACAAAACCG	ACCTGCTGCC	GTCTGAAGAA	CAAAACACGG
1001	GCATATGGCG	CGACGCTGCG	GGAAAAATTG	CGCCCGTCTG	CATTTCGGTT
1051	GCTGAAAAAT	CCGGTATAGA	CGCACTGCCG	CGAGCCATTG	CCGAGTCTTG
1101	TGCCCGCCGA	CCAAACACAG	ACGAAACCGA	AATGCCATTGA	

m538 . pep

1	MTGRTGGNGS	TQAOPEVRML	GVMLDKDGT	GSSAARLNGF	QTALAEAVEL
51	VKAAGDSVR	VETAKRRDPH	TALFVGTGKA	AELSEAAAD	GIDLVFVNH
101	LTPQQRNLE	KELKCRVLDR	VGLLAIARF	RARTQEGRIQ	VELAQLSHLA
151	GLRLRGYGLH	QSKRGGIMK	GGETKLETD	RRLIAHRINA	LIKQLANLKK
201	QRALRRKSRE	SGTIKTFALV	GYTNVGKSSL	FNRLTKSGIY	AKDKLSPPCS
251	IILTDTVGVF	SDLPHKLISA	FSXTLLEBTAQ	ADVLLHVUDA	AAPNSGQQIE
301	DVENVLGEIH	AGDAIPCIKY	NKTDLDPSEE	QNTGTIWRDAA	GKIAAVRISV
351	AENTGIDALER	EAIAESCAA	PNTDETPEM*		

Homology with a predicted ORF from *N. gonorrhoeae*

m538/q538

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVMLDKDGTGSSAARLNGFQTALAAEVELVKAAGGDSVR					
	: : : : :					
g538	MSGRGTGRNSATQAQPERVMLVGVMLDKDGTGSNAARLNGFQTALAAEVELVKAAGGDSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPHALTAVGTGKAAELSEAVAADGIDLVVFNHFLTPTQERNLEKELKCRVLDR					
	: :					
g538	VETAKRDRPHALTAVGTGKAAELSEAVAADGIDLVVFNHFLTPTQERNLEKILQCRVLDR					

812

	70	80	90	100	110	120
	130	140	150	160	170	180
m538.pep	VGLILAI FARRARTQ EGR LQVELAQLSHLAGRLIRGYGHLQSQRRGGIGMKGPGETKLETD					
g538	VGLILAI FARRARTQ EGR LQVELAQLSHLAGRLIRGYGHLQSQRRGGIGMKGPGETKLETD					
	130	140	150	160	170	180
	190	200	210	220	230	240
m538.pep	RRLIAHRINALIKQLANLKKQALRRKSRESGTIKTFALVGTYNVGKSSLFNRLTKSGIY					
g538	RRLTAHRINALKKQLANLKKQALRRKSRESGRITKTFALVGTYNVGKSSLFNRLTKSGIY					
	190	200	210	220	230	240
	250	260	270	280		
m538.pep	AKDKL-----SPEC SII L T D T V G F V S D L P H K L I S A F S X T L E E T A Q A D V L L H V					
	:					
g538	AKDQLFATLDTTARRLYISPAC SII L T D T V G F V S D L P H K L I S A F S A T L E E T V Q A D V L L H V					
	250	260	270	280	290	300
	290	300	310	320	330	340
m538.pep	VDAAAPNSGQQIEDVENVLQEIHAHDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
g538	VDAAARNSGQQIEDVENVLQEIHAHDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
	350	360	370	380		
m538.pep	ISVAENTGIDALREIAIESCAAAPNTDETEMPX					
g538	ISVAENTGIDALREIAIEYCAAAPNTDETEMPX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1559>:

```

a538.seq
1  ATGACAGGCA GAACAGGCCG CAACGGCAGT ACCCAAGCGC AACCCGAACG
51  CGTCATGCTG GTGGGCGTAA TGTGGACAA AGATGGTACG GGCAGCAGTG
101 CCACCCGTCT GAACGGTTTT CAGACGGCAT TGGCGGAAGC TGTCGAGCTG
151 GTCAAAGCGG CGGGCGGCGA TTCCGTGCGC GTGGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCGCGCTGT TTGTCGGCAC GGGCAAGGCG GCGGAGCTGT
251 CGGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301 CTTACGCCCA CGCAGGAACG CAATTGGA AATCCTCC ATGCCCGCT
351 ATTGGACAGA GTGGGGCTGA TTCTGCGCAT TTTCCGCCG CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CACAATTGAG CCATTGGCG
451 GGACGCTTGA TACGCGTTA CGGCCATCTG CAGAGCCAGC GCGCGGTAT
501 CGGCATGAAA GGCCCGCGCG AAACCAAACT GGAAACCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGAAAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TCGCCCGCAA GTCCCGCGAA TCGGGCACAA TCAAAACGTT
651 TCGCGTGGTC GGCTATACCA ATGTCGGCAA ATCCAGTCTG TTCAACCGGC
701 TGACCAAGTC CGGCATATAT GCGAAAGACC AGCTTTTCGC CACACTCGAC
751 ACGACGGCGC GCGGCTGTA CATCAGTCCC GAATGCAGCA TTATCCTGAC
801 CGATACCGTC GGATTCTGCA GCGATCTGCC GCACAACTG ATTTCCGCCT
851 TTTCCGCCAC GCTGGAAGAA ACCGCGCAAG CCGATGTGCT GCTGCACGTC
901 GTCGATGCCG CCGCTCCGAA CAGCGGACAG CAGATTGAAG ACGTGGAAAA
951 CGTACTGCAA GAAATCCATG CCGCGATAT TCCGTGCATC AAGGTGTACA
1001 ACAAAACCGA CCTGCTGCCG TCTGAAGAAC AAAACACGGG CATATGGCGC
1051 GACGCTGCGG GAAAAATTGC CGCCGTCCGC ATTTCCGTTG CTGAAAATAC
1101 CCGTATAGAC GCACTGCGCG AAGCCATTGC CGAGTATTGT GCCGCCGCAC
1151 CAAACACAGA CGAAACCGAA ATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1560; ORF 538.a>:

```

a538.pep
1  MTGRTGRNGS TQAQPERVML VGVMLDKDGT GSSATRLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVALD GIDLVVFNHE
101 LPTPTQERNLE KILQCRVLDR VGLILAI FAR RTQEGRLQ VELAQLSLHA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LKKQLANLKK

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813

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201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD
251 TTARRLYISP ECSIILTDTV GFVSDLPKLI ISAFSATLEE TAQADVLLHV
301 VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCI KVYNKTDLLP SEEQNTGIWR
351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*

```

m538/a538 94.6% identity in 392 aa overlap

```

          10      20      30      40      50      60
m538.pep  MTGRTGGNGSTQAQPERVMLVGVM LDKDGTGSSAARLNGFQTALAEAVELVKAAGGDSVR
          |||||  |||||  |||||  |||||  |||||  |||||
a538       MTGRTGRNGSTQAQPERVMLVGVM LDKDGTGSSATRLNGFQTALAEAVELVKAAGGDSVR
          10      20      30      40      50      60

          70      80      90     100     110     120
m538.pep  VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPTQERNLEKELKCRV LDR
          |||||  |||||  |||||  |||||  |||||  |||||
a538       VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPTQERNLEKILQCRV LDR
          70      80      90     100     110     120

          130     140     150     160     170     180
m538.pep  VGLILAI FARRARTQEGR LQVELAQ LSHLAGRLIRGYGHLQSQ RGGIGMKGPGETKLETD
          |||||  |||||  |||||  |||||  |||||  |||||
a538       VGLILAI FARRARTQEGR LQVELAQ LSHLAGRLIRGYGHLQSQ RGGIGMKGPGETKLETD
          130     140     150     160     170     180

          190     200     210     220     230     240
m538.pep  RRLIAHRINALIKQLANLKKQ RALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY
          |||||  |||||  |||||  |||||  |||||  |||||
a538       RRLIAHRINALKKQLANLKKQ RALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY
          190     200     210     220     230     240

          250     260     270     280
m538.pep  AKDKL-----SPECSIILTDTVGFVSDLPKLI SAFSXTLEETAQADVLLHV
          |||:|  |||||  |||||  |||||  |||||  |||||
a538       AKDQLFATLDTTARRLYISPECSIILTDTVGFVSDLPKLI SAFSATLEETAQADVLLHV
          250     260     270     280     290     300

          290     300     310     320     330     340
m538.pep  VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR
          |||||  |||||  |||||  |||||  |||||  |||||
a538       VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR
          310     320     330     340     350     360

          350     360     370     380
m538.pep  ISVAENTGIDALREAIAESCAA PNTDETEMPX
          |||||  |||||  |||||  |||||
a538       ISVAENTGIDALREAIAEYCAA PNTDETEMPX
          370     380     390

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1561>:

```

g539.seq
1  atggaggatc tgcaggaaat cgggttcgat gtcgcccgcg taaaggtagg
51  tcggcagcgc gaacatcatc gtctgcatca taccaggtcc ggcaacggca
101 aggcggacga tgtattgttt gcgttctttt tggttggcgg cttcgatttt
151 ttgcgcgtca tagggtgcgg cgggttagcc tgtctgccgg attttcaaca
201 gaatgtcggg gaggcggatt ttgccgtcgt cccagacgac gcggcagcgg
251 tgcgtgctgt aattgaggtc gatgcggacg atgccgtctg tgcgcaaaag
301 ctgctgttcg atcagccaga cgcaggcggc gcaggtaatg ccgctgagca
351 tcagactgc ttcgtgcgtg ccattatggg tttccacaaa gtcggatttg
401 acttcgggca ggtcgtacag gcggatttgg tcgaggattt cttggggcgg
451 cagttcggtt tttttcgcgt cggcggtgcg tcgtttgtaa taactgccca
501 agccggaatc gatgatgctt tgtgcgactg cctgacagcc gacgcagcag
551 gtttcgcggg cttcgccttc gtagcggacg gtcagatgca ggttttcggg
601 aacgtccagc ccgcagtggg aacaggtttt tttcatggca tttcggtttc

```

814

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651 gtctgtgttt ggtgcggcgg cacaatactc ggcaatggct tcgcgcagtg
701 cgtctatacc ggtattttca gcaacggaaa tgcggacggc ggcaattttt
751 cccgcagcgt cgcgccatat gcccggtgtt tgttcttcag acggcagcag
801 gtcgggtttt ttgtacacct tgatgcacgg aatatcgtgg gcatcgattt
851 cttgcagtac gttttccacg tcttcaatct gctgcccgct gttccggcg
901 gcagcatcga cgacgtgcag cagcacatcg gcttgcaagg tttcttccaa
951 ggtggcggaa aaggcggaaa tcagtttggt cggcagatcg ctgacgaatc
1001 cgacggatc ggtcaggata atgctgcatg cgggactgat gtacagccgc
1051 cgcgcgctcg tctcgagagt ggcgaaaagc tgggtctttcg catatatgcc
1101 cgacttggtc agccggttga acaggctgga tttgccgaca ttggtatag

```

This corresponds to the amino acid sequence <SEQ ID 1562; ORF 539.ng>:

g539.pep

```

1 MEDLQEIGFD VAAVKVGRQR EHHRLHHTQS GNGKADDVLF AFFLVGGFDF
51 LRVIGCGGVA CLPDFQQNVG EADFAVVPDD AAARAVIEV DADDAVCAQK
101 LLFDQPDAGG AGNAAEHQHC FVRAIMGFHK VGLDFGQVVO ADLVEDFLGR
151 QFGFFRVGGA SFVITAQAGI DDALCDCLTA DAAGFAVFAF VADGQMVFV
201 NVQPAVETGF FHGISVSSVF GAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISW AWISCSFST SSICCLPFA
301 AASTTCSSTS ACTVSSKVAE KAEISLCGRS LTNPTVSVRI MLHAGLMYSR
351 RAVVSRVAKS WSFAYPMDLV SRLNRLDLPT LV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1563>:

m539.seq (partial)

```

1 ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51 TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTTCCTTT TGGTTGGCGG CTTCGATTTT
151 TTGCGCGTCA TAGGGTGCAG CCGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCaGCGg
251 TGCGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGCTCTG TACGC AAAAG
301 CTGCTGTTTC ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTA AACCGC CTGCGCGGTG CCGCCGTGGG TTTCCACAAA GTCGGACTGG
401 ACTTCGGGCA GGTCTGACAG GCGGATTGCG TCGAGGATTT CTGCGGCGG
451 CAGCTCGGTT TTTTGCCTGT CCGCGGTGCG TTGTTGTGTA TAATGCCCA
501 AGCCCCGCTC AATAATGCTT TGTGCGACCG CCTGACAGCC GGCGCaAGg
551 GTTTCGCGGT CTTCGTTTTC GTAACGGACA GTCAGGTGGA GGTGTTGCGG
601 AACATCCAGA CCGCAGTGGA AACAGGTTTT TTTTCATGGA TTTGCGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAAGACTC GGCAATgGCT TCGCGCAGTG
701 CGCTATACCC GGTATTTTCA GCAACGGAAA TCGCGACGGC GGCAATTTTT
751 CCCGACGCGT CCGCCATAT GCCCGTGTTC TGTCTTCAG ACGGCAGCAG
801 TCGGTTTTTG TTGTACACCT TgATGCACGG AATATCGCCG GCATGGATT
851 CTTGCAGTAC GTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCGCGG TTTCTTCCAG
951 CGTGGcG.AA AAGGCGGAAA TCAGTTTgTG CGGCAGATCG CTnACGAATC
1001 CGACGGTATC GGTCAGGATA ATGCTGCATT CGGGAC...

```

This corresponds to the amino acid sequence <SEQ ID 1564; ORF 539>:

m539.pep (partial)

```

1 MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF
51 LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVFHK VGLDFGQVVO ADLVEDFLGR
151 QLGLFRVGGG LFVITAQARV NNALCDRLTA GAQGFVAVFV VTDSQVEVFG
201 NIQTAVETGF FHGISVSSVF GAAQDSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSFST SSICCLPFGA
301 AASTTCSSTS ACAVSSSVAX KAEISLCGRS LTNPTVSVRI MLHSG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 539 shows 89% identity over a 345 aa overlap with a predicted ORF (ORF 539.ng) from *N. gonorrhoeae*:

m539/g539

	10	20	30	40	50	60
m539.pep	MEDLQEIGFDVAAVKVGRQR	EHHRLHHPQP	GNGEADDVLF	FAFFLVGGFDF	FLRVIGCGGVA	
g539	MEDLQEIGFDVAAVKVGRQR	EHHRLHHTQS	GNGKADDVLF	FAFFLVGGFDF	FLRVIGCGGVA	

815

	10	20	30	40	50	60
	70	80	90	100	110	120
m539.pep	YLPDFQQNVGKADFVAVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
g539	CLPDFQQNVGEADFAVVPDDAAAVRAVIEVDADDAVCAQKLLFDQPDAGGAGNAAEHQHC					
	70	80	90	100	110	120
	130	140	150	160	170	180
m539.pep	LARAAVGFHKVGLDFGQVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA					
g539	FVRAIMGFHKVGLDFGQVQADLVEDFLGRQFGFFRVGGASFVITAQAGIDDALCDCLTA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m539.pep	GAQGFVAVFVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAAQDSAMASRSASIPVFS					
g539	DAAGFAVEAFVADGQMVFGNVQPAVETGFFHGISVSSVFGAAAQYSAMASRSASIPVFS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m539.pep	ATEMRTAAIFPAASRHMVFVFCSSDGSRSVLLYTLMHGISPWISCSTFTSSICCPLFGA					
g539	ATEMRTAAIFPAASRHMVFVFCSSDGSRSVLLYTLMHGISWAWISCSTFTSSICCPLFRA					
	250	260	270	280	290	300
	310	320	330	340		
m539.pep	AASTTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
g539	AASTTCSSTSACTVSSKVAEKAEISLCGRSLTNPTVSVRIMLHAGLMYSRRVAVSRVAKS					
	310	320	330	340	350	360
g539	WSFAYMPDLVSRLNRLDLPTLV					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1565>:

```

a539.seq
1  ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51  TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTTCCTTT TGGTTGGCGG CTTCGATTTT
151 TTGCGCGTCA TAGGGTGC GGTTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCAGCGG
251 TGGCTGCTGT AATTGAGGTC GATGCGGACG ATGCCGCTCTG TACGCCAAAAG
301 CTGCTGTTTC ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAAAACCGC CTCGCGCGTG CCGCCGTGGG TTTCCACAAA GTCGGACTGG
401 ACTTCGGGCA GGTGCTACAG GCGGATTGG TCGAGGATTT CTTGGGGCGG
451 CAGCTCGGTT TTTGCGCGT CGGCGGTGCG TTGTTTGTA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACTG CCTGACAACC GGCGCAGCAG
551 GTTTCGCGGT CTTGTTTTTC GTAACGGACG GTCAGATGCA GGTTTTCGGG
601 AACGTCCAGC CCGCAGTGGA AACAGGTTTT TTTCATGGCA TTTCGGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAATACTC GGCAATGGCT TCGCGCAGTG
701 CGCTATACCC GGTATTTTCA GCAACGGAAA TCGCGACGGC GGCAATTTTT
751 CCCGCAGCGT CCGGCCATAT GCCCGTGTTC TGTTCTTCAG ACGGCAGCAG
801 GTCGGTTTTG TTGTACACCT TGATGCACGG AATATCGCCG GCATGGATTT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGC GCGG TTTCTTCCAG
951 CGTGGCGGAA AAGGCGGAAA TCAGTTTGTG CCGCAGATCG CTGACGAATC
1001 CGACGGTATC GGTGAGGATA ATGCTGCATT CGGGACTGAT GTACAGCCGC
1051 CCGCGCGTCG TGTCGAGTGT GCGGAAAAGC TGGTCTTTCG CATATATGCC
1101 CGACTTGGTC AGCCGTTTGA ACAGACTGGA TTTGCCGACA TTGGTATAG

```

This corresponds to the amino acid sequence <SEQ ID 1566; ORF 539.a>:

```

a539.pep
1  MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF

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816

```

51  LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVFHK VGLDFGQVVQ ADLVEDFLGR
151 QLGFLRVGGA LFVITAQARV NNALCDCLTT GAAGFAVEVF VTDGQMVFVG
201 NVQPAVETGF FHGISVSSVF GAAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPFLGA
301 AASTTCSSTS ACAVSSVAE KAEISLCGRS LTNPVSVRI MLHSGLMYSR
351 RAVVSSVAKS WSFAYMPDLV SRLNRLDLPT LV*

```

m539/a539 97.1% identity in 345 aa overlap

	10	20	30	40	50	60
m539.pep	MEDLQEI	GFDAVAVKVGRQREHRLHHPQPGNGEADDVLF	FAFFLVGGFDFLRVIGCGGVA			
a539	MEDLQEI	GFDAVAVKVGRQREHRLHHPQPGNGEADDVLF	FAFFLVGGFDFLRVIGCGGVA			
	10	20	30	40	50	60
	70	80	90	100	110	120
m539.pep	YLPDFQQNVGKADFAVVPDDAAARAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
a539	YLPDFQQNVGKADFAVVPDDAAARAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m539.pep	LARAAGVFHKVGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA					
a539	LARAAGVFHKVGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDCLTT					
	130	140	150	160	170	180
	190	200	210	220	230	240
m539.pep	GAQGFVAVFVTDTSQVEVFGNIQTAVETGFFHGISVSSVFGAAAQDSAMASRSASIPVFS					
a539	GAQGFVAVFVTDGQMVFQVGNVQPAVETGFFHGISVSSVFGAAAQYSAMASRSASIPVFS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m539.pep	ATEMRTAAIFPAASRHMPVFCSSDGSRSVLLYTLMHGISPAPWISCSTFSTSSICCPFLGA					
a539	ATEMRTAAIFPAASRHMPVFCSSDGSRSVLLYTLMHGISPAPWISCSTFSTSSICCPFLGA					
	250	260	270	280	290	300
	310	320	330	340		
m539.pep	AASTTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
a539	AASTTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSGMLYSRRRAVVSSVAKS					
	310	320	330	340	350	360
a539	WSFAYMPDLVSRLNRLDLPTLVX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1567>:

```

g540.seq
1  atgccgccct cccgacgcgg caacgggggtg tttatcaaa acggcaaaact
51  tgccaatgcg gtttccgctt gccgattgcc aaaccggcaa acctttcccg
101  tgccggtgcc gaaccgatg ccgtctgaac cttcagacgg catcggtgtg
151  ttatttgtcc actcggacgg gtgcaggttc gtattgtgtc gattcgtcgc
201  cgtaatacag cacgccgagt ttgacgggga tgcgtccctg cgatttgccg
251  tgggcgttgg aatcgcgcaa ggaatgcgcg cagccgcagt attcctgctg
301  gtagaagttt tcgcgtttgc tgatttcaat catacgcgcg ccgccccgcg
351  ctttgcgcca gttgaagtc caataggcca catcatcgta aggcgcgcg
401  gcacggtgtc cgcagtcgtt gatttgcgcc atatttttcc agcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1568; ORF 540.ng>:

```

g540.pep
1  MPFSRRNGNV FYQNGKLANA VSACRLPNRQ TFPVPVNPMP FSEPSDGIGC

```

817

51 L FVHSDGCRF V LCRFVAVIQ HAEFDGDASL RFAVGVGIAQ GIRA AAVFLL
 101 VEVFAFADFN HTRAAAFAP VEVPIGHIIV RRGTVSAVV DLRHIFPA *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1569>:

m540.seq (partial)
 1 ..CCGAACCCGA TGCCGTCTGA ACCTTCAGAC GGCATCGGGT GTTATTTGT
 51 CCACCCGGAT GGGGCGAGGT TCGTATTGTG TCGATTCGTC GCCGTAATAC
 101 AGCAGCCCGA GTTTGATGGG GATTCTGCCC TGTGATTTGC GGTGGGCATT
 151 GGAATCCCTC AGGGAATAGG CACAACCGCA ATATTCCTGC TGGTAGAAGT
 201 TTTACGTTT GCTGATTCA ATCATGCGCG CGCTGCCGCC GCCTTTGCGC
 251 CAGTTGAAAT CCCAATACAC CACATCATCG TAAGGCGCGG CGGCGCGGTG
 301 TCCGCAGTCG TTGATTGCG CCATATTTT CCAGCGTGA

This corresponds to the amino acid sequence <SEQ ID 1570; ORF 540>:

m540.pep (partial)
 1 ..PNMPSEPSD GIGCLFVHPD GGRFVLCRFV AVIQHAEFDG DSAL*FAVGI
 51 GIPOGIGTTA IFLLEVFTF ADFNHARAAA AFAPVEIPIH HIIVRRGGAV
 101 SAVDLRHIF PA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 540 shows 85.7% identity over a 112 aa overlap with a predicted ORF (ORF 540.ng)

from *N. gonorrhoeae*:

m540/g540

m540.pep				10	20	30
				PNMPSEPSD	GIGCLFVHPD	GGRFVLCRFV
g540	GNGV	FYQNG	KLNAV	SACRL	PNRQT	FPVPV
	10	20	30	40	50	60

m540.pep	40	50	60	70	80	90
	AVIQHAEFDG	DSALXFAV	GIGIPQ	GIGTTAIF	LLVEVFTF	ADFNHARAAA
g540	AVIQHAEFDG	DASLRFAV	GVGIAQ	GIRA AAVF	LLVEVFAF	ADFNHTRAAA
	70	80	90	100	110	120

m540.pep	100	110
	HIIVRRGGAV	SAVVDLRHIF
g540	HIIVRRGGTV	SAVVDLRHIF
	130	140

L' estremita' N-terminale di meningococco e' assente perche' interviene la fine del contig

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1571>:

a540.seq
 1 ATGCCGTCCT CCCGACGCGG CAACGGGGTG TTTTATCAAA ACGGCAAACT
 51 TGCCAATGCG GTTTCGATT GCAGATTGCC AAACCGGCAA ACCTTCCCG
 101 TGCCGATGCC GAACCCGATG CCGTCTGAAC CTTACAGCGG CATCGGGTGT
 151 TTATTGTGCC ACCCGATGG GTGCAGGTTT GTATTGTGTC GATTGTCGCG
 201 CGTAATACAG CACGCCGAGT TTGATGGGGA TTCTGCCCTG TGATTGCGG
 251 TGGGCGTTGG AATCCCTCAG GGAATAGGCA CAACCGCAAT ATTCCTGCTG
 301 GTAGAAGTTT TCACGTTTGC TGATTCAAT CATACGCGCG CTGCCGCCGC
 351 CTTTGCGCCA GTTGAAATCC CAATACACCA CATCATCGTA AGGCGCGGCG
 401 GCGCGGCGGC CGCAGTGGTT AATCTGGTTC ATGTTTTC A

This corresponds to the amino acid sequence <SEQ ID 1572; ORF 540.a>:

a540.pep (partial)
 1 MPSSRRGNV FYQNGKLANA VSDCRLPNRQ TFPVPMNPM PSEPSDGIGC
 51 L FVHPDGRF V LCRFVAVIQ HAEFDGDASL *FAVGVGIPQ GIGTTAIFLL
 101 VEFTFADFN HTRAAAFAP VEIPIHHIIV RRGAAA AAVV NLVHVFP

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m540/a540 92.8% identity in 111 aa overlap

```

                                10      20      30
m540.pep                      PNPMPSEPSDGIGCLFVHPDGGRFVLCRFV
                                |||||
a540      GNGVFYQNGKLANAVSDCRLPNRQTFPVPMPNPMPSEPSDGIGCLFVHPDGGRFVLCRFV
              10      20      30      40      50      60

                                40      50      60      70      80      90
m540.pep      AVIQHAEFDGDSALXFAVGIGIPQIGITTAIFLLVEVFTFADFNHARAAAFAPVEIPIH
              |||||
a540      AVIQHAEFDGDSALXFAVGIGIPQIGITTAIFLLVEVFTFADFNHTRAAAFAPVEIPIH
              70      80      90      100     110     120

                                100     110
m540.pep      HIIIVRRGGAVSAVVDLRHIFPAX
              |||||
a540      HIIIVRRGGAAAVVNLVHVFP
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1573>:

```

g542.seq
1  atgccgaat ggtcgcgcac acggcggtgc agcgctcctt cgctgatgtt
51  cagcgcggt gtcagccggt tgacttggtg tgcgccgcgc tgcgaacgcgg
101 cattcagggt gcggtgaag tcttcagacg gcatagcgtc tgcttcgcc
151 gtttgcccg ccgccggtc gatgccgtct gaaaccgtgt cccacaaatc
201 cgacagcagc cgcaaacagt ccgcctcgcg gcgcaatgtt tcgccccaat
251 gccctttgg gacgggttgc aggcaggatg ccgccaagcc gcgcaggttt
301 gggggcaaat cccatatact gaccggttcg cggttaa

```

This corresponds to the amino acid sequence <SEQ ID 1574; ORF 542.ng>:

```

g542.pep
1  MPKWSRIRRC SVLSLMFSAA VSRLTWCAPP SNAAFRVLK SSDGIASASA
51  VCPAAGSMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTVC RQDAAKPRRF
101 GGKSHILTGS R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1575>:

```

m542.seq
1  ATGCCGAAAT GGTCGCGCAT ACGGCGTTGC AGCGTCCTTT CACTGATGTT
51  CAGCGCGTCT GTCAGCCGGT TGA CTGTTGGTG TGC GCCGTCG GCAAACGCGG
101 CATTTAGGGT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTTCGCC
151 GTTTGCCCG CCGCCGCCG GATGCCGTCT GAAACCGTGT CCCACAAGTC
201 CGACAGCAGC CGCAACAGT CCGCCTCGCG .CGCAATGTT TCGCCCAAAT
251 GCCCCTTTGG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTT
301 GGGGGCAAAT CCGATATCCT GACCGGTTTC CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1576; ORF 542>:

```

m542.pep
1  MPKWSRIRRC SVLSLMFSAS VSRLTWCAPS ANAAFVRVLK SSDGIASASA
51  VCPAAGSMPS ETVSHKSDSS RNTSASRAMF RNPAPLGRNV SPKCPFGTAF
101 RQDAAKPRRF GGKSHILTGS R*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 542 shows 93.7% identity over a 111 aa overlap with a predicted ORF (ORF 542.ng) from *N. gonorrhoeae*:

```

m542/g542

              10      20      30      40      50      60
m542.pep      MPKWSRIRRC SVLSLMFSASVSRLTWCAPSANAAFVRVLKSSDGIASASAVCPAAGPMPS
              |||||
g542      MPKWSRIRRC SVLSLMFSAAVSRLTWCAPP SNAAFVRVLKSSDGIASASAVCPAAGSMPS
              10      20      30      40      50      60

              70      80      90      100     110
m542.pep      ETVSHKSDSSRNTSASXRNVS PKCPFGTAF RQDAAKPRRF GGKSHILTGSRX

```

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```

|||||
g542  ETVSHKSDSSRNTSASRRNVSPKCPFGTVCRQDAAKPRRFGGKSHILTGSRX
      70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1577>:

```

a542.seq
1  ATGCCGAAAT  GGTCGCGCAT  ACGGCGTTGC  AGCGTCCTTT  CGCTGATGTT
51  CAGCGTGTCT  GCCAGCCGGT  TGAATTGATG  TGCGCCGCCG  GCAAACGCGG
101 CATTCAAGAT  GCGGCTGAAG  TCTTCAGACG  GCATAGCGTC  TGCTTCCGCC
151 GTTTGCCCCG  CCGCCGGCCC  GATGCCGTCT  GAAACCGTGT  CCCACAAGTC
201 CGACAGCAGC  CGCAACACGT  CCGCCTCGCG  GCGCAATGTT  TCGCCCAAAT
251 GCCCCTTTGG  GACGGCTTTC  AGGCAGGATG  CCGCCAAGCC  GCGCAGGTTC
301 GGGGGCAAAT  CCCATATCCT  GACCGGTTTC  CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1578; ORF 542.a>:

```

a542.pep
1  MPKWSRIRRC  SVLSLMFSVS  ASRLT*CAPP  ANAAFRMLK  SSDGIASASA
51  VCPAAGPMPS  ETVSHKSDSS  RNTSASRRNV  SPKCPFGTAF  RQDAAKPRRF
101 GGKSHILTGS  R*

```

m542/a542 94.6% identity in 111 aa overlap

```

      10      20      30      40      50      60
m542.pep  MPKWSRIRRCVLSLMFSVSASRLTWCAPSANAAFRVRLKSSDGIASASAVCPAAGPMPS
      |||||
a542       MPKWSRIRRCVLSLMFSVSASRLTXCAPPANAAFRMLKSSDGIASASAVCPAAGPMPS
      10      20      30      40      50      60

      70      80      90      100     110
m542.pep  ETVSHKSDSSRNTSASRRNVSPKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
      |||||
a542       ETVSHKSDSSRNTSASRRNVSPKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
      70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1579>:

```

g543.seq
1  atggtttgtc  gggtatttgc  cgcgcttttt  ggctttcaac  tcggcaatca
51  gcccgctgat  gcctttggct  ttgatgattt  cgcgcaattg  gttgcgggtac
101 acggtaacca  ggctcgtgcc  ttcatgagcg  acgttgtagg  tacggatttt
151 gccgcccgtt  tggtaggtgg  taaagtccat  attgacgggc  ttctgaccgg
201 ggatgccgac  ttccgacacg  acgacgattt  ccttgccgcc  cttattgacg
251 atgggattgt  ctttgacggt  gacggtcgcg  tttttgaatt  tcagcatcgt
301 gccggaatag  gtgcggatca  gcagggtttg  aaattctttg  gccaacgctt
351 gtttttgcgc  ytcggacgcy  gtacgccaa  ggttgccgac  cgccaatgcy
401 gtcatacgtt  ggaaatcgaa  atagggaacc  gcataggctt  cggcttttgg
451 gcgtgcagaa  gccgcgtcgc  cgcttttgag  gatggtcaaa  acctgtgtgg
501 cgttttggcg  gatttgcccc  actgcgtcgg  ccggggaggg  aaatgccatg
551 ccgatgctca  aaataccgat  gcccaatgcy  ctgatgaagg  aggatttttt
601 cacgatgtct  ttctgaaaa  tggatgtgta  tgttattctt  gcggcttttt
651 ccgcattgcc  gccctcagcg  tttttctcgg  cgaagctggt  catgaattta
701 ccgatcaggt  tttccagaa  cattgcagaa  ctggttacgg  agatggtgtc
751 gccggcagca  aggttttccg  tatcgccgcc  ctgctgcagc  ccgatgtact
801 gttcgcctaa  aagtcccga  gtcaggattt  gcgcggaacc  gtcactgctg
851 aactgatact  tgccgtccaa  atcaaggcgc  accctcgctt  gataggattt
901 cgggtcaagc  ccgatagcgc  cgacgcgccc  gaccaatacg  cctgcggatt
951 tgacgggggc  attgaccttc  aaacgcgcga  tgcgcgcgaa  atcggcataa
1001 acggcgtaag  ttttgctcga  accgccgaac  gccgcgccgc  ccgccacgcg
1051 gaaagcgaga  aaggcaaccg  ccgccgcgcc  gatcaagacg  aacagtccga
1101 cccaaaattc  caatatgttc  tttttcatta  a

```

This corresponds to the amino acid sequence <SEQ ID 1580; ORF 543.ng>:

```

g543.pep
1  MVCRLFAAVF  GFQLGNQPD  AFGFDDFAEL  VAVHGNQARA  FDGDVVGTVF

```

m543.seq

1	ATGGTTTGTCT	GGTTATTTGCG	CGCCGTTTTT	GGCTTTCAC	TCGGCAATCA
51	GTCCGTCCAC	GCCTTTCGCT	TTGATAATT	CGCGAATTG	GTTCGCGTAC
101	ACGGTAACCA	GGCTCGCGCG	TTCCAGTGGC	ACGTTGTAGG	TACGGTATT
151	ACCGCCGCTT	TGGTAGGTGG	TGAAGTCCAT	GTTCAGCGGT	TTTTCGCCG
201	GTACGCCGAC	TTCCGCGCGG	ACGATGATT	CTTTGCCGCC	TTTATTGACG
251	ATGGGATTGT	CTTTGACGTT	GACGTTGGCG	TTTTTTAATT	TCAGCATCGT
301	GCCCGAATAG	GTCCGGATCA	GCAGGGTTTG	AAATTCCTTG	GCCAAACGTT
351	GTTTTTGCG	GTCGGACGCG	GTGCGCAAG	GGTTGCCGAC	CGCCAAATGG
401	GTCATACGTT	GGAATCGAA	ATAGGGAAT	GCATAGGCTT	CGGCTTTTTG
451	GCGAGCGGTG	TTGGCATCGC	CGTTTTTTAA	GATGCTCAAT	ACTTGAGTGG
501	CGTTTTGACG	GATTTGGCTT	ACCGCGTCGG	CAGGGGCGGC	AAATGCCATG
551	CCGATGCTCA	AAATACCGAT	GCCCAATGCG	CTGATAGGG	AGGATTTTTT
601	CATGATTAAG	TGTCCTAGTT	TGAATATGAT	GGCATACGTT	TATTCCGGCG
651	CTTTTCCCG	ATTGCCCGCG	TCCGCAATTT	TCTCGGCAA	ACTCGTCATG
701	AATTTGCCGA	TAAGGTTTTT	CAGAACCAT	GCAGAACTGG	TTACGGAGAT
751	GGTGTCGCCG	GCAGCAAGGT	TTTCCGTGTC	GCCGCCCTGC	TGCAGCCCGA
801	TGTACTGCTC	GCCCAAAAGT	CCCCAAGTCA	GGATTTGCGC	GGAAACGTCG
851	CTGCTGAAGT	GATACCTTGC	GTCCAAATCG	AGGCGCACCC	TGCCTGATA
901	GGATTTCCGG	TCAAGTCCGA	TAGCGCCGAC	GCGCCCGACC	AAATACGCGT
951	CGGATTTGAC	GGGGGCATTG	ACCTTCAAAC	CGCCGATGTC	GCCGAAATCG
1001	GCATAAACGG	CGTAAGTTTT	GTCCGAACCG	CCGGAACCGG	CACCGCCGGC
1051	CACCGCGAAA	GCGAGAAAGT	CAACCGCCGC	CGCGCAATC	AGGACGAACA
1101	GTCCGACCCA	AAATTCCAAT	ATGTTCTTCT	TCATTAA	

m543 . pep

1	<u>MVCRLFAAVF</u>	<u>GFOGLNQSVH</u>	<u>AFRFDNF AEL</u>	<u>VAVHGNQARA</u>	<u>FDGDVVGVTVF</u>
51	TAALVGGEVH	VDGFLPGYAD	FGADDDFFAA	FIDDGIVFV	DVGVFVXFQHR
101	AGIGAQOQGL	KQFGQRLFLR	VGAGAPRVAD	RQCCHTLEIE	IGNRGIFGFL
151	ASGVGIAVFX	DAFFLHSGVLT	DLAYRVGRGG	KCHADAQNTD	QCADEGGFF
201	HDXVSXFEYD	GIRLFGGFFR	IAAVGI FLKG	TRHEFADKVF	QNHCR"GYGD
251	GVAGSKVFRV	AALLQPDVLL	AQKRSQDLAR	GNVAAELILA	VQIEAHPRLI
301	GFVKSDSAD	APDQYACGFD	GGIDLTQADV	AEINGVVSF	VRTAERTAG
351	HAESEKGNRR	RANQDEQSDP	KFYVLLH*		

ORF 543 shows 84.2% identity over a 379 aa overlap with a predicted ORF (ORF 543.ng) from *N. gonorrhoeae*:

m543/q543

	10	20	30	40	50	60
m543 . pep	MVCRLFAAVFGFQLGNQSVHAFRDNFAELVAVHGNQARAFDGDVVGTVFTAAALVGGVEVH					
g543	MVCRLFAAVFGFQLGNQPVDAFGFDDFAELVAVHGNQARAFDGDVVGTVFAAALVGGKVV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m543 . pep	VDGFLPGYADFGADDDFFAAFIDDGIVFDVDVGVFQFQHRAGIGADQOGLKFFGQRLFLR					
	: :					
g543	IDGLLTGDAADFGTDDDFLAALIDDGIVFDVDGRVFEFQFQHRAGIGADQOGLKFFGQRLFLR					
	70	80	90	100	110	120
	130	140	150	160	170	180

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```

m543.pep      VGRGAPRVADRQCGHTLEIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543          VGRGTPRVADRQCGHTLEIEIGNRIGFGFWACRSRVAAFEDGQNLCGVLADLSHCVGRGG
               130      140      150      160      170      180

               190      200      210      220      230      239
m543.pep      KCHADAQNTDAQCADEGGFFHDVXVSXFEYDG-IRLFGGFFRIAAGVIFLGKTRHEFADKV
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543          KCHADAQNTDAQCADEGGFFHDV---FPENGCVCLFCGFFRIAALSVFLGEAGHEFTDQV
               190      200      210      220      230

               240      250      260      270      280      290      299
m543.pep      FQNHCRRTGYGDGVAGSKVFRVAALLQPDVLLAQKRSRQDLRGNVAAELILAVQIEAHPRL
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543          FQNHCRRTGYGDGVAGSKVFRVAALLQPDVLFQAQKRSRQDLRGNVTAEILAVQIKAHPR
               240      250      260      270      280      290

               300      310      320      330      340      350      359
m543.pep      IGFRVKSDSADAPDQYACGFDGGIDLQADVAEIGINGVSFVRTAERRTAGHAESEKGNR
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543          IGFRVKPDSADAPDQYACGFDGGIDLQADVAEIGINGVSFVRTAERRAARHAESEKGNR
               300      310      320      330      340      350

               360      370      379
m543.pep      RRANQDEQSDPKFQYVLLHX
               |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543          RRADQDEQSDPKFQYVLFHX
               360      370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1583>:

```

a543.seq
1  ATGGCTTATG GATTACTTGC TGCCGTTTNT AGCCTTCAAC TCGNCAATCA
51  GTCCGTCCAC GCCTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
101 ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
201 NNACGCCGAC TTCGGCGCGG ACGATGATTT CTTTGCCGCC TTTATTGACG
251 ATNGGATTGT CTTTGACGTT GACGTTGGCG TTTTAAATT TCAGCATCGT
301 GCCGGAATAG GTGCGGATCA GCAGGGTTTG AAATCTTTG GCCAACGCTT
351 GTTTTTCGCG GTCCGACGCG GTGCCCAAG GGTGCCGAC CGCCAATGCG
401 GTCATACGTT GGAATCGAA ATAGGGAATC GCATAGCCTT CGGCTTTTGT
451 GCGGGCGGTG TTGGCATCAC CGCTTTTAA GATGCTCAAT ACTGAGTGG
501 CGTTTTGACG GATTGTTT ACCGCGTCGG CAGGGCGGCG AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAAGG AGGATTTTTT
601 CATGATTAAG TGTCCTAGTT TGAATATGAT GGCATACGTT TATTCGGCGG
651 CTTTTTCGCG ATTGCCGCG TCGGCATTTT TCTCGGCAA ACTCGTCATG
701 AATTTGCCGA TAAGTTTTT CAGAACCATT GCAGAACTGG TTACGGAGAT
751 GGTGTCGCCG GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
801 TGTACTGCTC GCCCAAAAGT CCCGAACTCA GGATTTCGCG GGAAACGTCG
851 CTGCTGAACT GATACTTGCC GTCCAAATCG AGGCGCACCC TCGCCTGATA
901 GGATTTCGGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCCTG
951 CGGATTGAC GGGGGCATTG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
1001 GCATAAACGG CGTAAGTTTT GTCCGAACCG CCGAACGCCG CACCGCCGGC
1051 CACGCGGAAA GCGAGAAAG CAACCGCCGC CGCGCCAATC AGGACGAACA
1101 GTCCGACCCA AAATTCCAAT ATGTTCTTTT TCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1584; ORF 543.a>:

```

a543.pep
1  MAYGLLAAXV SLQLXNOSVH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF
51  TAALVGGEVH VDGFLPGXAD FGADDDFFAA FIDDXIVFDV DVGVF*FQHR
101 AGIGADQOGL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL
151 AGGVGITAF* DAQYLSGVLT DLVYRVGRGG KCHADAQNTD AQCADEGGFF
201 HD*VS*FEYD GIRLFGGFFR IAAVGIFLGK TRHEFADKVF QNHCRRTGYGD
251 GVAGSKVFRV AALLQPDVLL AQKRSRQDLR GNVAAELILA VQIEAHPRLI
301 GFRVKSDSAD APDQYACGFD GGIDLQADV AEIGINGVSF VRTAERRTAG

```

351 HAESEKGNRR RANQDEQSDP KFQYVLFH*

m543/a543 96.0% identity in 378 aa overlap

	10	20	30	40	50	60
m543.pep	MVCRLFAAV	FGFQLGNQSV	HAFRFDNF	AELVAVHGN	QARAFDGD	VVGTVFTAALVGGEVH
	:	: :	: :	: :	: :	: :
a543	MAYGLLA	AVXSLQLXN	QSVHAFRFD	NFAELVAVH	GNQARAFD	GDDVVGTVFTAALVGGEVH
	10	20	30	40	50	60
	70	80	90	100	110	120
m543.pep	VDGFLPGY	ADFGADDD	FFAAFI	DDGIVFDV	DVGVFQHR	AGIGADQQGLKFFGQRLFLR
	:	: :	: :	: :	: :	: :
a543	VDGFLPGX	ADFGADDD	FFAAFI	DDXIVFDV	DVGVFQHR	AGIGADQQGLKFFGQRLFLR
	70	80	90	100	110	120
	130	140	150	160	170	180
m543.pep	VGRGAPRV	ADRQCGHT	LEIEIGNR	IGFGFLAS	GVGIAVFX	DAQYLSGVLTDLAYRVGRGG
	:	: :	: :	: :	: :	: :
a543	VGRGAPRV	ADRQCGHT	LEIEIGNR	IGFGFLAG	GVGITAFX	DAQYLSGVLTDLVYRVGRGG
	130	140	150	160	170	180
	190	200	210	220	230	240
m543.pep	KCHADAQNT	DAQCADEGG	FFHDXVSX	FEYDGI	RLFGGFFR	IAAVGIFLGKTRHEFADKVF
	:	: :	: :	: :	: :	: :
a543	KCHADAQNT	DAQCADEGG	FFHDXVSX	FEYDGI	RLFGGFFR	IAAVGIFLGKTRHEFADKVF
	190	200	210	220	230	240
	250	260	270	280	290	300
m543.pep	QNHCR	TGYGDG	VAGSKV	FRVAALL	QPDVLLA	QKSRSDLRGNVAAELILAVQIEAHPRLI
	:	: :	: :	: :	: :	: :
a543	QNHCR	TGYGDG	VAGSKV	FRVAALL	QPDVLLA	QKSRSDLRGNVAAELILAVQIEAHPRLI
	250	260	270	280	290	300
	310	320	330	340	350	360
m543.pep	GFRVKSDS	ADAPDQY	ACGFDGG	IDLQTA	DAVEIGI	NGVSEFVRTAERRTAGHAESEKGNRR
	:	: :	: :	: :	: :	: :
a543	GFRVKSDS	ADAPDQY	ACGFDGG	IDLQTA	DAVEIGI	NGVSEFVRTAERRTAGHAESEKGNRR
	310	320	330	340	350	360
	370	379				
m543.pep	RANQDEQSD	PKFQYVLLHX				
	:	: :				
a543	RANQDEQSD	PKFQYVLFHX				
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1585>:

g544.seq

```

1  atgaaaaaaa tactcaccgc cgcgcgcgtc gcactgatcg gcatectcct
51  cgccaccgtc ctcatecccg acagtaaaac cgcgcccgcc ttctccctgc
101 ccgacctgca cggaaaaacc gtttccaacg ccgacctgca aggcaaagtc
151 asccctgatta attttggtt tccctcctgt ccgggttggtg tgagcgaaat
201 gcccaaagtc accaaaacgg caaacgacta caaaaataaa gatttccaag
251 tcctcgccgt tgcccagccc atcgatccga tagaaagcgt ccgccaatac
301 gtcaaagact acggactgcc gtttaccgtc atttatgatg cggacaaagc
351 cgtcggacag gcattcggca cacagggtta tccgacttcc gtccttatcg
401 gcaaaaaagg cgaaatcctc aaaacttatg tcggcggaacc cgatttcggc
451 aaactctacc aagaaatcga taccgcgctg gcgcaatag

```

This corresponds to the amino acid sequence <SEQ ID 1586; ORF 544.ng>:

g544.pep

```

1  MKKILTAAAV ALIGILLATV LIPDSKTAPA FSLPDLHGKT VSNADLQGV
51  TLINFWFPSC PGCVSEMPKV TKTANDYKNK DFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV IYDADKAVGQ AFGTQVYPTS VLIGKKGEIL KTYVGEPDFG

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1587>:

1	ATGAwAAAAA	TACTCACCGC	CGCCGTCGTC	GCACTGATCG	GCATCCTCCT
51	TGCCATCGTC	CTCmTCCCG	ACAGCAAAAC	CGCGCCCGCC	TTCTCCmTGC
101	CCGACCTGCA	CGGAAAAAAC	GTTTCCAACG	CCGACCTGCA	AGGCAAAAGTA
151	ACCCTGATTA	ATTTTGGTT	TCCCTCCTGT	CCGGGTGTGT	TGAGCGAwAT
201	GCCCAAAATC	ATTAACAACG	CAAAATGACTA	TAAAwCAAA	AACTTCCAAG
251	TACTTGCCGT	CGCCACAGCC	ATCGATCCGA	TAGAAAGCGT	CCGCCAATAT
301	GTCAAAGACT	ACGGTTTGCC	GTTTACCGTC	ATGTATGATG	CGGACAAAGC
351	TGTGCGACAG	CGGTTTCGGCA	CACAGGTTTA	TCCGACTTCC	GTCTTATFCG
401	GCAAAATAAG	CGAAATCTTC	AAAACCTACG	TCGGCGTACC	CGATTTCCGC
451	AAACTCTACC	AAGAAATCGA	TACGCGCGTG	CGCAATAG	

m544.pgp

MS11: pep

1 MKKILTAADV ALIGILLAIV LXPDSKTAPA FSXPDLHGKT VSNADLQGVV
51 TLINFWFPSC PGCVSXMPKI IKTANDYKXK NFQVLAVAQP IDPIESVRQY
101 VKDYLGLPFTV MYDADKAVGQ AFGTQVYPTS VLIQ*GEIF KTYVGEPDFG
151 KLYOEIDTRV AO*

Homology with a predicted ORF from *N. gonorrhoeae*

m544/q544

	10	20	30	40	50	60
m544 . pep	MXKILTA	AAVVALIGILLAI	VLXPDSKT	APAFSXPDL	HGKTVSNADL	QGKVTLINFWFPSC
g544	MKKILTA	AAVVALIGILLAT	VLIPDSKT	APAFSLPDL	HGKTVSNADL	QGKVTLINFWFPSC
	10	20	30	40	50	60
	70	80	90	100	110	120
m544 . pep	PGCVSX	MPKIIKT	ANDYKX	KNFQVL	AVAQPID	PIESVRQYVKDYGLPFTVMYDADKAVGQ
g544	PGCVSE	MPKVTKT	ANDYKN	KDFQVL	AVAQPID	PIESVRQYVKDYGLPFTVIYDADKAVGQ
	70	80	90	100	110	120
	130	140	150	160		
m544 . pep	AFGTQV	YPTSVL	IGKKGEI	FKTYVG	EPDFGK	LYQEIDTRVAQX
g544	AFGTQV	YPTSVL	IGKKGEI	LKTYVG	EPDFGK	LYQEIDTALAQX
	130	140	150	160		

a544.seq

```

1      ATGAAAAAAA TACTCACCGC CGCGCTCGTC GCACTGATCG GCATCCTCCT
51     TGCCATCGTC CTCATCCCGC ACAGCAAAAC CGCGCCCGCT TTCTCCCTGT
101    CCGANGTCGA CGGAAAAANC GTTTNCAACG CCGAGCTGCA AGGCNAAGTT
151    ANCCTGATTA ANTTTGGTT TCCCTCCTGT CCGGGTTGTG TGAGCGGAAT
201    GNCCANAATC ATTAAAACGG CAAATGACTA TAAAAACAAA AACTCTCAAG
251    TCCTTGCCGT CGCCAGCCG ATCGATCCGA TAGAAAGCGT CCGCCAATAT
301    GTCAAAGACT ACGGTTTGCC GTTTACCGTC ATGTATGATG CGGACAAAGC
351    TGTCCGACAG CGATTCCGCA CACAGGTTTA TCCGACTTCC GTCTTATTCG
401    GCAAAAAAGG CGAAATCTC AAAACTTATG TCGGCGTAAC CGATTCGGGC
451    AAACCTTACC AAGAAATCGA TACCGCGCTG GCACAATAG

```

a544.pep

1 MKKILTA^{AVV} ALIGILLA^{IV} LIPDSKTAPA FLSXLHGKX VXNADLQGXV
51 XLIXFWF^{PSC} PGCVSEMXXI IKTANDYKNK NFOVLAVQ^P IDPIESVRQY
101 VKDYG^LPFTT MYDADKAVGQ AFGTQVYPTS V^LIGKKGEIL KTYVGE^PDFG

824

151 KLYQEIDTAL AQ*

m544/a544 88.9% identity in 162 aa overlap

	10	20	30	40	50	60
m544 . pep	MXKILTAAVVALIGILLAIVLXPDSKTAPAFSXPDLHGKTVSNADLQGKVTLINFWFPSC					
a544	MKKILTAAVVALIGILLAIVLIPDSKTAPAFSLSLHGKXVXNADLQGXVXLIXFWFPSC					
	10	20	30	40	50	60
m544 . pep	PGCVSXPMPKIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ					
a544	PGCVSEMXXIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ					
	70	80	90	100	110	120
m544 . pep	PGCVSXPMPKIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ					
a544	PGCVSEMXXIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ					
	70	80	90	100	110	120
m544 . pep	AFGTQVYPTSVLIGKXGEIFKTYVGEPDFGKLYQEIDTRVAQX					
a544	AFGTQVYPTSVLIGKKGEILKTYVGEPDFGKLYQEIDTALAQX					
	130	140	150	160		
m544 . pep	AFGTQVYPTSVLIGKXGEIFKTYVGEPDFGKLYQEIDTRVAQX					
a544	AFGTQVYPTSVLIGKKGEILKTYVGEPDFGKLYQEIDTALAQX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1591>:

g547 . seq

```

1  atgttcgtag  ataacggatt  taataaaacg  gtacgcgagtt  ttgccccaaat
51  cgtcgaact  ttcgacgtat  tcttcttttag  gaacgattgc  gcctttttta
101 cgcagatgaa  acagcgggtgc  ggttgggtct  gctcgttggt  atatctcggt
151 gatataatta  caagatgcgg  cttcgagatt  ccgaaccgct  cctttaaaga
201 gcttgggctt  ttgatacaga  taagtctgtc  ggaacgtttt  aggactaatg
251 ccgaagtcga  gatggatgcc  cattacttcc  ccttactcag  aaaatattta
301 aaatttataa  tgttacatat  agttacaaat  attagagttt  tttgtgtgtg
351 cgtcaaggaa  ttgttgacaa  ttttagttaa  aaatttgtct  ccaaaccgaa
401 aaaagcgggt  tgttttttgt  tgtttaa

```

This corresponds to the amino acid sequence <SEQ ID 1592; ORF 547.ng>:

g547 . pep

```

1  MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
51  DIFPRCGFEI PNRSPKELGL LIQISLSERF RTNAEVEMDA HYFPLLRKYL
101 KFIMLHIVTN IRVFCVCVKE LLTILVKNLN PNGKKRFVFC C*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1593>:

m547 . seq

```

1  ATGTTTCGTAG ATAACGGATT TAATAAAACG GTACCGAGTT TTGCCCAAAT
51  CGTCGAAACT TTCGACGTAT TCTTCTTTAG GAACGATTGC GCCTTTTFTA
101 CGCAGATGAA ACAGCGGTGC GGTGCGGTCT GCTCGTTGCT ATATCTCGTT
151 GATATCTTTC CAAGATGCGG ATTCGAGATT CCGAACCCTT CTTTAAAGA
201 GCTTGGGCTT TTGATACAGA TAAGTCTGTC GGAACGTTT AGGACTAATG
251 CCGAAGTCGA GATGGATGCT CATTACTTCC CCTTACTCAG AAAATATTTA
301 AAATTTATAA TGTTACATAT ATTTACAAAT ATTAAAGTTT TTTTGTGTGT
351 GTGCGTCAAG GAATTGTTGA CAATTTTAGT TAAAAATTG TCTCCAAACG
401 GAAAAAAGCG GTTTGTTTTT TGTGTGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1594; ORF 547>:

m547 . pep

```

1  MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
51  DIFPRCGFEI PNRSPKELGL LIQISLSERF RTNAEVEMDA HYFPLLRKYL
101 KFIMLHIFTN IKVFXCVCKV ELLTILVKNL SPNGKKRFVF CC*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 547 shows 97.2% identity over a 142 aa overlap with a predicted ORF (ORF 547.ng) from *N. gonorrhoeae*:

m547/g547

825

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
g547	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFTRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIFTNIKVFXCVCVK					
g547	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIVTNIRVF-CVCVK					
	70	80	90	100	110	
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCCX					
g547	ELLTILVKNLSPNGKKRFVFCCX					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1595>:

```
a547.seq
1  ATGTTCTAG  ATAACGGATT  TAATAAACG  GTAGCGAGTT  TTGCCCAAAT
51  CGTCGAACT  TTCGACGTAT  TCTTCTTAG  GAACAATTGC  ACCTTTTSTA
101 CGCAGATGAA  ACAGCGGTGC  GGTGGGTCT  GCTCGTTGGT  ATATCTCGTT
151 GATATCTTTC  CAAGATGCGG  CTTGAGATT  CCGAACCGCT  CCTTTAAAGA
201 GCTTGGGCTT  TTGATACAGA  TAAGTCTGTC  GGAACGTTT  AGGACTAATG
251 CCGAAGTCGA  GATAGATGCT  CATTACTTCC  CCTTACTCAG  AAAATATTTA
301 AAATTTATAA  TGTACATAT  ATTACAAAT  ATTAAAGTTT  TTTT.TGTGT
351 GTGCGTCAAG  GAATTGTTGA  CAATTTTAGT  T
```

This corresponds to the amino acid sequence <SEQ ID 1596; ORF 547.a>:

```
a547.pep
1  MFVDNGFNKT  VASFAQIVET  FDVFFFRNNC  TFFTQMKQRC  GWVCSLVYLV
51  DIFPRCGFEI  PNRSFKELGL  LIQISLSERF  RTNAEVEIDA  HYFPLLRLKY
101 KFILMLHIFTN  IKVFXCVCVK  ELLTILV
```

m547/a547 97.6% identity in 127 aa overlap

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
a547	MFVDNGFNKTVASFAQIVETFDVFFFRNCTFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIFTNIKVFXCVCVK					
a547	PNRSFKELGLLIQISLSERFRTNAEVEIDAHYFPLLRLKYLKFIMLHIFTNIKVFXCVCVK					
	70	80	90	100	110	120
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCCX					
a547	ELLTILV					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1597>:

```
g548.seq
1  atgttttccg  taccgcgttc  ctttttgccg  ggcgttttcg  tacttgccgc
51  gcttgccgcc  tgcaaacctc  aagacaacag  tgcggcgcaa  gccgcttctt
101 caagtgcac  cgcgccggtc  gcggaaaatg  cggcaaacgc  gcaaacgcgc
151 ggtacggata  tgcgtaagga  agacatcggc  ggcgatttca  cactgaccga
201 cggcgaaggc  aagcctttca  gcctgagcga  tttgaaaggc  aaggctcgtga
251 ttctgtcttt  cgcctttacg  cactgtcccc  atgtctgccc  gacagggtct
```

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```

301 ttgacgtaca gcgacacttt gaagcagttg ggcgggcagg ctaaggacgt
351 gaaagtggty ttcgtcagca tcgatccgga acgcgacacg cctgaaatca
401 tcggcaagta tgccaaacag ttcaatccgg actttatcgg tctgacggca
451 acggggcgcc aaaacctgcc ggtcatcaag cagcaatacc gcgtggtttc
501 tgccaaaatc aatcaaaaag acgacagcga aaactatttg gtcgaccact
551 cttccggtgc gtatcttata gataaaaacg gtgaggttgc cattttctcg
601 ccttacggaa gcgagccgga aacgattgct gccgatgtaa ggaccctgct
651 ctga

```

This corresponds to the amino acid sequence <SEQ ID 1598; ORF 548.ng>:

```

g548.pep
1  MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ AASSSASAPA AENAAKPOTR
51  GTDMRKEDIG GDFTLTDGEG KPFSLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSDTLKQL GGQAKDVKVV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGGQNLPIVK QQYRVVSAKI NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1599>:

```

m548.seq
1  ATGTTTTCCG TACCGCGTTC CTTTTTGCCG GCGGTTTTTC TACTTGCCGC
51  GCTTGCCGCC TGCAAACCTC AAGACAACAG TCGCGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAAATG CGGCAAAGCA AnACACGCGC
151 GGTACGGATA TCGTAAGGA AGACATCGGC GCGGATTTCa CGCTGACCGA
201 CCGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCTGTA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGGACAG CTAAGGACGT
351 GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGs TCTGACGGCA
451 ACGGGCGGCC AAAACCTGCC GGTATCAAG CAGCAATACc GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAmG ACGACAGCGA AAActATTtG GTCGACCACT
551 CTTCGGGTGC GTATCTCATC GACAAAACG GTGAGGTTGC CATTTTCTCG
601 CCTTACGGA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1600; ORF 548>:

```

m548.pep
1  MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKQXTR
51  GTDMRKEDIG GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSDTLKQL GGQAKDVKVV FVSIDPERDT PEIIGKYAKQ FNPDFIXLTA
151 TGGQNLPIVK QQYRVVSAKV NQXDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 548 shows 95.9% identity over a 217 aa overlap with a predicted ORF (ORF 548.ng) from *N. gonorrhoeae*:

```

m548/g548
          10      20      30      40      50      60
m548.pep  MFSVPRSFLPGVFVLAALAAACKPQDNSAAQVASSSASASAENAAKQXTRGTDMRKEDIG
          |||
g548       MFSVPRSFLPGVFVLAALAAACKPQDNSAAQAASSSASAPAAENAAKPQTRGTDMRKEDIG
          |||
          10      20      30      40      50      60

          70      80      90     100     110     120
m548.pep  GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKVV
          |||
g548       GDFTLTDGEGKPFSLSDLKGKVVILSFGFTHCPDVCPTGLLTYSDTLKQLGGQAKDVKVV
          |||
          70      80      90     100     110     120

          130     140     150     160     170     180
m548.pep  FVSIDPERDTP EIIGKYAKQFNPDFIXLTATGGQNLPIVKQQYRVVSAKVNQXDDSENYL
          |||
g548       FVSIDPERDTP EIIGKYAKQFNPDFIGLTATGGQNLPIVKQQYRVVSAKINQKDDSENYL
          |||
          130     140     150     160     170     180

```

827

```

                190      200      210
m548.pep      VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLX
                |||||
g548          VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLX
                190      200      210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1601>:

```

a548.seq
1  ATGTTTTCCTG TACCGCGTTC CTTTTTGCCG GCGTTTTTCG TACTTGCCCG
51  GCTTGCCGCC TGCAAACCTC AAGACAACAG TCGGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGCTC GCGGAAAATG CGGCAAAGCC GCAAACGCGC
151 GGTACGGATA TCGCTAAGGA AGACATCGGC GCGGATTTCG CGCTGACCGA
201 CCGCGAAGGC AAGCCTTTCG ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCG GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGG TCTGACGGCA
451 ACGGGCGACC AAAACCTGCC GGTCAACAAG CAGCAATACC GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAAG ACGACAGCGA AAATATTGTC GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAAACG GTGAGGTTGC CATTTTCTCG
601 CTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA EGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1602; ORF 548.a>:

```

a548.pep
1  MFSVPRSFPLGVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKPQTR
51  GTDMRKEDIG GDFLTLDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTFL
101 LTYSDTLKQL GGQAKDVKV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGDQNLPIVK QQYRVVSAKV NQKDDSENYL VDHSSGAYLI DNKGEVAIFS
201 PYGSEPETIA ADVRTL*

```

m548/a548 97.7% identity in 217 aa overlap

```

                10      20      30      40      50      60
m548.pep      MFSVPRSFPLGVFVLAALAAACKPQDNSAAQVASSSASASAAENAAKQXTRGTDMRKEDIG
                |||||
a548          MFSVPRSFPLGVFVLAALAAACKPQDNSAAQVASSSASASAAENAAKPQTRGTDMRKEDIG
                10      20      30      40      50      60

                70      80      90      100     110     120
m548.pep      GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSIDLKQLGGQAKDVKV
                |||||
a548          GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSIDLKQLGGQAKDVKV
                70      80      90      100     110     120

                130     140     150     160     170     180
m548.pep      FVSIDPERDTP E IIGKYAKQFNPD F IXL TATGGQNLPIVKQYRVVSAKVNQKDDSENYL
                |||||
a548          FVSIDPERDTP E IIGKYAKQFNPD F IGL TATGDQNLPIVKQYRVVSAKVNQKDDSENYL
                130     140     150     160     170     180

                190     200     210
m548.pep      VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLX
                |||||
a548          VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLX
                190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1603>:

```

g550.seq
1  atgataacgg acaggtttca tctctttcat tttccagtat ctttcattta
51  tcaatctgac aacaaaatgc cgcctgaaaa cagttcagac ggcatthtaa
101 ccacaaacgg cttacagctt ccattcgccc aacttggcag cgtaagcttc

```

828

```

151  caaatctgca atcgacggg ttgccacgcc gctttccatc gctgctttgg
201  cggcagccgt agcgacgcga ggcagcaggc gggaaatcgaa cggagtagga
251  atcaggtatt ccgcgccgaa ttcgaatttc ttaccgtaag cggcaaccac
301  ttcttcgggt acttcttcca tcgccaaatc tgccaaagca tacacgcagg
351  cgcgtttcat ttcttcggtg atggtggttg cgcgcacatc caacgcgccc
401  cggaagatga acgggaagca caatacgttg ttcacttggt tcgggaagtc
451  ggagcggccg gtaccgataa ccacgtcccg acgggtttct ttccgcagcg
501  gcggcaggat ttccggattc gggttggcca tggcgaacac gatgggtttt
551  tcgttcacgc tgttcaacat ttcaggcgtc agcagggttg cgcgcgagag
601  gcccagaag atgtctttgc ctttaaccgc atcggcaagt acgcgcgggc
651  cgttgtcttc aacggcgtag aatttttttg attcgtccat gcggtctttg
701  tcttcgcggg tttggtaaat cacgcctttg gagttagcaa cgtttacgtt
751  ttcacgtttc aagcccaaat ccagcagttg gttcaggcag gcaatcgcgg
801  cggcacctgc gccggagcac accaaagtcg cttcttcgat ttacggccg
851  gtataacgca gggcggttcaa tacggcgcg cggtaatga tggcgtgcc
901  gtgctggtca tcatgaaata cggggatttt gcagcggttg cgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1604; ORF 550.ng>:

g550.pep

```

1  MITDRPHLFH FPVSFIYQSD NKMPPENSSD GILTTNGLQL PFAQLGVSFV
51  QICNRTGCHA AFHRCFGGSR SDARQQAGIE RSRNQVFRAE FEFLTVSGNH
101 FFGYFFHRQI CQSIHAGAFH FFVDGGCADI QRAPEDEREA QVVVHLVREV
151 GAAGTDNHVR TGFFRQRRQD FRIRVGHGEH DGFFVHRVQH FRRQQVCAGE
201 AQEDVFAFNR IGKYAPAVVF NGVEFFGFVH AVFVFAGLVN HAFGVANGYV
251 FTFQAQIQQL VQAGNRGGTC AGAHQSRFFD FTAGITQGVQ YGGGGNDGRA
301 VLVIMKYGDF AAFA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1605>:

m550.seq (partial)

```

1  ..GACGGCATCG GCAAGCACGC GCTGGCCGTT GTCTTCAATG GCGTAGAACT
51  GTTGGACTC GTCCATACGG TCTTTGTCTT CGCGGGTTTG GTAAATCACG
101 CCTTGGAGT CGCAAACGGT CACGTTTTCG CGTTTCAAGC CCATATCCAG
151 CAATTGGwTC AAGCAGGCAA TCGCGGCCGC ACCTGCGCCG GAACACACCA
201 AAGTCGCTTC TTCGATTITA CGGCCGGTAA AACGCAKGGC GTTCAATACG
251 GCGGCGGCCG TAATGATGGC CGTGCCGTGC TGGTCGTCGT GGAATACGGG
301 GATTTTGCAG CGTTTGCGTA A

```

This corresponds to the amino acid sequence <SEQ ID 1606; ORF 550>:

m550.pep (partial)

```

1  ..DGIGKHALAV VFNGVELFGL VHTVVFVAGL VNHAFGVANG HVFAFQAQIQ
51  QLXQAGNRGR TCAGTHQSRF FDFTAGKTXG VQYGGGGNDG RAVLVVVEYG
101 DFAAFA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 550 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 550.ng) from *N. gonorrhoeae*:

m550/g550

m550.pep				10	20	30	
				DGIGKHALAVVFNGVELFGLVHTVVFVAGLVN			
				: : : : : : :			
g550	DGFFVHRVQHFR	RQQVCAGEAQED	VFAFNRIGKYAP	AVVFNGVEFFGFV	HAVFVAGLVN		
	190	200	210	220	230	240	
m550.pep		40	50	60	70	80	90
		HAFGVANGHVFA	FQAQIQQLXQAG	NRGRTCAGTHQSR	FFDFTAGKTXGV	QYGGGGNDGRA	
		: : : : :		: : : : :			
g550		HAFGVANGYVFT	FQAQIQQLVQAG	NRGGTCAGAHQSR	FFDFTAGITQGV	QYGGGGNDGRA	
		250	260	270	280	290	300
m550.pep		100					
		VLVVVEYGDFAAF	AX				
		: : : : :					
g550		VLVIMKYGDFAAF	AX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1607>:

```
a550.seq
1  CTATATCAAT CTGACAGCAA AATGCCGCCT GAAAACAGTT CAGACGGCAT
51  TTAAACCGCA AACGGCTTAC AGCTTCCATT CGCTCAGCTT GGCAGCGTAA
101 GCTTCCAAAT CTGCAATCGG ACGGGTTGCC ACGCCGCTTT CCATCGCTGC
151 TTTGGCGGCA GCCGTAGCAA CGCGCGGAG CAGGCGGGAA TCGAACGGAG
201 TCGGAATCAG GTATTCCGCG CCGAATTCAA ATTTCTTACC GTAAGCGGCA
251 ACCACTTCTT CGGTTACCTC TTCCATCGCC AAATCCGCCA AAGCATACAC
301 GCAGGCGCGT TTCATTCTTT CGTTGATGGT CGTCGCGCCG ACATCCAACG
351 CACCGCGGAA GATGAACGGG AAGCACAATA CATTGTTCAC TTGGTTCGGG
401 AAGTCGGAGC GGCCGGTACC GATAACCACG TCCGGACGGG TTTCTTTCGC
451 CAGCGCGGCG AGGATTTCGG GATTGCGGTT GGCCATAGCG AACACGATGG
501 GTTTTTTCGT CATGGTGTTT AGTATTTCAG GCGTCAGCAG GTTCGCGCCG
551 GAGAGGCCCA AGAAGATGTC TTTGCCTTTG ACGGCATCGG CAAGCAGCGG
601 CTGGCCGTTG TCTTCAATGG CGTAGAACTG TTTGGACTCG TCCATACGGT
651 CTTTGTCTTC GCGGGTTTGG TAAATCACGC CTTTGGAGTC GCAAACGGTC
701 ACGTTTTTCG GTTTCAGGCC CAAATCCAGC AATTGGTTCA AGCAGGCAAT
751 CGCGGCGGCA CCTGCGCCGG AACACACCAA AGTCGCTTCT TCGATTTTAC
801 GGCCCGTAAA ACGCAGGGCG TTCAATACGG CAGCGCGCGT AATGATGGCC
851 GTGCCGTGCT GGTCTCGTG GAATACGGGG ATTTTGCAGC GTTTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1608; ORF 550.a>:

```
a550.pep
1  LYQSDSKMPP ENSSDGILTA NGLQLPFAQL GSVSFQICNR TGCHAAFHRC
51  FGGSRSNARQ QAGIERSRNO VFRAEFKFLT VSGNHFFGYL FHRQIRQSIH
101 AGAFHFFVDG RRADIQRTAE DEREAYIVH LVREVGAAGT DNHVRTGFFR
151 QRRQDFRIRV GHSEHDGFFV HGVQYFRRQQ VRAGEAQEDV FAFDGIGKHA
201 LAVVFNGVEL FGLVHTVFVF AGLVNHAFGV ANGHVFAFQA QIQQLVQAGN
251 RGRTCAGTHQ SRFFDFTAGK TQGVQYGS GG NDGRAVLVVV EYGDFAAFA*
```

m550/a550 97.2% identity in 106 aa overlap

```
m550.pep                                10      20      30
                                DGICKHALAVVFNGVELFGLVHTVFVFAGL
                                |||
a550      EHDGFFVHGVQYFRRQQVRAGEAQEDVFAFDGIGKHALAVVFNGVELFGLVHTVFVFAGL
              170      180      190      200      210      220

              40      50      60      70      80      90
m550.pep      VNHAFGVANGHVFAFQAQIQQLXQAGNRGRTCAGTHQSRFFDFTAGKTXGVQYGGGGNDG
              |||
a550      VNHAFGVANGHVFAFQAQIQQLVQAGNRGRTCAGTHQSRFFDFTAGKTQGVQYGS GGNDG
              230      240      250      260      270      280

              100
m550.pep      RAVLVVVEYGDFAAFAX
              |||
a550      RAVLVVVEYGDFAAFAX
              290      300
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1609>:

```
g552.seq
1  atgaagctga aaaccttggt attgcccttc gccgcactgg cattgtgtgc
51  caacgcattt gccgccccgc ccggcgacgc gtcgttggca cgttggtcgg
101 atacgcagaa tttcgaccgg gatatagaaa aaaatatgat tgaaggcttt
151 aatgccggat ttaaaccgta tgcggacaaa gcccttgccg aaatgccgga
201 agcgaaaaaa gatcaggcgg cagaagcctt taatcggtat cgtgagaatg
251 ttttgaaaga tttgattacg cccgaagtga aacaggctgt ccgcaatacc
301 ttattgaaga atgcccgatg aatatacacg caagaagaaa ttgacggcat
351 gattgccttt tacggttcgc ctgtcggtca gtccgctcgt gccaaaaatc
401 cgcgcttaat caagaaatcg atgagtgaat tagcggtatc ttggactgca
```

830

451 ttgtcaggga aaatcgcgcg acatcatctg cccgagttaa cggaagagtt
501 acggcgcatc atctgcgcg gtatagtga ttaa

This corresponds to the amino acid sequence <SEQ ID 1610; ORF552.ng>:

g552.pep
1 MKLKTLLLPF AALALCANAF AAPPGDASLA RWLDTQNFDR DIEKNMIEGF
51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAHHHL PEFTEELRRI ICGGIVD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1611>:

m552.seq (partial)
1 ..ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
51 CAATGCTTTT GCCGCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG
101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
151 AATGCCGGAT TTAAACCGTA TCGGCACAAA GCCCTTGCCG AAATGCCGGA
201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
501 GCGGCGCATC ATCTGCGCGG GTAAAAATCC CGATGCGGGC TGTAACAAG
551 CCGACAGGT TGGGAAAAG CATCAGAAAT AA

This corresponds to the amino acid sequence <SEQ ID 1612; ORF 552>:

m552.pep (partial)
1 ..IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAHHHL PEFTEELRRI ICGKKNPDAG CKQAGQVGR HQK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 552 shows 97.1% identity over a 174 aa overlap with a predicted ORF (ORF 552.ng) from *N. gonorrhoeae*:

m552/g552

	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	: : : : : :					
g552	MKLKTLLLPFAALALCANAFAPPGDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m552.pep	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	: : : : :					
g552	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m552.pep	YGSPVGQSVVAKNPRLIKSMSEIAVSWTALSGKIAHHHLPEFTEELRRIICGGKKNPDAG					
	: : : : :					
g552	YGSPVGQSVVAKNPRLIKSMSEIAVSWTALSGKIAHHHLPEFTEELRRIICGGIVDX					
	130	140	150	160	170	
	190					
m552.pep	CKQAGQVGRHQKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1613>:

a552.seq
1 ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
51 CAATGCTTTT GCCGCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG
101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
151 AATGCCGGAT TTAAACCGTA TCGGCACAAA GCCCTTGCCG AAATGCCGGA

831

```

201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAACAACG
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1614; ORF 552.a>:

```

a552.pep
  1 IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
 51 NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTEELRRI ICGGKNPDAG CKQAGQVGKR HQK*

```

m552/a552 100.0% identity in 193 aa overlap

	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
a552	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m552.pep	ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
a552	ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m552.pep	YGSPVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG					
a552	YGSPVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG					
	130	140	150	160	170	180
	190					
m552.pep	CKQAGQVGKRHHQKX					
a552	CKQAGQVGKRHHQKX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1615>:

```

m552-1.seq
  1 TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
 51 GTGCACCAAT GCTTTTGCCG CCCCGCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAR CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCTGTG CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAGCCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1616; ORF 552-1>:

```

m552-1.pep
  1 LNIKLTLLP PFATLALCTN AFAAPPSDAS LARWLDTQNF DRDIEKNMIE
 51 GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVKDL ITPEVKQAVR
101 NTLKNAREI YTQEEIDGMI AFYGSVPVQS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPFTEELR RIICGGKNPD AGCKQAGQVG KRHHQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1617>:

a552-1.seq

832

```

1  TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
51  GTCCACCAAT GCTTTTGCCG CCCC GCCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAT CCGCAACAT CATCTGCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAGCCGG ACAGGTTGGG AAAAGGCATC AGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1618; ORF 552-1.a>:

a552-1.pep

```

1  LNIKLTLL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE
51  GFNAGFKPYA DKALAEMPEA KKDQAAEFN RYRENVKDL ITPEVKQAVR
101 NTLLKNAREI YQEEIDGMI AFYGSVPVQS VVAKNPRIK KSMSEIAVSW
151 TALSGKIAQH HLPFTEELR RIICGKNPD AGCKQAGQVG KRHKQ*

```

a552-1/m552-1 100.0% identity in 195 aa overlap

	10	20	30	40	50	60
a552-1.pep	LNIKLTLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYA					
m552-1	LNIKLTLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYA					
	10	20	30	40	50	60
a552-1.pep	DKALAEMPEAKKDQAAEFNRYRENVKDLITPEVKQAVRNTLLKNAREIYQEEIDGMI					
m552-1	DKALAEMPEAKKDQAAEFNRYRENVKDLITPEVKQAVRNTLLKNAREIYQEEIDGMI					
	70	80	90	100	110	120
a552-1.pep	AFYGSVPVQSVVAKNPRIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGKNPD					
m552-1	AFYGSVPVQSVVAKNPRIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGKNPD					
	130	140	150	160	170	180
a552-1.pep	AGCKQAGQVGRHKHX					
m552-1	AGCKQAGQVGRHKHX					
	190					
a552-1.pep	AGCKQAGQVGRHKHX					
m552-1	AGCKQAGQVGRHKHX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1619>:

g553.seq

```

1  atggattatc tgcaaacctt gtctttgggc ttgacaaaaa agctgcccg
51  tatactgcaa acagaagtag cggagtgttg cttggcatgt ctacggcgtg
101 tggccggatt ttatggtttc tatacggatt tgcgcgcact gcgttcaaaa
151 tactgtctgt cacttaaggg tgagaatttg gcagatattg ttcgtttg
201 tgatgatatg gggctgacgg gacgggcgtt gaggtggat ttagacgaat
251 tgggcagttt gcgcctgccc tgtattctac attgggattt gaatcatttt
301 gtggtgcttg aatcggatc ttcggacggg gctgcccgtc tggatccggc
351 ttcgggacga cgcaaaagtc agacggagga aatatcgcgc aagttacgg
401 gaattgcttt ggaactgttg ccaaacacgc gtttcgaggc aggggaagaa
451 aagcaggaaa tccgcatoct acccatgttg cgcgggattt ctgggctggg
501 gcggacattg tttcagcttt tggctttggc agcagcaatg gaagtgtttg
551 cttttttaca aaacgtcagc ttcaagatcg gacgtggtga atcgtttg
601 ttaatcggac gatcgggctg cggtaaatcg acacttttgg atattttaag
651 cggcaatcta cctccgaat caggcaaat catgataaat gggcacgaca
701 tttacagctt accgccacct tttattccgc aatttgagtg cgatggtcaa
751 ggcaggacga tgttttatag tggattaaat ttaaaccggt ag

```

This corresponds to the amino acid sequence <SEQ ID 1620; ORF 553.ng>:

g553.pep

833

```

1 MDYLQNLISLG LTKKLPVILQ TEVAECGLAC LAAVAGFYGF YTDLRALRSK
51 YCLSLKGENL ADIVRFADDM GLTGRALRLD LDELGSLRLP CILHWDNLNH
101 VVLESVSSDG AAVMDPASGR RKVKTEEISR KFTGIALELW PNTRFEAGEE
151 KQEIRILPML RGISGLGRTL FQLLALAAAM EVFAFLQNVF FKIGRGESLA
201 LIGRSGCGKS TLLDILSGNL PPESGKVMIN GHDIYSLPPP FIPQFECDGQ
251 GRTMFYSGLN LNR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1621>:

```

m553.seq (partial)
1 ATGGATTATT TATCAAGACT GTCCTTGGGA TTTAACAAAA AGCTACCTGT
51 CATTCTGCAA ACAGAAGTTG CTGAATGTGG TTTAGCATGC CTGACATCCA
101 TCTTGCTCTA TTATGGCTTT CACACTGATT TAAGAACGTT ACGCCAAAAA
151 TACACCTGT CATTAAAGGG CGCAATCTT GCAGACATCA TGAGATTGG
201 CAATGAAATG AATTTAACGC CACGAGCTTT GCGTTTAGAG TTAGATGAGC
251 TGTCAAATTT ACAACTACCC TGCATTCTCC ATTGGAACCT AAACCATTTT
301 GTTGTACTTT GTTCCATTTC CAAAGACAGT ATCGTCATTA TGGACCCTGC
351 TGTCGGTATG CGAAAAATCA AAATGGACGA AGTTTCACAA AAATTCACAG
401 GGATTGCCCT AGAATTATTC CCCAATACCC ATTTTGAAGA GAAAAAGAA
451 ACAAAGAAAA TCAAAATATT ATCTCTATTA AGGGGGGG.T CAGGCTTAAA
501 ACGCTCTTTA ATTCAAATGC TTATATTAGC TATTTCTTTG GAAGTCTTTG
551 CATTG...

```

This corresponds to the amino acid sequence <SEQ ID 1622; ORF 553>:

```

m553.pep (partial)
1 MDYLSRLSFG FNKKLPVILQ TEVAECGLAC LTSILSYYG HTDLRLTRQK
51 YTLISLKGANL ADIMRFGNEM NLTPRALRLE LDELSNLQLP CILHWNLNHF
101 VVLCISKDS IVIMDPAVGM RKIKMDEVSO KFTGIALELF PNTHFEKKE
151 TTKIKILSL RGXSLKRSI IQMLILAIISL EVFAL...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 553 shows 65.5% identity over a 185 aa overlap with a predicted ORF (ORF 553.ng) from *N. gonorrhoeae*:

m553/g553

	10	20	30	40	50	60
g553.pep	MDYLQNLISGLTKKLPVILQTEVAECGLAC	LAAVAGFYGFYTDLRALRSKYCLSLKGENL				
m553	MDYLSRLSFGFNKKLPVILQTEVAECGLAC	LTSILSYYGHTDLRLTRQKYLTLISLKGANL				
	10	20	30	40	50	60
g553.pep	ADIVRFADDMGLTGRALRLDLDELGSLRLP	CILHWDNLNHFVVLESVSSDGAAVMDPASGR				
m553	ADIMRFGNEMNLTPRALRLELDELSNLQLP	CILHWNLNHFVVLCISKDSIVIMDPAVGM				
	70	80	90	100	110	120
g553.pep	RKVKTEEISRKFTGIALELWPNTREAGEEKQEIRILPMLRGISGLGRTL	FQLLALAAAM				
m553	RKIKMDEVSOQKFTGIALELFPNTHFEKKETTKIKILSLRGXSLKRSI	IQMLILAIISL				
	130	140	150	160	170	180
g553.pep	EVFAFLQNVFVKIGRGESLALIGRSGCGKSTLLDILSGNLPPESGKVMIN	GHDIYSLPPP				
m553	EVFAL					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1623>:

```

a553.seq
1 ATGCCCCATC TGCAAAACCT GTCTTGGGC TTAAGAAAA AGCTGCCTGT
51 TATCCTGCAA ACAGAAATAT CAGAATGCGG CTGGCATGT CTGGCGGCTG
101 TGGCGGGATT TCATGGTTTC CATACGAATT TACGCGCACT GCGTTCAAAA
151 TAC

```

This corresponds to the amino acid sequence <SEQ ID 1624; ORF 553.a>:

```
a553.pep
      1  MPHLQNLSLG LKKKLPVILQ TEISECGLAC LAAVAGFHGF HTNLRALRSK
     51  Y
```

m553/a553 62.7% identity in 51 aa overlap

	10	20	30	40	50	60
m553.pep	MDYLSRLSFGFNKKLPVILQTEVAECGLACLT	SILSYYGFTDLRTL	RQKYTL	SLKGANL		
	: : : : : : : : : :	: : : : : : : : :	: : : : : : : : :	: : : : : : : : :		
a553	MPHLQNLSLGLKKKLPVILQTEISECGLACLA	AVAGFHGFHTNLRALRSKY				
	10	20	30	40	50	
	70	80	90	100	110	120
m553.pep	ADIMRFGNEMNLT	PRALRLELDELSNL	QLPCILHWNLNH	FVVLCSISKDS	SIVIMDPAVGM	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1625>:

```
g554.seq..
      1  atgacagcac ataaaatcct gccgcctcct cttcccatca tcttaggcgt
     51  ttctcacgca acggctgcat cgcccgcgcc caacagaccg acggtacacg
    101  ccgccccac gctccaaaca ccgaaacccc tcacggcggc acacatcggt
    151  atcgaccttc aaagcaggca gactttatcc gccaaaaaca ccaatacccc
    201  tgtcgaaccg gcggcactaa cccaactgat gaccgcatat ttggttttca
    251  aaaacatgaa atcgggaaat atccaatctg aagaaaactt aaaaaatccc
    301  gaatccgcat gggcttcaga aggaagcaga atgtttgtac gtcccgcgca
    351  tacggtcagc accgacaaac tcttaaaagg catgattgcc ctatgcgcaa
    401  acgatgccgc cctaaccctt gccgaccggc tgggcaacgg ctcgattgaa
    451  aattttgtgc aacaaatgaa caaagaagcc cgacgcttgg gcatgaagaa
    501  caccgtatcc aaaaaccgga caggcttggg tagagaagga caggtttcca
    551  ccgccaaga cctctccctg ctgtctgaag cattgatgcg cgactttccg
    601  gaatattacc cgctgttttc catcaaatcg ttcaagtttg aaaacataga
    651  acaaaacaac cgcaatatcc ttttatatag ggacaacaat gtaaacggcc
    701  tgaaagccgg gcacacagaa agcggcggtt acaaccttgc cgtgtcatac
    751  tccggcaacg gcaggcacat ccttgtcatc acactagggt cggaatcggc
    801  ggaaaccgc gcacgggaca acagcaagct gctgaaccgg gcattgcagg
    851  ccttcgatac gcccaaaata tatccgaaag gcaaaaccgt tgcccaaatc
    901  caaatttccg gaggcagcaa aaaaaccgtc cgcgagggtt tcctcaaaga
    951  agcctacatc actctgccac ataaagaagc gaaaatggca gaacagattt
   1001  tggaaaccat acagccgatt cccgccccgg taaaaaaagg gcagatttta
   1051  ggaaaaatca aaatcaggca aaacggacat accattgccg aaaaagaaat
   1101  cgtcgcactg gaaaacgtag aaaaaagaag ccggtggcaa aggctttgga
   1151  cgcgtctgac agggcagtaa
```

This corresponds to the amino acid sequence <SEQ ID 1626; ORF 554.ng>:

```
g554.pep..
      1  MTAHKILPVL LPIILGVSHA TAASPAENRP TVHAAPTLOT PETLTAHIV
     51  IDLQSRQTLA AKNTNTPVEP AALTQLMTAY LVFKNMKSGN IQSEENLKIP
    101  ESAWASBGSR MFVRPGDTVS TDKLLKGMIA LCANDAALTL ADRLNGSIE
    151  NFVQQMNKEA RRLGMKNTVF KNPTGLGREG QVSTAKDLSL LSEALMRDFP
    201  EYYPLFSIKS FKFENIEONN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
    251  SGNGRHILVI TLGSESAETR ASDNSKLLNR ALQAFDTPKI YPKGKTVAQI
    301  QISGGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
    351  GKIKIRQNGH TIAKEIVAL ENVEKRSRWQ RLWTRLTGQ*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1627>:

```
m554.seq..
      1  ATGACAGCAC ATAAAATCCT GCCCGTCCTG CTTTCCATCA TCTTAGGCGT
     51  TTCTCACGCA ACGGCTGCAT CGCCCGCGCC CAACAGACCG ACGGTACACG
    101  CCGCCCCAC GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
    151  ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAAACA TCAATACCCC
    201  TGTGTAACCG GCGGCACTAA CCAACTGAT GACCGCATAT CTGGTTTTCa
    251  AAAACATGAA ATCGGGCAAT ATCCAATCTG AAGAAAACCT AAAAAATACC
```

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```

301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTAC GTCCCGCGCA
351 TACGGTCAGC ACCGACAAAC TCTTAAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCTT GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAACCAGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCTG CTGTCTGAAG CATTGATGCG CGACTTCCG
601 GAATATTACC CGCTGTTTTC CATCAAATCT TTCAAATTC AAAATATAGA
651 ACAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTGCATC
751 TCCGGCAACG GCAGGCACAT CCTTGTATC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAACTGG GCATTGCAGG
851 CCTTCGATAC GCCCAAATA TATCCGAAAG GCAAAACCGT TGCCCAAATC
901 CAAATTTCAG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAATGCGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1628; ORF 554>:

m554.pep..

```

1 MTAHKILPVL LSIILGVSHA TAASPAPNRP TVHAAPTFTQ PETLTAAHIV
51 IDLSKQILS AKNINTPVEP AALTQMTAY LVFKNMKSGN IQSEENLKIP
101 ESAWASEGSR MFVRPGDIVS TDKLLKGMIA LSANDAALTL AGRNGSIE
151 NFVQMNKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAL LSEALMRDFP
201 EYYPLFSIKS FKFKNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SGNRHLVITL GSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKQIL
351 GKIKIRONGY TIAEKEIVAL ENVKKRSRWQ RLWACLTGQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 554 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 554.ng)

from *N. gonorrhoeae*:

m554/g554

	10	20	30	40	50	60
m554 . pep	MTAHKILPVLLSIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIVIDLQSKQILS					
g554	MTAHKILPVLLPIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIVIDLQSRQTL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m554 . pep	AKNINTPVEPAALTQMTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDIVS					
g554	AKNTNTPVEPAALTQMTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDIVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m554 . pep	TDKLLKGMIALSANDAALTLAAGRLNGSIE NFVQMNKEARRLGMKNTVFNPTGLSREG					
g554	TDKLLKGMIALCANDAALTLADRLNGSIE NFVQMNKEARRLGMKNTVFNPTGLGREG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m554 . pep	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNGLKAGHTE					
g554	QVSTAKDLSLLSEALMRDFPEYYPLFSIKSFKFENIEQNNRNILLYRDNNVNGLKAGHTE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m554 . pep	SGGYNLAVSYSGNRHLVITL GSESAETR ASDNSKLLNWALQAFDTPKIYPKGKTVAQI					

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```

g554      SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNRLAQAFDTPKIYPKGKTVAQI
           250      260      270      280      290      300

           310      320      330      340      350      360
m554 . pep QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRONGY
           |||||:|||||:|||||:|||||:|||||:|||||:
g554      QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRONGH
           310      320      330      340      350      360

           370      380      390
m554 . pep TIAEKEIVALENVKRSRWQRLWACLTGQX
           |||||:|||||:|||||:
g554      TIAEKEIVALENVKRSRWQRLWTRLTGQX
           370      380      390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1629>:

```

a554 . seq
1  ATGACAGCAC ATAAATCCT GCCCGTCTG CTTTCCATCA TCTTAGGCGT
51  TTCTCAGCA ACGGCTGCAT CGCCCGCGCC CAACAGACCG ACGGCACACG
101 CCGCCCCAC GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
151 ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAAACA TCAATACCCC
201 TGTGGAACCG GCGGCACTAA CCCAACTGAT GACCGCATAT CTGGTTTCA
251 AAAACATGAA ATCGGGAAAT ATCCGATCTG AAGAAACTT AAAAATACCC
301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTAC GTCCCGGCGA
351 TACGGTCAGC ACCGACAAC TCTTAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCTT GCGGCCGCG TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAATCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCAG CTGTCTGAAG CATTGATGCG CGACTTTCCG
601 GAATATTACC CGCTGTTTC CATCAAATCT TCAAATTC AAAATATAGA
651 GCAAAACAAC CGCAATATCC TTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTGCG CGTGTATAC
751 TCCGGCAACG GCAGGCACAT CCTTGTATC ACATTGGGTG CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAACTGG GCATTGCAAG
851 CCTTCGATAC GCCCAARATA TATCCGAAAG GCAAAACCGT TGCCCAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCGCCCGAG TAAAAAAGG GCAAATTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1630; ORF 554.a>:

```

a554 . pep
1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TAHAAPTFTQ PETLTAAHIV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKSNG IRSEENLKIP
101 ESAWASEGSR MFVRPGDTVS TDKLLKGMIA LSANDAALTL AGR LGNGSIE
151 NFVQQMNKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAQ LSEALMRDFP
201 EYYPLFSIKS FKFKNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SNGNRHILVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKTV RAGFLKEAYI TLPHKEAKMA EQILETIQPI PAPVKKGQIL
351 GKIKIRONGY TIAEKEIVAL ENVKRSRWQ RLWACLTGQ*

```

m554/a554 99.2% identity in 389 aa overlap

```

           10      20      30      40      50      60
m554 . pep MTAHKILPVLLSIILGVSHATAASPAPNRPVHAAPTFTQ PETLTAAHIVIDLQSKQILS
           |||||:|||||:|||||:|||||:|||||:|||||:
a554      MTAHKILPVLLSIILGVSHATAASPAPNRPVHAAPTFTQ PETLTAAHIVIDLQSKQILS
           10      20      30      40      50      60

           70      80      90      100     110     120
m554 . pep AKNINTPVEPAALTQLMTAYLVFKNMKSNGIQSEENLKIPESAWASEGSRMFVRPGDTVS
           |||||:|||||:|||||:|||||:|||||:|||||:
a554      AKNINTPVEPAALTQLMTAYLVFKNMKSNGIRSEENLKIPESAWASEGSRMFVRPGDTVS

```

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	70	80	90	100	110	120
m554 . pep	130	140	150	160	170	180
	TDKLLKGMIALSANDAALTLAGRLNGSNIENFVQOMNKEARRLG MKNTVFKNPTGLSREG					
a554	TDKLLKGMIALSANDAALTLAGRLNGSNIENFVQOMNKEARRLG MKNTVFKNPTGLSREG					
	130	140	150	160	170	180
m554 . pep	190	200	210	220	230	240
	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFNIEQNNRNILLYRDNNVNLKAGHTE					
a554	QVSTAKDLAQLSEALMRDFPEYYPLFSIKSFKFNIEQNNRNILLYRDNNVNLKAGHTE					
	190	200	210	220	230	240
m554 . pep	250	260	270	280	290	300
	SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI					
a554	SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI					
	250	260	270	280	290	300
m554 . pep	310	320	330	340	350	360
	QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQIPAPVKKGQILGKIKIRONGY					
a554	QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQIPAPVKKGQILGKIKIRONGY					
	310	320	330	340	350	360
m554 . pep	370	380	390			
	TIAEKEIVALENVKKRSRWQRLWACLTGQX					
a554	TIAEKEIVALENVKKRSRWQRLWACLTGQX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1631>:

g556. seq..

```

1 atggacaata agaccaaact gcgcttgggc ggcctgattt tactgaccac
51 cggcggttta agcctcatta tcgtattgat tgctgattcc tggccgcttg
101 ccatacctgct tggcgccgctc atcgctcgccg ccgctgcccgg cggttttgtt
151 tggacatccc gccgacagca acgccagttt atcgaacgctc tgaaaaaatt
201 cgacatcgat ccgaaaaaag gcagaatcaa cgaggcaaac ctgcgccgta
251 tgtaccacag cggcgggaaa caccagaaaag atgcgattac cctgatctgc
301 ctgtcgcaaa aatgttcggt ggacgaggcg cagcgtatgt tcaaaaaacg
351 cccgacacgt caggaaatca atcaaattggc ggcaaaacag tcgcgcggtc
401 agaaacgtcc gcaccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1632; ORF 556.ng>:

g556. pep.

```

1 MENKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51 WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC
101 LSOKCSVDEA HAMFKRPRTR QEINQMAAKO SRGQKRPHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1633>:

m556. seq..

```

1 ATGGACAATA AGACCAAAC TCGCTTGGGC GGCCTGATTT TACTGACCAC
51 CGCCGTTTTA AGCCTCATT TCGTATTGAT TGTCGATTCC TGGCCGCTTG
101 CCATCCTGCT TGCAGCCGTC ATGTGCGCTG CCGCTGCGGG CGGTTTGTG
151 TGGACATCCC GCCGACAGCA ACGCCAGTTT ATCGAACGCC TGAAAAAATT
201 CGACATCGAT CCCGAAAAAG GCAGAATCAA CGAGGCAAAC CTGCGCCGTA
251 TGTACCACAG CGGCGGACAA CACCAGAAAAG ATGCGATTAC CCTGATCTGC
301 CTGTCGCAAA AATGTTTCGT GGACGAGGCG CAGCCTATGT TCAAAAAACG
351 CCCGACACGT CAGGAAATCA ATCAAATGGC GGCAAAACAG TCGCGCGGTC
401 AGAAACGTCC GCACCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1634; ORF 556>:

m556. pep..

```

1 MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51 WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC

```

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101 LSQKCSVDEA HAMFKKRPTR QEINQMAAKQ SRGQKRPHR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 556 shows 100.0% identity over a 139 aa overlap with a predicted ORF (ORF 556.ng) from *N. gonorrhoeae*:

m556/g556

	10	20	30	40	50	60
m556.pep	MDNKT	KLRLG	LILLT	TAVLS	LIIVL	IVDSW
	PLAIL	LA	IVAAA	AGGFV	WTSRR	QQRQF
g556	MDNKT	KLRLG	LILLT	TAVLS	LIIVL	IVDSW
	PLAIL	LA	IVAAA	AGGFV	WTSRR	QQRQF
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKK	FDIDP	EKGRIN	EANLR	RRMYH	SGGQH
	QKDAIT	LICLS	QKCSV	DEAH	AMFKK	RPTR
g556	IERLKK	FDIDP	EKGRIN	EANLR	RRMYH	SGGQH
	QKDAIT	LICLS	QKCSV	DEAH	AMFKK	RPTR
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQ	MAAKQ	SRGQK	RPHRX		
g556	QEINQ	MAAKQ	SRGQK	RPHRX		
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1635>:

a556.seq

1	ATGGACAATA	AGACCAA	ACT	GCGCTT	TGGGC	GGCCTG	ATTT	TACTG	ACCAC
51	CGCCGTTT	TA	AGCCTC	ATTA	TCGTAT	TGAT	TGTCG	ATTCC	TGGCCG
101	CCATCCTG	CT	TGCCG	CCGTC	ATCGTC	GCCG	CCGCTG	CCGG	CGGCTT
151	TGGACATCC	C	GCCGAC	AGCA	ACGCCA	GT	TT	ATCGA	ACGTC
201	CGACATCG	AT	CCGAAA	AAG	GCAGA	ATCAA	CGAGG	CAAAC	CTGCGC
251	TGTACCAC	AG	CGGCGG	ACAA	CACCAA	AAG	ATGCG	ATTAC	CCTGAT
301	CTGTGCA	AAA	AATGTT	CGGT	GGACG	AGGCG	CACGCT	ATGT	TCAAAA
351	CCCGACAC	GT	CAGGAA	ATCA	ATCAA	ATGGC	GGCAA	AACAG	TCGCGC
401	AGAAACG	TCC	GCACCG	TTAA					

This corresponds to the amino acid sequence <SEQ ID 1636; ORF 556.a>:

a556.pep

1	MDNKT	KLRLG	GLILL	TTAVL	SLIIV	LIVDS	WPLAIL	LA	IVAAA	AGGFV
51	WTSRR	QQRQF	IERLKK	FDIDP	EKGRIN	EANLR	RRMYH	SGGQ	HQKDAIT	LIC
101	LSQKCS	VDEA	HAMFKK	RPTR	QEINQ	MAAKQ	SRGQK	RPHR	*	

m556/a556 100.0% identity in 139 aa overlap

	10	20	30	40	50	60
m556.pep	MDNKT	KLRLG	LILLT	TAVLS	LIIVL	IVDSW
	PLAIL	LA	IVAAA	AGGFV	WTSRR	QQRQF
a556	MDNKT	KLRLG	LILLT	TAVLS	LIIVL	IVDSW
	PLAIL	LA	IVAAA	AGGFV	WTSRR	QQRQF
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKK	FDIDP	EKGRIN	EANLR	RRMYH	SGGQH
	QKDAIT	LICLS	QKCSV	DEAH	AMFKK	RPTR
a556	IERLKK	FDIDP	EKGRIN	EANLR	RRMYH	SGGQH
	QKDAIT	LICLS	QKCSV	DEAH	AMFKK	RPTR
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQ	MAAKQ	SRGQK	RPHRX		
a556	QEINQ	MAAKQ	SRGQK	RPHRX		
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1637>:

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g557.seq

```

1  atgaacaaaa ttttccttac tgccgcagcc ttggtgctgg gcgcgtgcgg
51  tttccacctg aaaggtgcag acggcatttc tccgccgctg acctaccgga
101 gctggcacat cgaaggcgga caggcattgc aatttccttt ggaaaccgcg
151 ctgtatcagg cttcgggcag ggtggacgat gctgccggcg cgcagatgac
201 cctgcgctata gacagcgttt cccaaaacaa ggaaacctat accgttacct
251 gtgcggcagt catcaacgaa tatcttttga tattgacggt tgaagcgag
301 gtattgaaac gcggcgagcc ggtcggcaaa ccgatgaccg tgtccgtccg
351 ccgcattttg gattatgccg acaacgaaat ttggggcaaa caggaagaag
401 aagaaaccct gtgggcggaa atgcggcagg atgttgccga acagattgtc
451 cgccgcctga cttttctgaa ggcggaatga

```

This corresponds to the amino acid sequence <SEQ ID 1638; ORF 557.ng>:

g557.pep..

```

1  MNKIFLTAAL LVLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA
51  LYQASGRVDD AAGAQMTRLI DSVSONKETY TVTRAAVINE YLLILTVEAQ
101 VLKRGEFVGK PMTVSVRRIL DYADNEILGK QEEEEELWAE MRQDVAEQIV
151 RRLTFLKAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1639>:

m557.seq..

```

1  ATGAACAAAC TGTTCCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGGCG
51  TTTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA
101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC GGTTCCTTTT GGAAACCGCG
151 CTGTATCAGG CTTCCGGCAG GGTGGACGAT GCTGCCGGCG CGCAGATGAC
201 CCTGCGTATA GACAGCGTTT CCCAAAACAA GGAAACCTAC ACCGTTACCC
251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG
301 GTATTGAAAC GCGGCGAGCC GGTGCGTAAA CCGATGACCG TGTCCGTCCG
351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAAA CAGGAAGAGG
401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC
451 CGCCGCCTGA CTTTCTGAA GCGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1640; ORF 557>:

m557.pep..

```

1  MNKFLTAAL LMLGACGFHL KGADGISPPL TYRSWHIEGG QALRFPLETA
51  LYQASGRVDD AAGAQMTRLI DSVSONKETY TVTRAAVINE YLLILTVEAQ
101 VLKRGEFVGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAAEQIV
151 RRLTFLKAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 557 shows 94.3% identity over a 159 aa overlap with a predicted ORF (ORF 557.ng) from *N. gonorrhoeae*:

m557/g557

	10	20	30	40	50	60
m557.pep	MNKFLTAALVLMGACGFHLKGADGISPPLTYRSWHIEGGQALRFPLETALYQASGRVDD					
	: :					
g557	MNKIFLTAALVLMGACGFHLKGADGISPPLTYRSWHIEGGQALQFPLETALYQASGRVDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m557.pep	AAGAQMTRLIDSVSONKETYTVTRAAVINEYLLILTVEAQVLKRGEFVGKPMTVSVRRVL					
g557	AAGAQMTRLIDSVSONKETYTVTRAAVINEYLLILTVEAQVLKRGEFVGKPMTVSVRRIL					
	70	80	90	100	110	120
	130	140	150	160		
m557.pep	AYADNEILGKQEEEAALWAE MRQDAAEQIVRRLTFLKAEX					
g557	DYADNEILGKQEEETLWAE MRQDVAEQIVRRLTFLKAEX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1641>:

840

```

a557.seq
1  ATGAACAAAC TGTTCCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGCGG
51  TTTCACACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA
101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC AGTTTCCTTT GGAAACCGCG
151 CTGTATCAGG CTTCGGGTAG GGTGGACGAT GCTGCCGCGC CGCAGATGAC
201 CCTGCGTATA GACAGCGTTT CCAAAACAA GGAAACCTAC ACCGTTACCC
251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG
301 GTATTGAAAC GCGGCGAGCC GGTCCGCCAA CCGATGACCG TGTCCTGTCG
351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAAA CAGGAAGAGG
401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC
451 CGCGCCTGA CCTTCTGAA GCGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1642; ORF 557.a>:

```

a557.pep
1  MNKLFLTAAV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA
51  LYQASGRVDD AAGAQMTRLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ
101 VLKRGEVPGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAAEQIV
151 RRLTLKAE*

```

m557/a557 99.4% identity in 159 aa overlap

	10	20	30	40	50	60
m557.pep	MNKLFLTA	AVLMLGAC	GFHLKGAD	GISPPLTY	RSWHIEGG	QALRFPLE
a557	MNKLFLTA	AVLMLGAC	GFHLKGAD	GISPPLTY	RSWHIEGG	QALRFPLE
	10	20	30	40	50	60
m557.pep	AAGAQMTR	IDSVSQNK	ETYTVTRA	AVINEYLL	ILTVEAQV	LKRGEVPG
a557	AAGAQMTR	IDSVSQNK	ETYTVTRA	AVINEYLL	ILTVEAQV	LKRGEVPG
	70	80	90	100	110	120
m557.pep	KPMTVSVR	RVLAYADN	EILGKQEE	EAALWAE	MRQDAAE	QIVRRLTL
a557	KPMTVSVR	RVLAYADN	EILGKQEE	EAALWAE	MRQDAAE	QIVRRLTL
	130	140	150	160		
m557.pep	KAE					
a557	KAE					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1643>:

```

g558.seq..
1  ATGGATGCTT GTTTTTTCGT CATTCCCGCA CAGGCGGGAA TTCGGAGATT
51  CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCAGGAATGA
101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGCTTCAACA GGGGACGGCA
151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGCTGCC CTCGATTAG
201 ATTCTATCGC TATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
251 AGTCCATTTC CGACACCTCT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
301 CTTTCAGACG GCATTGTTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1644; ORF 558.ng>:

```

g558.pep..
1  MDACFFVIPA QAGIRRFQIV FKRSGRILAG AGMMPLYTFS ELYMLQQGTA
51  HQAPHCVLPE RGCPPIRFYR YKQTGFNRKG MGIKSISDTS RAMPSENQSP
101 LSDGIV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1645>:

```

m558.seq..
1  ATGAATGCTT GTTTTTTCGT CATTCCACAA CAGGCGGGAA TTCGGAGATT
51  CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCAGGAATGA
101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGCTTCAACA GGGGACGGCA
151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGACTACC CTCGATTAG
201 ATTCTATCGC CATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
251 AGTCCATTTC CGACATCTsT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
301 CTTTCAGACG GCATTGTTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1646; ORF 558>:

841

m558.pep.
 1 MNACFFVIPT QAGIRREGIV FKRSGRILAG AGMMPLYTFS ELYMFQQGTA
 51 HQAPHCVLPE RDYPPIRFYR HKQTGFNRKG MGIKSISDIX RAMPSENQSP
 101 LSDGIV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 558 shows 92.5% identity over a 106 aa overlap with a predicted ORF (ORF 558.ng) from *N. gonorrhoeae*:

m558/g558

	10	20	30	40	50	60
m558.pep	MNACFFVIPTQAGIRREGIVFKRSGRILAGAGMMPLYTFSELYMFQQGTAHQAPHCVLPE					
	: :					
g558	MDACFFVIPTQAGIRREGIVFKRSGRILAGAGMMPLYTFSELYMLQQGTAHQAPHCVLPE					
	10	20	30	40	50	60
	70	80	90	100		
m558.pep	RDYPPIRFYRHKQTGFNRKGMGIKSISDIXRAMPSENQSPSLSDGIVX					
	: :					
g558	RGCPPIRFYRYKQTGFNRKGMGIKSISDTSRAMPSENQSPSLSDGIVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1647>:

a558.seq
 1 ATGAATGCTT GTTTTTTCGT CATTCCCACA CAGGCGGGAA TTCGGAGATT
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCGGGAATGA
 101 TGCCCTTATA TATAGTGGAT TAAATTAAA TCAGGACAAG GCGACGAAGC
 151 CGCAGACAGT ACAAATAGTA CGGCAAGGCG AGGCAACGCC GTACTGGTTT
 201 AAATTTAATC CACTATACTT TCTCCGAGCT TTATATGTTT CAACAGAGGA
 251 CGGCACATCA AGCACCGCAC TGCCTGTTGC CCGAACGAGA CTGCCCTCCG
 301 ATTAGATTCT ATCGCTATAA ACAGACGGGT TTCAACCGAA AAGGAATGGG
 351 AATGAAGTCC GTTTCGACA CCTCTCGGGC GATGCCGTCT GAAAACCAAT
 401 CTCCACTTTC AGACGGCATT GTTTAG

This corresponds to the amino acid sequence <SEQ ID 1648; ORF 558.a>:

a558.pep
 1 MNACFFVIPT QAGIRREGIV FKRSGRILAG AGMMPLYIVD *I*IRTRRRS
 51 RRQYK*YGKA RQRTGLNLI HYTFSELYMF QORTAHQAPH CVLPERDCPP
 101 IRFYRYKQTG FNRKGMGMKS VSDTSRAMPS ENQSPLSDGI V*

m558/a558 70.2% identity in 141 aa overlap

	10	20	30		
m558.pep	MNACFFVIPTQAGIRREGIVFKRSGRILAGAGMMPLY-----				
a558	MNACFFVIPTQAGIRREGIVFKRSGRILAGAGMMPLYIVDXIXIRTRRRSRQYKXYGKA				
	10	20	30	40	50
					60
	40	50	60	70	80
m558.pep	-----TFSELYMFQQGTAHQAPHCVLPERDYPPIRFYRHKQTGFNRKGMGIKS				
a558	RQRTGLNLIHYTFSELYMFQORTAHQAPHCVLPERDCPPIRFYRYKQTGFNRKGMGMKS				
	70	80	90	100	110
					120
	90	100			
m558.pep	ISDIXRAMPSENQSPSLSDGIVX				
	:				
a558	VSDTSRAMPSSENQSPSLSDGIVX				
	130	140			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1649>:

g560.seq
 1 atgtcatca tccgaacct gatttactgg ctgatactct g-tccagcct

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```

51  gattttctctc tttcccttta tgetgctcgc ctgccttttc cgggacgggg
101 cgcacaagat ggcgcgggtc tgggtcgga tctcaactg gtcgctcaaa
151 cacatcgctc ggctcaaata ccgcatcatc ggcgcggaac acattccgga
201 ccgcccctcc gtcactctgc ccaaacacca aagcggtcg gaaacgctcg
251 cgctccaaga gatttttccg ccgcaggttt acgttgcaa gcgcgagttg
301 ttcaaaatcc ctttttccg ctggggcttg aaactggtca aaaccatagg
351 catagaccgc aacaaccgcc gcgaagccaa cgaacagctc ataaaacagg
401 gtttgccgcg caaaaacgaa ggttattgga ttaccatttt ccccgaaggc
451 acgcgccttg cgcgcggaaa acgcggcaaa taaaaactcg gcggcgcgcg
501 catggcgaaa atgtttgaga tggacatcgt ccccgctgcc ctcaacagcg
551 gcgaattttg gccgaaaaat tcctttctga aatatccggg ggaaatcacc
601 gtcacatctt gtccgaccat cccgcacgca agcggcagcg aagccgaatt
651 gatggaaaaa tgcgaacacc tcattgaaac gcaacaaccg cttatttccg
701 gcgcaggccc gtttgccgcc gaaatgccgt ctgaaaccgc atga

```

This corresponds to the amino acid sequence <SEQ ID 1650; ORF 560.ng>:

g560.pep..

```

1  MLIIRNLIYW LILCSSLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
51  HIVGLKYRII GAEHIPDRPS VICAKHSGW ETLALQEIFP PQVYVAKREL
101 FKIPFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
151 TRLAPGKRK YKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VIICPTIPHA SGSEAELEMEK CEHLIETQQP LISGAGPFAA EMPSET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1651>:

m560.seq

```

1  ATGCTCATCA TCCGCAACCT GATTACTGCG CTGATACTCT GTTCCACCCT
51  GATTTCCTC TTTCCCTTTA TGCTGCTCGC CTCGCCTTTC CGGGACGGGG
101 CGCACAAGAT GGCGCGGGTC TGGGTGCGCA TTCTCAACTG GTCGCTCAAA
151 CACATCGTCG GGCTCAAATA CCGCATCATC GGCGCGGAAA ACATCCCCGA
201 CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251 CCCTTCAGGA CATTTTTCCG CCGCAGGTTT ACCTTGCCAA ACGCGAGTTG
301 TTCAAATCC CTTTTTTCGG CTGGGGCTTG AAACGTGTCA AAACCATAGG
351 CATAGACCGC AACAAACGCC GCGAAGCCAA CGAGCAGCTC ATAAACAGG
401 GGTGGTGCG CAAAACGAA GGCTATTGGA TTACCATTTT CCCCGAAGGC
451 ACGCGCCTTG CGCCCGGAAA ACGCGGCAA TACAACTCG GCGGCGCGCG
501 CATGCGGAAA ATGTTTGAGA TGGACATCGT CCCCGTCGCC CTCAACAGCG
551 GCGAATTTTG GCCGAAAAAC TCCTTTCTGA AATATCCGGG GGAAATCACC
601 GTCGTCATCT GTCCGACCAT CCGCACGCA AGCGGCAGCG AAGCCGAATT
651 GATGAAAAAA TGCGAACATC TCATCGAAAC GCAACAACCG CTATTTCGG
701 GCGCAGGCC GTTTGCCGCC AAAATGCCGT CTGAAACCGC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1652; ORF 560>:

m560.pep

```

1  MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
51  HIVGLKYRII GAENIPDRPA VICAKHSGW ETLALQDIFP PQVYVAKREL
101 FKIPFGWGL KLVKTIGIDR NNRREANEQL IKQGLVRKNE GYWITIFPEG
151 TRLAPGKRK YKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VVICPTIPHA SGSEAELEMEK CEHLIETQQP LISGAGPFAA KMPSETA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 560 shows 97.2% identity over a 246 aa overlap with a predicted ORF (ORF 560.ng) from *N. gonorrhoeae*:

m560/g560

```

          10      20      30      40      50      60
m560.pep  MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK HIVGLKYRII
          |||||
g560      MLIIRNLIYW LILCSSLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK HIVGLKYRII
          10      20      30      40      50      60

          70      80      90     100     110     120
m560.pep  GAENIPDRPA VICAKHSGW ETLALQDIFP PQVYVAKREL FKIPFGWGL KLVKTIGIDR
          |||||
g560      GAEHIPDRPS VICAKHSGW ETLALQEIFP PQVYVAKREL FKIPFGWGL KLVKTIGIDR

```

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```

      70      80      90      100     110     120
      130     140     150     160     170     180
m560.pep  NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA
          |||||:|||||
g560      NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA
          130     140     150     160     170     180

      190     200     210     220     230     240
m560.pep  LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAEIMKCEHLIETQQPLISGAGPFAA
          |||||:|||||
g560      LNSGEFWPKNSFLKYPGEITVIICPTIPHASGSEAEIMKCEHLIETQQPLISGAGPFAA
          190     200     210     220     230     240

m560.pep  KMPSETAX
          :||||
g560      EMPSETX
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1653>:

```

a560.seq
1  ATGCTCATCA TCCGCAACCT GATTACTGCG CTGATACTCT GTTCCACCCCT
51  GATTTTCCTC TTTCCCTTTA TGCTGCTCGC CTCGCCTTTC CGAGACGGGG
101 CGCACAAAGAT GCGCGGGGTC TGGGTCAAAA TCCTCAACCT CTCGCTCAAA
151 CACATCGTCG GGCTCAAATA CCGCATCATC GGCGCGGAAA ACATCCCCGA
201 CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251 CCCTTCAGGA CATTTTTCGG CCGCAGGTTT ACGTTGCCAA ACGCGAGTTG
301 TTCAAAATCC CCTTTTTCGG CTGGGGCTTG AAACCTGGTCA AAACCATAGG
351 CATAGACCGC AACAACCGCC GCGAAGCCAA CGAGCAGCTC ATAAACAGG
401 GGTGGCGCG CAAAAACGAA GGCTATTGGA TTACCATTTT CCCCAGAGGC
451 ACACGCCCTG CGCCCGGAAA ACGCGGCAA TACAACTCG GCGGCGCGCG
501 CATGGCGAAA ATGTTTGAGA TGGACATCGT CCCCCTCGCC CTCACAGCG
551 GCGAATTTTG GCCGAAAAAC TCCTTTCTGA AATATCCGGG GGAAATCACC
601 GTCGTCATCT GTCCGACCAT CCGCACGCA AGCGGCAGCG AAGCCGAATT
651 GATGGGAAAA TCGAACACC TCATCGAAAC GCAGCAGCCG CTCATTTCCG
701 GCGCAGGCC GTTGCCGCC AAAATGCCGT CTGAAACCGC ATGA
```

This corresponds to the amino acid sequence <SEQ ID 1654; ORF 560.a>:

```

a560.pep
1  MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK
51  HIVGLKYRII GAENIPDRPA VICAQHSGW ETLALQDIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
151 TRLAPGKRGK YKLGARMAMK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VVICPTIPHA SGSEAEIMGK CEHLIETQQP LISGAGPFAA KMPSETA*
```

m560/a560 98.4% identity in 247 aa overlap

```

      10      20      30      40      50      60
m560.pep  MLIIRNLIYWLILCSTLIFLFPFMLLASPFRDGAHKMARVWVGILNWSLKHIVGLKYRII
          |||||
a560      MLIIRNLIYWLILCSTLIFLFPFMLLASPFRDGAHKMARVWVKILNLSLKHIVGLKYRII
          10      20      30      40      50      60

      70      80      90      100     110     120
m560.pep  GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR
          |||||
a560      GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR
          70      80      90      100     110     120

      130     140     150     160     170     180
m560.pep  NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA
          |||||:|||||
a560      NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA
```

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	130	140	150	160	170	180
	190	200	210	220	230	240
m560 . pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAE	LMKCEHLIETQQPLISGAGPFAA				
a560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAE	LMGKCEHLIETQQPLISGAGPFAA				
	190	200	210	220	230	240
m560 . pep	KMPSETAX					
a560	KMPSETAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1655>:

```

m561 . seq.
1  ATGATACTGC CAGCCCGTTT TTCAGACGGC ATCAGCCTTT CCCTGCGCCT
51  GAAACTCCTG ACCGGACTGT GGGTCGGGTT GCGCGCATTG TCTGTCGTTT
101 TGACACTGCT GCTCTCTTTG CGTCTGGAAG ACGCGCCTC CGTCATCGAA
151 GAGGCGGGCA ACTTGAGAAT GCAGGCATAC CGTCTGGCAT ACATGGCGGG
201 TGAAGGCTCG CCCCGTGC GC AAATTGACAA TCAGGTGCC GAATTTGAAA
251 AAAGTTTAAA ACGCATTGCC CAAAGCGATG CCATCCATCC GCTGATTCCT
301 TCGGACACCC CTCTTGCTTA TGATTGATA CAATCCATGC TGATTATAGA
351 TFGGACGGCA CACATCCTCC CCCCGCTCCA GTCCATCCGG CGACCGACTC
401 AGGTCGATCT CTACCGCTTT GCCGGAACA TCGAACTGTT TTTGCAGGCA
451 TTGGAAAATG CCAACGAAAA AAACACATGG TGGCTCAGGC GTTTTCAATG
501 GGCAATTATG TTGATGACGC TGGTGTCTGC TGTACTGATG CTGTTTGGC
551 ACCAGATTTG GGTATCCGG CCGCTGCAGG CGTTAAGGGA AGGTGCGGAA
601 CGCATCGGAC GGAGGTGTTT CGATATTCCG GTTCCCGAAG GCGGTACGCC
651 GGAAATCAAA CAGGTCGGGC GTTGTTCCTT TCAAATGGGC GGCAGGTTGA
701 AAATTTTATA TGATGATTTG GAAGGACAAG TCGCCGAGCA GACACGCAGT
751 CTCGAAAAAC AAAATCAAAA CCTGACCTG CTGTACCAA CTACACGGGA
801 CCTGCACCAA TCCTACATAC CGCAACAGGC TGCAGAACAT TTTCTAAACC
851 GTATCCTGCC CGCCGTAGGA GCAGATCCG GCAGAGTTTG TTTGGACGGC
901 GGATCCGATG TTTATGTTTC CATTTCATCAT GCGGATTGCG GCACAGCAGC
951 TTCGGATTTG GGAAGTACC ATGAGGAAAT CTTCCCAT GAGTACCAGA
1001 ACGAAACATT GGGCAGGCTG TTGCTCAGCT TTCCAACCG CATTCTCTT
1051 GATGAAGACG ACCGCATCCT GCTTCAAACA CTAGGCAGGC AATTGGGCGT
1101 ATCGCTTGCC GCGCAAAAC AGGAGGAAGA AAAACGCCTG CTTCAGTAT
1151 TCGAGGAACG CAACCTGATT GCGCAAGGAT TACATGACAG CATCGACAA
1201 GCATTAACGT TCCTAAACCT ACAGGTACAG ATGCTGGAAG CCGCCTTTGC
1251 CGAAACAAA CCGGAGGAAG CCGCAGAAA CATCAGCTTT ATCAAACAG
1301 GCGTGACGGA ATGTTATGAA GATGTCGCG AACTGCTGCT CAACTTCCGT
1351 ACCAAATCA GCAATAAGA ATTTCCCGAA GCCGTTGCCG ACCTATTCGC
1401 CCGCTTTACG CAACAAACCG GGATAACGCT CGAAACCGCC TGGGAAACG
1451 GTTCGTTTCT GCGCCTCAG GAAGCGCAGC TCCAAATGAT TTTATCCTG
1501 CAGGAAAGCC TGTCCAACAT CCGCAAACAC GCCCGCGCCA CCCATGTAAA
1551 ATTCACCCTT TCCGAACACG GCGGACGCTT TACCATGACC ATCCAAGACA
1601 ACGGACAAGG TTTTCGACACG GAGAAAATAG GAGAACCAC GGCAGCCAT
1651 GTCGGACTGC ACATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1656; ORF 561>:

```

m561 . pep
1  MILPARFSOG ISLSRLKLL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
51  EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFOWAIM LMTLVSSVLM LFWHQIWRV FLQALREGAE
201 RIGRRCFDIP VPEGTPPEFK QVGRCFNQM GRKILYDDL EGQVAEQTRS
251 LEKQNQNLT LYQTRDLHQ SYIPQAAEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIH ADCGTAASDL GKYHEEIFPI EYQNETLRL LLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEERL LAVLQERNLI AQLHDSIAQ
401 ALTFNLQVQ MLETAFENK REEAENISF IKTGVQECYE DVRELLLNFR
451 TKISNKEFPE AVADLFARF QQTGITVETA WENGSLPQPQ EAQLQMIFIL

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501 QESLSNIRKH ARATHVKFTL SEHGRFTMT IQDNGQFDT EKIGEPTGSH
 551 VGLHIMQERA KRIHAVLEIR SQAQGGTTVS LTVASEESLK *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m561/g561 89.7% identity in 223 aa overlap

	10	20	30	40	50	60
m561.pep	MILPARFSDGISLSRLKLLTGLWVGLAALS	VVLTL	LSRL	ENAA	SVIEE	EAGNLRMQAY
g561	MILPTRFSDGIPLSLRLKLLTGLWVGLAALS	VVLTL	LSRL	ENAA	SVIEE	EAGNLRMQAY
	10	20	30	40	50	60
m561.pep	RLAYMAGEGSPRAQIDNQVAE	FEKSLKRIAQSDAIH	PLIPSDT	PLAYDL	IQSMLI	IDWQA
g561	RLAYMAGEGSPRAQIDNQIAE	FEKSLKRISQSDAIH	PLIPSDN	PLAYDL	IQSMLI	IDWQA
	70	80	90	100	110	120
m561.pep	HILPPLQSYRRPTQVDLYR	FAGNIELFLQALENANE	KNTWWLRR	FCQWAIM	MLTVSS	VLM
g561	NILPPLQAYRRPTQIELYR	FAGNIELFLQALENAGE	KNTWWLRR	FCQWIM	MLTVSS	VLM
	130	140	150	160	170	180
m561.pep	LFWHQIWVIRPLQALREGA	ERIGRRCFDIP	VEGGTPE	FKQVGR	CFNQMG	GRKLKILYDDL
g561	LFWHQIWVIRPLQALREGA	ERIGRRCFDIP	VEGGTPE	FKQVGR	CFNQMG	GRKLKILYDDL
	190	200	210	220	230	240
m561.pep	EGQVAEQTRSLEKQNLTL	LYQTTRDLH	QSYIPQQA	AHFLNR	ILPAVG	ADSGRVCLDG
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1657>:

a561.seq

1	ATGATACTGC	CAGCCCGTTT	TTCAGACGGC	ATCAGCCTTT	CCCTGCGCCT
51	GAAACTCCTG	ACCGGACTGT	GGGTCGGGTT	GGCGGCATTG	TCTGTCGTTT
101	TGACACTGCT	GCTCTCTTTG	CGTCTGGAAA	ACGCGGCCTC	CGTCATCGAA
151	GAGGCGGGCA	ACTTGAGAA	GCAGGCATAC	CGTCTGGCAT	ACATGGCGGG
201	TGAAGGCTCG	CCCCGTGCGC	AAATTGACAA	TCAGGTTGCC	GAATTTGAAA
251	AAAGTTTAAA	ACGCATTGCC	CAAAGCGATG	CCATCCATCC	GCTGATTCCT
301	TCGGACACCC	CTCTTGCTTA	TGATTTGATA	CAATCCATGC	TGATTATAGA
351	TTGGCAGGCA	CACATCCTCC	CCCCGCTCCA	GTCCTACCGG	CGACCGACTC
401	AGGTGCATCT	CTACCGCTTT	GCCGGAACA	TCGAAGTGT	TTTGCAAGCA
451	TTGGAAAATG	CCAACGAAAA	AAACACATGG	TGGCTCAGGC	GTTTTCATG
501	GGCAATTATG	TTGATGACGC	TGGTGTCTGC	TGTACTGATG	CTGTTTGGC
551	ACCAGATTG	GGTATCCGG	CCGCTGCAGG	CGTTAAGGGA	AGGTGCGGAA
601	CGCATCGGAC	GGAGGTGTTT	CGATATTCCG	GTTCCCGAAG	GCGGTACGCC
651	GGAAATCAAA	CAGGTCGGGC	GTGTTTCAA	TCAAATGGGC	GGCAGGTTGA
701	AAATTTTATA	TGATGATTG	GAAGGACAAG	TCGCCGAGCA	GACACGCAGT
751	CTCGAAAAAC	AAAATCAAAA	CCTGACCCTG	CTGTACCAAA	CTACACGGGA
801	TCTGCACCAA	TCCTACATAC	CGCAACAGGC	TGCAGAACAT	TTTCTAAACC
851	GTATCTTGCC	CGCCGTAGGA	GCAGATTCCG	GCAGAGTTTG	TTTGGACGGC
901	GGATCCGATG	TTTATGTTTC	CATTATCAT	GCGGATTGCG	GCACAGCAGC
951	TTCGGATTG	GGGAAGTACC	ATGAGGAAAT	CTTCCCCATT	GAGTACCAGA
1001	ACGAAACATT	GGGCAGGCTG	TTGCTCAGCT	TTCCAAACGG	CATTCTCTT
1051	GATGAAGACG	ACCGCATCCT	GCTTCAAACA	CTAGGCAGGC	AATTGGGCGT
1101	ATCGCTTGCC	GGCGCAAAAC	AGGAGGAAGA	AAAACGCTG	CTTGAGTAT
1151	TGCAGGAACG	CAACCTGATT	GCGCAAGGAT	TACATGACAG	CATCGCACAA
1201	GCATTAACTG	TCCTAAACCT	ACAGGTACAG	ATGCTGGAAA	CCGCTTTTGC
1251	CGAAAAACAA	CGGGAGGAAG	CCGCAGAAAA	CATCGGCTTC	ATCAAAACAG
1301	GCGTGCAGGA	ATGTTATGAA	GATGTCCGCG	AACTGCTGCT	CAACTCCGT
1351	ACCAAAATCA	GTAATAAAGA	ATTTCCCGAA	GCCGTTGCCG	ACCTATTCTC

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1401 GCGCTTTACG CAACAGACCG GCACGACTGT CGAAACCGCT TGGGAAAACG
1451 GCACGCACCT GCCTACACAG GACGAGCAGC TCCAAATGAT TTTCATCCTG
1501 CAAGAAAGCT TGTCCAACAT CCGAAAACAT GCCCAGCCCA CCCATATCAA
1551 ATTCAGACTG CTCAAACAGG ATGGAAGTTT TACAATGACC ATTCAGACA
1601 ACGGACAGGG TTTTGACACG GAAAACATTG GAGAACCATC GGGCAGCCAT
1651 GTCGGACTGC ATATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1658; ORF 561.a>:

```

a561.pep
1  MILPARFSDG ISLSRLKLL TGLWVGLAAL SVVLTLLSL RLENAASVIE
51  EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFESLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMIIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFWHQIWVIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQM GRLKILYDDL EGQVAEQTRS
251 LEKQNQNLTL LYQTTRDLHQ SYIPQAAEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGR LLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEKRL LAVLQERNLI AQGLHDSIAQ
401 ALTFNLQVQ MLETAFENK REEAAENIGF IKTGVQECYE DVRELLNFR
451 TKISNKEFPE AVADLFSRFT QQTGTTVETA WENGTHLPTQ DEQLQMIFIL
501 QESLSNIRKH AHATHIKFRL LKQDGSFTMT IQDNGQCFDT ENIGEPSGSH
551 VGLHIMQERA KRIHAVLEIR SQAQGTTVS LTVASEESLK *

m561/a561 96.9% identity in 590 aa overlap

10      20      30      40      50      60
m561.pep MILPARFSDGISLSRLKLLTGLWVGLAALSVVLTLLSLRLENAASVIEEAGNLRMQAY
|||||
a561      MILPARFSDGISLSRLKLLTGLWVGLAALSVVLTLLSLRLENAASVIEEAGNLRMQAY
10      20      30      40      50      60

70      80      90      100     110     120
m561.pep RLAYMAGEGSPRAQIDNQVAEFESLKRIAQSDAIHPLIPSDTPLAYDLIQSMIIIDWQA
|||||
a561      RLAYMAGEGSPRAQIDNQVAEFESLKRIAQSDAIHPLIPSDTPLAYDLIQSMIIIDWQA
70      80      90      100     110     120

130     140     150     160     170     180
m561.pep HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM
|||||
a561      HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM
130     140     150     160     170     180

190     200     210     220     230     240
m561.pep LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGRCLKILYDDL
|||||
a561      LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGRCLKILYDDL
190     200     210     220     230     240

250     260     270     280     290     300
m561.pep EGQVAEQTRSLEKQNQNLTLTYQTTRDLHQSYIPQAAEHFLNRILPAVGADSGRVCLDG
|||||
a561      EGQVAEQTRSLEKQNQNLTLTYQTTRDLHQSYIPQAAEHFLNRILPAVGADSGRVCLDG
250     260     270     280     290     300

310     320     330     340     350     360
m561.pep GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLLSFPNGISLDEDDRILLQT
|||||
a561      GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLLSFPNGISLDEDDRILLQT
310     320     330     340     350     360

370     380     390     400     410     420
m561.pep LGRQLGVSLAGAKQEEKRLAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK
|||||
a561      LGRQLGVSLAGAKQEEKRLAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK

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847

	370	380	390	400	410	420
	430	440	450	460	470	480
m561.pep	REEAAENISFIKTGVQECYEDVRELLLNFR	TKISNKEFPEAVADLFARETQQTGITVETA				
a561	REEAAENIGFIKTGVQECYEDVRELLLNFR	TKISNKEFPEAVADLFSRFTQQTGTTVETA				
	430	440	450	460	470	480
	490	500	510	520	530	540
m561.pep	WENGSLFPQEAQLQMIFILQESLSNIRKHARATHVKFTLSEHGGRFTMTIQDNGQGFDT					
a561	WENGTHLPTQDEQLQMIFILQESLSNIRKHAHATHIKFRLLKQDGSFTMTIQDNGQGFDT					
	490	500	510	520	530	540
	550	560	570	580	590	
m561.pep	EKIGEPTGSHVGLHIMQERAKRIHAVLEIRSQAQQGTTVSLTVASEESLKK					
a561	ENIGEPSGSHVGLHIMQERAKRIHAVLEIRSQAQQGTTVSLTVASEESLKK					
	550	560	570	580	590	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1659>:

g562.seq..

```

1  atggcaagcc cgtcgagtct gcctttcaat tcgggcaaga ccaaaccgac
51  ggcttttggcc gcgccggttt tggtcggaat catgttttcc acgccgctgc
101  gggcgcgccg caggtctttg tggcgacagt cggtaacggt ttggtcgttg
151  gtcagtgcgt ggatgggtgt cattgcgcct ttgacgatgc cgacgctttc
201  gctcaacact ttggcaaccg gcgagaggca gttggtggtg caggaagcgt
251  tggaaacgac ggtcatgtcg gcggtcagga cgctgtcggt caccgcgtac
301  acgacggttg catcgacatc gtcgccgccc ggtgcggaat tgaggacttt
351  ttccgcgcgc ctttcgaggt ggattttggc tttttctttg ctggtgaacg
401  cgccggtgca ttccatgacc aaatcgacac cgagttcttt ccacggcagt
451  tcggcagggg tcggggtcga gaagaagggg attttgtcgc cgttgacgat
501  gaggttgccg ccgtcgtggg atacgtcggc ttcaaagcgt ccgtgtacgg
551  tgtcgaaatt ggtcagatgg gcgttggttt caaggctgcc gctggcggtg
601  acggcgacga ttggagttg gtcttga

```

This corresponds to the amino acid sequence <SEQ ID 1660; ORF 562.ng>:

g562.pep

```

1  MASPSSLPFN SGTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51  VSAWMVVIAP LTMPTLSLNT LATGERQLVV QEALTTVMS AVRTLSFTPY
101  TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSM TSTPSSFHGS
151  SAGLRVEKKG ILSPLTMRLP PSWDTASAKR PCTVSNLVRW ALVSRPLPLA
201  TATIWSWS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1661>:

m562.seq

```

1  ATGGCAAGCC CGTCGAGCCT GCCTTTCAAT TCGGGCAGTA CCAAACCGAC
51  GGCTTTTGCC GCGCCGTTT TGGTCGGAAT CATGTTTTC ACGCCGCTGC
101  GGGCGCGCGC CAGGTCTTTG TGGCGCACGT CGGTAACGCT TTGGTCGTTG
151  GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTTC
201  GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT
251  TGGAAACGAC GGTGATGTCG GCGGTCAGGA CGCTGTCGTT CACGCCGTAC
301  ACGACGGTTG CATCGACATC GTCGCCGCCC GGTGCGGAAA TGAGGACTTT
351  TTTCGCGCCG CTTTCGAGGT GGATTTTGGC TTTTCTTTG CTGGTGAACG
401  CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT
451  TCGGCAGGGT TCGGGTCTGA GAAGAAGGGG ATTTTGTGCG CGTTGACGAT
501  GAGGTTGCCG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGCACGG
551  TGTCGAAATT GGTGAGATGG GCGTTGTTT CAAGGCTGCC GCTGGCGTTG
601  ACGGCGACGA GTTGAGTTG GTCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1662; ORF 562>:

m562.pep

```

1  MASPSSLPFN SGTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51  VSAWMVVIAP LTMPTLSLNT LATGERQLVV QEALTTVMS AVRTLSFTPY

```


848

```

101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSM TSTPSSFHGS
151 SAGLRVEKKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRLPLAL
201 TATSWWS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m562/g562 99.0% identity in 208 aa overlap

```

              10      20      30      40      50      60
m562.pep      MASPSSLPFNSGSKPTAFAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMMVVIAP
              |||||
g562           MASPSSLPFNSGSKPTAFAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMMVVIAP
              10      20      30      40      50      60

              70      80      90      100     110     120
m562.pep      LTMTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPTTVASTSSPPGAEMRTFFAP
              |||||
g562           LTMTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPTTVASTSSPPGAEMRTFFAP
              70      80      90      100     110     120

              130     140     150     160     170     180
m562.pep      LSRWILAFSLLVNAPVHSM TSTPSSFHGS SAGLRVEKKG ILSPLTMLRP PSWDTASAKR
              |||||
g562           LSRWILAFSLLVNAPVHSM TSTPSSFHGS SAGLRVEKKG ILSPLTMLRP PSWDTASAKR
              130     140     150     160     170     180

              190     200     209
m562.pep      PCTVSNLVRWALVSRLPLALTATSWWSX
              |||||
g562           PCTVSNLVRWALVSRLPLALTATSWWSX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1663>:

```

a562.seq
1  ATGGCAAGCC CGTCGAGTTT GTCTTTCAAT TCGGGCAGTA CCAAACCGAC
51  GGCTTTTGCC GCGCCAGTTT TGGTCGGAAT CATGTTTTC ACGCCGCTGC
101 GGGCGCGGCG CAGGTCTTTG TGGCGCACGT CGGTAACGGT TTGGTCGTTG
151 GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTTC
201 GCTCAACACT TTGGCAACCG CCGAGAGGCA GTTGGTGGTG CAGGAAGCGT
251 TGGAAACGAC GGTCAATGTCG CCGTCAGGA TGCTGTCGTT CACGCCGTAC
301 ACGACGGTTG CATCGACATC CTCGCCGCC GGTGCGGAAA TGAGGACTTT
351 TTTCGCGCCG CTTTCCASAT GAACTTTGGC TTTTCTTTG CTGGTGAACG
401 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT
451 TCGGCAGGGT TCGGGTCNA GAAGAANGGG ATTTTGTCGC CGTTGACGAT
501 GAGGTGCGCG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGACGCG
551 TGTCGAATTT GGTGAGGTGG GCGTTGGTTT CAAGGCTGCC GCTGGCGTTG
601 ACGGCGACGA TTTGGAGTTG GTCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1664; ORF 562.a>:

```

a562.pep
1  MASPSSLSFN SGSTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51  VSAWMVVIAP LTMTLSLNT LATGERQLVV QEALETTVMS AVRMLSFPT
101 TTVASTSSPP GAEMRTFFAP LSR*TLAFSL LVNAPVHSM TSTPSSFHGS
151 SAGLRVKKXG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRLPLAL
201 TATIWSWS*

```

m562/a562 96.6% identity in 208 aa overlap

```

              10      20      30      40      50      60
m562.pep      MASPSSLPFNSGSKPTAFAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMMVVIAP
              |||||
a562           MASPSSLSFN SGSTKPTAFA APVLVGIMFS TPLRARRRSLWRTSVTVWSLVSAMMVVIAP
              10      20      30      40      50      60

```

849

	70	80	90	100	110	120
m562.pep	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSTFTPYTTVASTSSPPGAEMRTFFAP					
a562	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRMLSTFTPYTTVASTSSPPGAEMRTFFAP					
	70	80	90	100	110	120
m562.pep	LSRWILAFSLLVNAPVHSMTKSTPSSFHGSSAGLRVEKKGILSPLTMRLLPPSWDTSASKR					
a562	LSRXTLAFSLLVNAPVHSMTKSTPSSFHGSSAGLRVXKXGILSPLTMRLLPPSWDTSASKR					
	130	140	150	160	170	180
m562.pep	LSRWILAFSLLVNAPVHSMTKSTPSSFHGSSAGLRVEKKGILSPLTMRLLPPSWDTSASKR					
a562	LSRXTLAFSLLVNAPVHSMTKSTPSSFHGSSAGLRVXKXGILSPLTMRLLPPSWDTSASKR					
	130	140	150	160	170	180
m562.pep	PCTVSNLVRWALVSRLPLALTATSWWSX					
a562	PCTVSNLVRWALVSRLPLALTATSWWSX					
	190	200	209			
m562.pep	PCTVSNLVRWALVSRLPLALTATSWWSX					
a562	PCTVSNLVRWALVSRLPLALTATSWWSX					
	190	200				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1665>:

g563.seq

```

1  ATGAACAAAA CCCTCTATCG TGTGATTTTC AACCGCAAAC GCGGTGCTGT
51  GGTAGCTGTT GCCGAAACCA CCAAGCGCGA AGGTAAAAGC TGTGCCGATA
101 GTGGTTCGGG CAGCGTTTAT GTGAAATCCG TTTCTTTTCAT TCCTACTCAT
151 TCCAAAGCCT TTTGTTTTTC TGCATTAGGC TTTTCTTTAT GTTTGGCTTT
201 GGGTACGGTC AATATTGCTT TTGCTGACGG CATTATTACT GATAAAGCTG
251 CTCCTAAAAC CCAACAAGCC ACGATTCTGC AAACAGGTAA CGGCATACCG
301 CAAGTCAATA TTCAAACCCc tACTTCGGCa ggGGTTTCTG TTAATCAATA
351 TGCCCAGTTT GATGTGGGTA ATcgCGGGC GATTTTAAAC AACAGTCGCA
401 GCAACACCCA AACACAGCTA GGCGGTTGGA TTCAAGGCAA TCCTTGGTTG
451 ACAAGGGGCG AAGCACGTGT GGTGTAAAC CAAATCAACA GCAGCCATCC
501 TTCACAACTG AATGGCTATA TTGAAGTGGG TGGACGACGT GCAGAACTCG
551 TTATTGCCAA TCCGGCAGGG ATTGCAGTCA ATGGTGGTGG TTTTATCAAT
601 GCTTCCCGTG CCACTTTGAC GACAGGCCAA CCGCAATATC AAGCAGGAGA
651 CTTTAGCGGC TTTAAGATAA GGCAAGGCAA TGCTGTAATC GCCGGACACG
701 GTTTGGATGC CCGTGATACC GATTTCACAC GTATTCTTTT GTATGCCAAC
751 AAAATCACCT TGATCAGTAC GGCCGAACAA GCAGGCATTC GTAATCAAGG
801 GCAGTTGTTT GCTTCTTCCG GTAATGTGGC GATTGATGCA AATGGCCGTT
851 TGGTCAATAG TGGCACGATG GCTGCGCCA ATGTGCAAGA TATGAATAAT
901 ACAGCGGAAC ACAAAGTCAA TATCCGCACT CAAGCCTTTG AAAACAGCGG
951 TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAA TCGATTCAAA
1001 ACACCTGGCA ATTATTGTCG GCAGGAACAG AGGATTTAGC CGTTTCAGGC
1051 AGCCTGAACA ATCAAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT
1101 TCACGATGGT CAGCAATCTA CCGTTGTCAT TGATAATACG AATGGCACGA
1151 TACAATCAGG CCGTGATGTT GCCATTGAG CAAATCGTT ATCCAACAAC
1201 GGCACACTTG CCGCTGATAA TAACTGGAT ATTGCGTTAC AAGATGATTT
1251 TTATGTAGAA CGCAAGATCG TGGCGGGCAA TGAATTGTCG CTCAGTACAC
1301 GAGGCAGCCT GAAAAATTCA CATACCTTGC AAGCAGGAAA ACGCATTCCG
1351 ATTAAAGCAA ATAACCTTGA TAATGCAGTA CAAGGCAACA TTCAATCCGG
1401 CCGTACGACA GACATTGGCA CGCAGCACAA TTAAACCAAT AGAGGCTTGA
1451 TTGACGGACA ACAAAACCAA ATCCAAGCCG GGCAATGAA TAATATCGGT
1501 ACAGGTGCGA TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA
1551 CAATCAAGAT GAAAACGGTA CAGGTGCCGC CATTGCGGCA CGCGAAAACC
1601 TGAATTAGG CATTGAACAA TTAAATAACC GTGAAAACAG TCTGATTTAC
1651 AGCGGTAAAC ATATGGCGGT TGGCGGCGCA TTAGATACCA ATGACCAAGC
1701 CACAGGCAAA GCCCAAAGGA TACAATGTC CCGCGCAATC ATTGAAGCTG
1751 CAGGCAAAAT GCGTTAGGT GTAGAAAAGC TGCACAATAC CAATGAGCAT
1801 TTGAAAACGC AGTTGGTAGA AACAGGGCGC GAGCGTATTG TTGATTACGA
1851 AGCATTGGA CGACACGAAT TATTGCGAGA AGGCACGCAA CATGAATTAG
1901 GCTGTTTGT CTACAACAAT GAATCAGACC ACTTACGCAC CCCTGATGGA
1951 GTGGCGCATG AAAATTGGCA TAAATACGAT TATGAAAAAG TAACGCAAGA
2001 AACTCAAGTA ACCGGAACGT CGCTGCTAA AATCATTGCA GGTAGCGATT
2051 TGATTATTGA TAGCAAAGCA GTCTTCAACA GCGACAGCCG AATCATTGCC

```

2101 GCGCGCCAAT TGCTTGTGCA AACAGAAAAA GACGGTTTGC ATAACGAGCA
 2151 AACCTTTGGC GAGAAGAAAAG TCTTCAGCGA AAATGGTAAG TTGCACAACT
 2201 ACTGGCGTGC GCGTCGTAAA GGACATGATG AAACAGGGCA TCGTGAACAA
 2251 AATTATACCT TGCCGGAGGA AATCACACGC GACATTTTAC TGGGTTTCACT
 2301 TGCCTATGAA TCGCATAGCA AAGCATTAAAG CCGTCATGCG CCCAGCCAAG
 2351 GCACTGAGTT GCCACAAAGT AACCGGGATA ATATCCGTAC TCGCAAAAGC
 2401 AACGGTATTT CGCTACCTTA TACGCCCAAT TCTTTTACCC CATTACCCGG
 2451 CAGCAGCTTA TACATTATCA ATCCTGCCAA TAAAGGCTAT CTTGTTGAAA
 2501 CCGATCCACG CTTTGCCAAC TACCGTCAAT GGTGGGTAG TGACTATATG
 2551 CTGGGCAGCC TCAAACTAGA CCCAAACAAT TTACATAAAC GTTTGGGTGA
 2601 TGGTTATTAC GAGCAACGTT TAATCAATGA ACAAATCGCA GAGCTGACAG
 2651 GGCATCGTCG TTTAGACGGT TATCAAAACG ACGAAGAACA ATTTAAAGCC
 2701 TTAATGGATA ATGGCGCGAC TGCGGCACGT TCGATGAATC TCAGCGTTGG
 2751 CATTGCAATTA AGTGCCGAGC AAGCAGCGCA ACTGACCAGC GATATTGTTT
 2801 GGTGGGTACA AAAAGAAGTT AAACCTCCTG ATGGCGGCAC ACAAACCGTA
 2851 TTGATGCCAC AGGTTTATGT ACGCGTTAAA AATGGCGGCA TAGACGGTAA
 2901 AGGTGCATTG TTGTCAGGCA GCAATACACA AATCAATGTT TCAGGCAGCC
 2951 TGAAAAACTC AGGCACGATT GCAGGGCGCA ATGCGCTTAT TATCAATACC
 3001 GATACGCTAG ACAATATCGG TGGGCGTATT CATGCGCAAA AATCAGCGGT
 3051 TACGGCCACA CAAGACATCA ATAATATTGG CGGCATTCTT TCTGCCGAAC
 3101 AGACATTATT GCTCAATGCG GGTAACAACA TCAACAACCA AAGCACGGCC
 3151 AAGAGCAGTC AAAATGCACA AGGTAGCAGC ACCTACCTAG ACCGAATGGC
 3201 AGGTATTTAT ATCACAGGCA AAGAAAAAGG TGTTTTAGCA GCGCAGGCAG
 3251 GCAAAAGACAT CAACATCATT GCCGGTCAAA TCAGCAATCA ATCAGATCAA
 3301 GGGCAAACCC GGCTGCAGGC AGGACGCGAC ATTAACCTGG ATACGGTACA
 3351 AACCGGCAAA TATCAAGAAA TCCATTTTGA TGCCGATAAC CATAACATCC
 3401 GAGTTTCAAC GAACGAAGTC GGCAGCAGCA TTCAAACAAA AGGCGATGTT
 3451 ACCCtattGT CAGGGAATAA TCTCAATGCC AAAGCTGCCG AAGTCGGCAG
 3501 CGCAAAAGGC ACACCTTGCCG TGTATGCTAA AAATGACATT ACTATCAGCT
 3551 CAGGCATCCA TGCCGGCCAA GTTGATGATG CGTCCAAACA TACAGGCAGA
 3601 AGCGGCGGCG GTAATAAATT AGTCATTACC GATAAAGCCC AAAGTCATCA
 3651 CGAAACTGCT CAAAGCAGCA CCTTTGAAGG CAAGCAAGTT GTATTGCAGG
 3701 CAGGAAACGA TGCCAACATC CTTGGCAGTA ATGTTATTTC CGATAATGGC
 3751 ACCCGGATTC AAGCAGGCAA TCATGTTTCG ATTTGGTACAA CCCAAACTCA
 3801 AAGCCAAAGC GAAACCTATC ATCAAACCCA AAAATCAGGA TTGATGAGTG
 3851 CAGGTATCGG CTTCACTATT GGCAGCAAGA CAAACACACA AGAAAACCAA
 3901 TCCCAAAGCA ACGAACATAC AGGCAGTACC GTAGGCAGCC TGAAAGGCGA
 3951 TACCACCATT GTTGCAAGCA AACACTACGA ACAAACCGGC AGCAACGTTT
 4001 CCAGCCCTGA GGGCAACAAC CTTATCAGCA CGCAAAGTAT GGATATTGGC
 4051 GCAGCACAAA ACCAATTAAA CAGCAAAACC ACCCAAACCT ACGAACAAAA
 4101 AGGCTTAACG GTGGGCATTG AGTTCGCCCG TTACCGATTG GGCACAACAA
 4151 GCGATTGCGG TAGCACACAA AGCAGCAAAC AAGTCGGACA AAGCAAAAAA
 4201 GACCGCGTTA ATGCCATGGC GGCTGCCAAT GCAGGTTGGC AGGCCTATCA
 4251 AACAGGCAAA GGCACACAAA ACTTAGCCAA TGGTACAACC AATGCCAAAC
 4301 AAGTCAGCAT CTCCATAACC TACGGCGAAC AGCAAAACCG ACAAACCACC
 4351 CAAGTTCAAG CCAATCAAGC CCAAGCGAGT CAAATTCAAG CAGGCGGCAA
 4401 AACTACCCCT TATTGCCGAA GGTGCGGCGA ACAATCCAAT ATCAACATCA
 4451 CAGGCTCAGG TGTTTCAGGC AGAGCAGGAA CCGGCCTGAT TGCCGATAAG
 4501 CAAATCCATC TGCAATCAGC CGAGCAAAGC AATACCGAAC GCAGCCAAAA
 4551 CAAATCAGCA GGCTGGAACG CAGGTGCTGC CGTATCATTC GGACAAGGAG
 4601 GCTGGTCATT AGGCGTTGCC GCAGGCGGCA ATGTCGGCAA AGGCTACGGC
 4651 TATGGCGATA GCGTAACCCA CCGCCATAGC CATATTGGCG ACAAAGGCAG
 4701 CCAAACCCCT ATCCAAAGTG GTGGCGATAC CATCATCAA GCGCGCAAG
 4751 TACGCGGCAA AGGCGTACAA GTCAATGCCA AAAACCTAAG CATTCAAAGT
 4801 GTACAAGATA GAGAACTTA TCAAAGCAA CAACAAAACG CCGGTGCACA
 4851 AGTTACCGTA GGTATGGCT TCAAGTCCAG TGGCGATTAC AGCCAAAGCA
 4901 AAATCCGAGC CGACCATGCT TCGGTAACCG AGCAAAGCGG TATTTATGCC
 4951 GGAGAAGACG GCTATCAAAT CAAGGTCCGA AACCATACAG GCCTCAAAGG
 5001 CGGCATCATC ACCAGCAGCC AAAGCGCAAA AGACAAGGGT AAAAACCGAT
 5051 TCAGCACAGG CACACTCGCC GGCAGTGATA TTCAAAATTA CAGCCAATAC
 5101 GAAGGAAAAA GTTTTGGATT GGGTGCCAGC GTTGCCGTAA GCGGCAAAAC
 5151 ACTGGGACAG GGCACAAAAA ATAAACCTCA AGACAAACAC CTGACAAGCA

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5201 TAGCCGATAA AAACGGCGCA AGTTCATCAG TAGGGTACGG CAGCGACAGC
5251 GACAGTCAAA GCAGCATCAC AAAAAGCGGC ATCAATACCC CCAAAAACAT
5301 TCAAATCACA GACGAAGCCG CACAAATCAG GCTGACAGGC AAAATAGCGG
5351 CACAAACCAA AGCCGATATT GATACAAACG TAACCACAGA CACCGCCGAA
5401 CGACATTCCG GCAGCCTGAA AAACATATTT GACAAAGATA GAGTGCAAAG
5451 TGAACGGGAT TTACAAAgAa CCGTCAGCCA AGATTTTAGT AAAAAATGTTT
5501 AACAAACCAA TACCGAGATT AACCAACATT TAGACAAACT CAAAGCAGAC
5551 AAAGAAGCAG CCGAAACAGC AGCAGCCGAG GCATTAGCCA ATGGCGATAT
5601 GGAAACTGCC AAACGCAAGC CCCATGAAGC TCAAGATGCG GCAGCAAAAG
5651 CAGATAATTG GCAACAAGGC AAAGTCATT CCAACATGTT AGCCTCAGGT
5701 TTAGCTGAGC CGACCCAAAG CGGAGCgggc ATCGCTGCGG CTACCGCATC
5751 GCCAgAaCGTA TCGTATGCGA TTGGACAGCA CTTTAAagaT TTAGCCGGTC
5801 AAAACGCGAA TGGCAAAC TAACGCCAGT CgagAACCGC TCACGTTCTT
5851 GCCCACGCGG TATTAGGAGC AGCGGTGCGC GCAGCATGAG GCAACAATGC
5901 CCCGGCAGGA GCATTGGGTG CGGGCGGGTc ggAagcggCC GCCCAATCA
5951 TCGGCAAAAT GCTGTACGGC AAAGGAGAcg gcggcagcCT GAATgcggag
6001 gaaaAAGaga CCGTTTCGGC GATTACAAGG ATGCTGggtA cGgctGCCGG
6051 AGCAGCTGAG GGAAACTCGT CCGCCGATGC TGTGTGGGGT TGTTTTcaaa
6101 cggctTCaga TTTCGCTTCC TCTTTTTCAT ATCCTATAAA CATGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1666; ORF 563.ng>:

g563.pep..

```

1 MNKTLRYRVF NRKRGAVVAV AETTKREGKS CADSGSGSVY VKSVSFIPTH
51 SKAFCFSAIG FSLCLALGTV NIAFADGIIT DKAAPKTOQA TILQTGNIGP
101 QVNIQTPTSA GVSVNQYAQF DVGNRGAILN NSRSNTQTQL GGWIQGNPWL
151 TRGEARVVVN QINSSHPSQL NGYIEVGRR AEVVIANPAG IAVNGGGFIN
201 ASRATLTGQ PQYQAGDFSG PKIRQGNVAV AGHGLDARDT DFTRILLYAN
251 KITLISTAEQ AGIRNQGLF ASSGNVAIDA NGRLVNSGTM AAANVQDMNN
301 TAEHKVNIRS QAFENSGTAV SQOQTQIHSQ SIONTGKLLS AGTEDLAVSG
351 SLNNQNGEIA TNQQLIHDG QQSTVIDNT NGTIQSGRDV AIQAKSLSN
401 GTLAADNKLD IALQDDFYVE RKIVAGNELS LSTRGSLKNS HTLQAGKRIR
451 IKANNLDNAV QGNIQSGGTT DIGTQHNLTN RGLIDGQQTK IQAGQMNNIG
501 TGRYIGDNIA IAATRLDNQD ENGTAAGIAA RENLNLGIEQ LNNRENSLIY
551 SGNDMAVGGG LDTNDQATGK AQRHINAGAI IEAAGKMRLG VEKLNHTNEH
601 LKTQLVETGR ERIVDYEAFG RHELLREGTQ HELGWVYNN ESDHLRTPDG
651 VAHENWHKYD YEKVTQETQV TGTAPAKIIA GSDLIIDSKA VFNSDSRIIA
701 GGQLLVQTEK DGLHNEQTFG EKKVFSENGK LHNYYWRARRK GHDETGHRREQ
751 NYTLPEBITR DISLGSFAYE SHSKALSRHA PSQGTQLPQS NRDNIRTAKS
801 NGISLPTPN SFTPLPGSSL YIINPANKGY LVETDPRFAN YRQLGSDYM
851 LGSCLKDPNN LHKRLGDGYY RQRLINEQIA ELTGHRRLDG YQNDEEQFKA
901 LMDNGATAAR SMNLSVGIAL SAEQAAQLTS DIVVLVQKEV KLPDGGTQTV
951 LMPQVYVRVK NGGIDGKGAL LSGSNTQINV SGSLKNSGTI AGRNALIINT
1001 DTLDNIGGRI HAQKSAVTAT QDINNIGGIL SAEQTLNNA GNNINNQSTA
1051 KSSQNAQSS TYLDRMAGIY ITGKEKGVLA AQAGKDINI AGQISNQSDQ
1101 GQTRLQAGRD INLDTVQTGK YQEIHFDADN HTIRGSTNEV GSSIQTGKDV
1151 TLLSGNNLNA KAAEVGSAKG TLAVYAKNDI TISSGIHAGQ VDDASKHTGR
1201 SGGGNKLVIIT DKAQSHHETA QSSTFEKGQV VLQAGNDANI LGSNVISDNG
1251 TRIQAGNHVR IGTQTQTSQS BTYHQTKSG LMSAGIGFTI GSKTNTQENQ
1301 SOSNEHTGST VGSCLKGDTTI VASKHYEQTG SNVSSPEGNN LISTQSMDIG
1351 AAQNQLNSKT TQTYEQKGLT VGIQFARYRF GTTSDCRSTQ SSKQVGQSKN
1401 DRVNAMAAN AGWQAYQTGK GAQNLANGTT NAKQVSISIT YGEQQNRQTT
1451 QVOANQAQAS QIQAGKTTL YCRRCEQSN INITSGSVSG RAGTGLIADK
1501 QIHLQSAEQS NTERSQNKSA GWNAGAAVSF QGGGWSLGA AGGNVKGKYG
1551 YGDSVTHRHS HIGDKGSQTL IQSGGDTI IK GAQVRGKGVQ VNAKNLSIQS
1601 VQDRETYQSK QQNAGAQTIV GYGFSASGDY SQSKIRADHA SVTEQSGIYA
1651 GEDGYQIKVG NHTGLKGGII TSSQSAKDKG KNRFTGTALA GSDIQNYSQY
1701 EGKSFGLGAS VAVSGKTLGQ GAKNKPQDKH LTSIADKNGA SSSVGYGSDS
1751 DSQSSITKSG INTPKNIQIT DEAAQIRLTG KIAAQTKADI DTNVTDTAE
1801 RHSGSLKNIF DKDRVQSELD LQRTVSQDFS KNVQQTNTET NQHLDKLKAD
1851 KEAAETAATAE ALANGDMETA KRKAHEAODA AAKADNWQQG KVILNMLASG
1901 LAEPTQSGAG IAAATASPDV SYAIGQHFKE LAGQNANGKL TASQETAHVL
1951 AHAVLGAAVA AAXGNNAPAG ALGAGGSEAA APIIGKWLYG KDGGSGLNAE
2001 EKETVSAITR MLGTAAGAAE GNSSADAVWG CFQTASDFAS SFSYPINM*

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The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1667>:

m563.seq.

```

1  ATGAATAAAA CTCTCTATCG TGTAATTTTC AACCGCAAAC GTGGGGCTGT
51  GGTAGCCGTT GCTGAAACTA CCAAGCGCGA AGGTAAAAGC TGTGCCGATA
101 GTGATTCAGG CAGCGCTCAT GTGAAATCTG TTCCTTTTGG TACTACTCAT
151 GCACCTGTTT GTCGTTCAAA TATCTTTTCT TTTCTTTTAT TGGGCTTTTC
201 TTTATGTTTG GCTGTAGGTA CGGCCAATAT TGCTTTTGCT GATGCGATTA
251 TTGCTGATAA AGCTGCTCCT AAAACTCAAC AAGCCACGAT TCTGCAAACA
301 GGTAACGGCA TACCGCAAGT CAATATTCAA ACCCTTACTT CGGCAGGGGT
351 TTCTGTAAAT CAATACGCCC AGTTTGATGT GGGTAATCGC GGGGCGATT
401 TAAACAACAG CCGCAGCAAC ACCCAAACAC AGCTAGGCGG TTGGATTCAA
451 GGTAATCCTT GGTGCGCAAG GGGCGAAGCA CGTGTGGTTG TAAACCAAAAT
501 CAACAGCAGC CATTCTTCAC AAATGAATGG CTATATTGAA GTGGGCGGAC
551 GACGTGCAGA AGTCGTATT GCCAATCCGG CAGGGATTGC AGTCAATGGT
601 GGTGGTTTTA TCAATGCTTC CCGTGCCACT TTGACGACAG GCCAACCGCA
651 ATATCAAGCA GGAGACCTTA GCGGCTTTAA GATAAGGCAA GGCAATGTTG
701 TAATCGCCGG ACACGGTTTG GATGCCCGTG ATACCGATT TACACGTATT
751 CTCAGTTATC ATTCCAAAAT TGATGCACCC GTATGGGGAC AAGATGTTCC
801 TGTCGTGCGG GGACAAAACG ATGTGGTCGC AACAGGTAAT GCACATTTCG
851 CTATTCTCAA TAATGCTGCT GCCAATACGT CAAACAATAC AGCCAACAAC
901 GGCACACATA TCCCTTTATT TGCGATTGAT ACAGGCAAAT TAGGAGGTAT
951 GTATGCCAAG AAAATCACCT TGATCAGTAC GGCCGAGCAA GCAGGCATT
1001 GTAATCAAGG GCAGTTGTTT GCTTCTTCCG GTAATGTGGC GATTGATGCA
1051 AATGGCCGTT TAGTCAATAG TGGCACGATG GCTGCCGCCA ATGCCGAAAG
1101 TACGGATAAT ACAGCGGAAC ACAAGTCAA TATCCGCAGT CAGGCGGTTG
1151 AAAACAGCGG TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAG
1201 TCGATTCAAA ACACTGGCAC ATTATGTCC TCAGGCGAAA TATTGATTCA
1251 CAATTGCGGC AGCCTGAAAA ATGAAACATC AGGCACCATT GAAGCCGCTC
1301 GTTTGGCTAT TGATACCGAC ACACCTAATA ATCAAGGCAA ACTCTCTCAA
1351 ACAGGTTTCA AAAAATCCCA TATTGATGCA CAAGGCAAAA TGGATAACCG
1401 TGGCCGCATG GGTTTACAAG ATACCGCACC AACCGCGTCA AATGGTTCAA
1451 GCAATCAAAC CGGCAATAGT TACAATGCAT CTTTCCATT ATCCACTACC
1501 ACACCAACAA CGGCAACAGG TACGGGTACT GCAACCGTTT CTATATCAAA
1551 CATAACTGCG CCTACCTTTG CTGATGGGAC AATTGCGACT CATGGTGCAC
1601 TGGATAATTC AGGCAGTATT ATTGCCAATG GTCAAACAGA TGTTAGTGCG
1651 CAACAAGGTT TAAATAATGC AGGACAAATA GACATTATC AGTTAAATGC
1701 AAAAGGTTTC GCGTTTGACA ATCACAATGG AACAAATTAT AGTGATGCGG
1751 TCCACATTCA AGCCGCGCAGC CTGAATAATC AAAATGGCAA CATCACAACA
1801 CGCCAACAGT TAGAGATTGA AACCGATCAA CTGGATAACG CTCATGGCAA
1851 GTTATTATCA GCAGAAATAG CGGATTAGC CGTTTCAGGC AGCCTGAACA
1901 ATCAAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT TCACGATGGT
1951 CAGCAATCTA CCGCTGTCAT TGATAATACG AATGGCACGA TACAATCAGG
2001 CCGTGATGTT GCTATTCAGG CAAAATCGTT ATCCAACAAC GGCACACTTG
2051 CCGCTGATAA TAAACTGGAT ATTGCGTTAC AAGATGATT TATGTAGAA
2101 CGCAATATCG TGGCGGGCAA TGAATTGTCG CTCAGTACAC GAGGCGCCT
2151 GAAAAATTCA CATACTTTGC AAGCAGGAAA ACGCATTCGG ATTAAGCAA
2201 ATAACCTTGA TAATGCAGCA CAAGGCAACA TTCAATCCGG CGGTACGACA
2251 GACATTGGCA CGCAGCACAA TTTAACCAAT AGAGGCTTGA TTGACGGACA
2301 ACAAACCAAA ATCCAAGCGG GGCAAAATGAA TAATATCGGT ACAGGTCGGA
2351 TTTATGCGCA CAATATCGCT ATTGCGGCTA CCCGCTTAGA CAATCAAGAT
2401 GAAACGGTA CAGGTGCCGC CATTGCGGCA CGTGAAAACC TGAATTAGG
2451 CATCGGACAA TTAACAACAC GTGAAAACAG TCTGATTAC AGCGGTAACG
2501 ATATGGCGGT TGGCGGCGCA TTAGATACCA ATGGCCAAGC CACAGGCAAA
2551 GCCCAAGGA TACACAATGC CGGCGCAACC ATTGAAGCTG CAGGCAAAAT
2601 GCGTTTAGGT GTAGAAAAGC TGCACAATAC CAATGAGCAT TTGAAAACGC
2651 AGTTGGTAGA AACAGGCGCG GAGCATATTG TTGATTACGA AGCATTGGGA
2701 CGACACGAAT TATTGCGAGA AGGCACGCAA CATGAATTAG GCTGGTCTGT
2751 CTATAACGAT GAATCAGACC ACTTACGCAC CCCTGATGGA CGGCGCATG
2801 AAAATTGGCA TAAATACGAT TATGAAAAAG TCACCCAAAA AACCCAAGTT
2851 ACCCAAACG CGCCAGCCAA AATCATTTCA GGTAAATGAT TAACCATTGA
2901 TGGTAAAGAA GTATTTAATA CCGATAGCCA AATCATTGCT GGTGCAATC
2951 TCATTGTACA AACAGAAAAA GACGGTTTGC ATAACGAGCA AACCTTTGGC

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3001 GAAAAGAAAG TATTCAGTGA AAATGGCAAA TTACACAGCT ATTGGCGTGA
3051 GAAACATAAA GGACGAGACT CAACGGGACA TAGCGAACAA AATTACACTT
3101 TGCCGGAGGA AATCACACGC AACATTTTAC TGGGTTTCAAT TGCCTATGAA
3151 TCGCATCGCA AAGCATTAAAG CCATCATGCG CCCAGCCAAG GCACTGAGTT
3201 GCCGCAAAGC AACGGTATTT CGCTACCCCTA TACGTCCAAT TCTTTTACCC
3251 CATTACCCAG CAGCAGCTTA TACATTATCA ATCCTGTCAA TAAAGGCTAT
3301 CTTGTTGAAA CCGATCCACG CTTTGCCAAC TACCGTCAAT GGTGGGTAG
3351 TGACTATATG CTGGACAGCC TCAAACCTAGA CCCAAACAAT TTACATAAAC
3401 GTTTGGGTGA TGGTTATTAC GAGCAACGTT TAATCAATGA ACAATTCGCA
3451 GAGCTGACAG GGCATCGTCG TTTAGACGGT TATCAAAACG ACGAAGAACA
3501 ATTTAAAGCC TTAATGGATA ATGGCGCGAC TGCGGCACGT TCGATGAATC
3551 TCAGCGTTGG CATTGCATTA AGTGCCGAGC AAGTAGCGCA ACTGACCAGC
3601 GATATTGTTT GGTGGGTACA AAAAGAAGTT AAGCTTCTTG ATGGCGGCAC
3651 ACAAACCGTA TTGGTGCCAC AGGTTTATGT ACGGTTAAAT AATGGCGACA
3701 TAGACGGTAA AGGTGCATTG TTGTCAAGCA GCAATACACA AATCAATGTT
3751 TCAGGCAGCC TGA AAAAATC AGGCACGATT GCAGGCGCA ATGCGCTTAT
3801 TATCAATACC GATACGCTAG ACAATATCGG TGGCGGTATT CATGCGCAAA
3851 AATCAGCGGT TACGGCCACA CAAGACATCA ATAATATTGG CGGCATGCTT
3901 TCTGCGAAC AGACATTATT GCTCAACGCA GGCAACAACA TCACAGCCA
3951 AAGCACCAAC GCCAGCAGTC AAAATACACA AGGCAGCAGC ACCTACCTAG
4001 ACCGAATGGC AGGTATTTAT ATCACAGGCA AAGAAAAAGG TGTTTATGCA
4051 GCGCAGGCAG GAAAAGACAT CAACATCATT CGCGGTCAA TCAGCAATCA
4101 ATCAGAGCAA GGGCAAACCC GGTGCAAGC AGGGCGCGAC ATTAACCTAG
4151 ATACGGTACA AACCAGCAAA CATCAAGCAA CCCATTTTGA TGCCGATAAC
4201 CATGTTATTC GCGGTTCAAC GAACGAAGTC GGCAGCAGCA TTCAAACAAA
4251 AGGCGATGTT ACCCTATTGT CAGGGAATAA CCTCAATGCC AAAGCTGCCG
4301 AAGTCAGCAG CGCAAACGGT ACACTCGCTG TGTCTGCCAA AAATGACATC
4351 AACATCAGCG CAGGCATCAA CACGACCCAT GTTGATGATG CGTCCAAACA
4401 CACAGGCAGA AGCGGTGGTG GCAATAAATT AGTCATTACC GATAAAGCCC
4451 AAAGTCATCA CGAAACCGCC CAAAGCAGCA CCTTTGAAGG CAAGCAAGTT
4501 GTATTGCAGG CAGGAAACGA TGCCAACATC CTTGGCAGCA ATGTTATTTT
4551 CGATAATGGC ACCCAGATTG AAGCAGGCAA TCATGTTTCG ATTGGTACAA
4601 CCCAAACTCA AAGCCAAAGC GAAACCTATC ATCAAACCCA GAAATCAGGA
4651 TTGATGAGTG CAGGTATCGG CTTCACTATT GGCAGCAAGA CAAACACACA
4701 AGAAAACCAA TCCCAAAGCA ACGAACATAC AGGCAGTACC GTAGGCAGCT
4751 TGAAAGGCGA TACCACCATT GTTGCAAGCA AACACTACGA ACAATCGGC
4801 AGTACGGTTT CCAGCCCGGA AGGCAACAAT ACCATCTATG CCCAAAGCAT
4851 AGACATTTCA GCGGCACACA ACAATTAAAT CAGTAATACC ACCCAAACCT
4901 ATGAACAAAA AGGCCTAACG GTGGCATTCA GTTCGCCCCG TACCGATTTG
4951 GCACAACAAG CGATTGCCGT AGCACAAGC AGCAACAAG TCGACAAAG
5001 CAAAACGAC CGCGTTAATG CCATGGCGGC TGCCAATGCA GGCTGGCAAG
5051 CCTATCAAAC AGGTAAGAGT GCACAAAAT TAGCCAATGG TACAACCAAT
5101 GCCAAACAAG TCAGCATCTC CATAACCTAC GGCGAACAGC AAAACCGACA
5151 AACCACCCAA GTTCAAGCCA ATCAAGCCCA AGCGAGTCAA ATTCAAGCAG
5201 GTGGTAAAAC CACATTAATC GCCACAGGCG CAGCAGAACA ATCCAATATC
5251 AACATCGCAG GCTCAGATGT TGCCGGCAAA GCAGGCACAA TCCTGATTGC
5301 CGATAACGAC ATCACACTCC AATCAGCCGA GCAAAGCAAT ACCGAACGCG
5351 GCCAAAACAA ATCGGCAGGC TGGAAACGAG GTGCTGCCGT ATCATTCGGA
5401 CAAGGAGGCT GGTCAATTAGG CGTTACCGCA GCGGCAATG TCGGCAAGG
5451 CTACGGCAAT GCGCAGACGA TCACCACCG CCATAGCCAT ATCGGCGACA
5501 AAGGCAGCCA AACCCCTATC CAAAGCGGTG GCGACACTAC CATCAAAGGC
5551 GCGCAAGTAC GCGGCAAAGG CGTACAAGTC AATGCCAAAA ACCTAAGTAT
5601 TCAAAAGCGTA CAAGATAGAG AAACCTATCA AAGCAACAAA CAAAACGCCA
5651 GTGCACAAAGT TACCGTAGGT TATGGCTTCA GTGCCGGTGG CGATTACAGC
5701 CAAAGCAAAA TCCGAGCCGA CCATGTTTCA GTAACCGAGC AAAGCGGTAT
5751 TTATGCCGGA GAAGACGGCT ATCAAATCAA GGTCCGAAAC CATACAGACC
5801 TCAAAGGCGG CATCATCACC AGTACCCAAA GCGCAGAAGA CAAGGGTAAA
5851 AACCGCTTTC AGACGGCCAC CCTACCCCAT AGCGACATCA AAAACCCAG
5901 CCAATACAAA GGCGAAAGTT TTGGATTGGG CGCAAGTGCG TCCTAAGCG
5951 GCAAAACACT GGGACAGGGC GCACAAAATA AACCTCAAAA CAAACACCTG
6001 ACAAGCGTAG CCGATAAAAA CAGCGCAAGT TCATCAGTGG GTTATGGCAG
6051 CGACAGCGAC AGTCAAAGCA GCATCACAAA AAGCGGCATC AACACCCGCA

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6101 ACATTCAAAT CACCGACGAA GCCGCACAAA TCCGGCTGAC AGGCAAAACA
6151 GCGGCACAAA CCAAAGCCGA TATTGATACA AACGTAACCA CAGACACCGC
6201 CGAACGACAT TCGGGCAGCT TGAAGAACAC CTTCAACAAA GAAGCGGTGC
6251 AAAGTGAAC TGGATTACAA AGAACCGTCA GCCAAGATTT TAGTAAAAAT
6301 GTTCAACAAG CCAATACCGA GATTAACCAA CATTTAGACA AACTCAAAGC
6351 AGACAAAGAA GCAGCCGAAA CAGCAGCAGC CGAGGCATTA GCCAATGGCG
6401 ATATGGAAAC TGCCAAACGC AAAGCCCATG AAGCTCAAGA TGCGGCAGCA
6451 AAAGCAGATA ATTGGCAACA AGGCAAAGTC ATTCTCAACA TGTTAGCCTC
6501 AGGTTTAGCT GCGCCGACCC AAAGCGGAGC GGGCATCGCT GCGGCTACCG
6551 CATCGCCAGC CGTATCGTAT GCGATTGGAC AGCACTTTAA AGATTTAGCC
6601 GGTCAAAACG CGAATGGTAA ACTAACCGCC AGTCAAGAAA CCGCACACGT
6651 TCTTGCCAC GCGGTATTAG GAGCAGCGGT TGCCGCAGTA GGAGACAACA
6701 ATGCTCTAGC AGGAGCATTG AGTGCGGCG GGTGCGAAGC GGCTGCGCCT
6751 TACATCAGCA AATGGTTATA CGGCAAAGAA AAAGGAAGCG ACTTAACGGC
6801 GGAAGAGAAA GAGACTGTAA CAGCGATTAC AAATGTATTG GGTACGGCTA
6851 CGGGTGC GCGC AGTCGCAAC AGCGCAACAG ATGCAGCGCA AGGCAGCCTG
6901 AATGCGCAAA GTGCGGTGGA GAATAATGAT ACTGTAGAGC AAGTGAAATT
6951 TGCTCTTAGG CACCCTAGAA TTGCTATTGC AATTGGATCT GTACATAAAG
7001 ATCCTGGCTC TACATTAGAG CCTAATATTT CAACAATTGC TTCAACTTTT
7051 CAATTAATAA TATTTCTTAA TAGTGAATTT GGTGGTGAAG GTGGAGTTGG
7101 CAATGCATTG AGGCACGTTT TATGGCAAGC AACCATCACA CGAGAATTTG
7151 GCAAAGATAT TGCTGTTAAA GTAGGAAATA GTCATGAAAG TGGGGAAAAA
7201 ATTAATTATT CTATAAGACG TAATCTTTCA TTAGATAAAG CAGATGAAAT
7251 GATTGATCAA CTAAATAACG AAATAGGAAG AGAAATAGCA TTAAATACCA
7301 ATAGGTTAAA CACAAAAGAG TTAGTTGGAT TAATCTGGA AACTTATAAA
7351 AATAATGGTT TTTATCAAGC AGAAAGAAAC AGTAATGGAA ATTATGATGT
7401 TGTAAGAAAA AGATTATCTG AAAAAGATTA CCAGAATACA AGCAATATAT
7451 TGATTCACCT AGATAATACT GGTGCCGGAT TTAATTTCA GCAGAGGAGA
7501 AAACAAATCA GAGCACAAT TTCAGCCAGA CAATGGAGAA GATAA

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This corresponds to the amino acid sequence <SEQ ID 1668; ORF 563>:

m563 . pep . .

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1 MNKTLRYVIF NRKRGAVVAV AETTKREGKS CADSDSGSAH VKSVFPGTTH
51 APVCRSNIFS FSLLGFSLCL AVGTANIAFA DGIADKAAP KTQQTILQT
101 GNGIPQVNIQ TPTSAGVSVN QYAQFDVGNR GAILNNSRSN TQTQLGGWIQ
151 GNPWLARGEA RVVVNQINSS HSSQMNGYIE VGGRRAEVVI ANPAGIAVNG
201 GGFINASRAT LTTGQPQYQA GDLSGFKIRQ GNVVIAGHGL DARDTDFTRI
251 LSYHSKIDAP VWGQDVRVVA QONDVVATGN AHSPILNNA ANTSNNNTANN
301 GTHIPLFAID TGKLGMYAN KITLISTAEQ AGIRNQGLF ASSGNVAIDA
351 NGRLVNSGTM AAANAKDTDN TAEHKVNIRS QGVENSATV SQQGTQIHSQ
401 SIQNTGTLLS SGEILIHNSG SLKNETSGTI EAARLADTD TLNNQGLKLSQ
451 TGSQKLHIDA QGKMDNRGRM GLQDTAPTAS NGSSNQTGNS YNASFHSSTT
501 TPTTATGTGT ATVSI SNITA PTFADGTIRT HGALDNSGSI IANGQTDVSA
551 QQGLNNAGQI DIHQLNAKGS AFDNHNGTII SDAVHIQAGS LNNQNGNITT
601 RQQLIEITDQ LDNAHGKLLS AEIADLAVSG SLNNQNGEIA TNQQLIHDG
651 QQSTAVIDNT NGTIQSGRDV AIQAKSLSN GTLAADNKLD IALQDDFYVE
701 RNIVAGNELS LSTRGSLKNS HTLQAGKRIR IKANNLDNAA QGNIQSGGTT
751 DIGTQHNLTN RGLIDGQQT IAGQMNNIG TGRIYGDNIA IAATRLDNQD
801 ENGTTGAIAA RENLNLGIGQ LNNRENSLIY SGNDMAVGG A LDTNGQATGK
851 AQRINHAGAT IEAAGKMLRG VEKLHNTNEH LKTQLVETGR EHIVDYEAFG
901 RHELLREBGTQ HELGWSVYND ESDHLRTPDG AAHENWHKYD YEKVTQKTQV
951 TQTAPAKIIS GNDLTIDGKE VFNTDSQIIA GGNLIVQTEK DGLHNEOTFG
1001 EKKVFSENGK LHSYWREKHK GRDSTGHSEQ NYTLPEBITR NISLGSFAYE
1051 SHRKALSHHA PSQGTLPQS NGISLPYTSN SFTPLPSSSL YIINPVNKG Y
1101 LVETDPRFAN YRQWLGS DYM LDSLKLDPNN LHKRLGDGY Y EORLINEQIA
1151 ELTGHRRLDG YONDEEQFKA LMDNGATAAR SMNLSVGIAL SAEQVAQLTS
1201 DIVWLQKEV KLPDGGTQTV LVPQVYVRVK NGDIDKGAL LSGSNTQINV
1251 SGSLKNSGTI AGRNALIINT DTLDNIGGRI HAQSAVTAT QDINNIGGML
1301 SAEQTLNNA GNNINSQSTT ASSQNTQSS TYLDRMAGIY ITGKEKGVLA
1351 AQAGKDINII AQQISNQSEQ QQTRLQAGRD INLDTVQTSK HQATHFDADN
1401 HVIRGSTNEV GSSIQTGQDV TLLSGNNLNA KAAEVSSANG TLAVSAKNDI
1451 NISAGINTTH VDDASKHTGR SGGGNKLVI DKAQSHHETA QSSTFEGKQV
1501 VLQAGNDANI LGSNVISDNG TQIQAGNHVR IGTQTQSQS ETYHQTQKSG

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855

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1551 LMSAGIGFTI GSKTNTQENQ SQSNEHTGST VGS�KGDTTI VAGKHYEQIG
1601 STVSSPEGNN TIYAQSIDIQ AAHNKLNSNT TQTYEQKGLT VAFSSPVTDL
1651 AQQAIIVAQSKQVQSKND RVNAMAANA GWQAYQTGKS AQNLANGTTN
1701 AKQVSIISITY GEOQNRQTTO VQANQAQASQ IQAGGKTTLI ATGAAEQSNI
1751 NIAGSDVAGK AGTILIADND ITIQSAEQSN TERGQNKASG WNAGAAVSFG
1801 QGGWSLGVTA GGNVKGKGYGN GDSITHRHS IGDKGSQTLI QSGGDTTIKG
1851 AQVRGKGVQV NAKNLSIQSV QDRETYQSKQ QNASAQVTVG YGFSAGGDYS
1901 QSKIRADHVS VTEQSGIYAG EDGYQIKVGN HTDLKGGIIT STQSAEDKKG
1951 NRPQTATLTH SDIKNHSQYK GESFGLGASA SISGKTGQAG AQNKPNKHL
2001 TSVADKNSAS SSVGYGSDSD SQSSITKSGI NTRNIQITDE AAQIRLTGKT
2051 AAQTKADIDT NVTTDTAERH SGSLKNTFNK EAVQSELDLQ RTVSQDFSKN
2101 VQQANTEINQ HLDKLKADKE AAETAAAEAL ANGDMETAKR KAHEAQDAAA
2151 KADNWQQGV ILNMLASGLA APTQSGAGIA AATASPAVSY AIGQHFCDLA
2201 GQANANGKLT SQETAHVLAH AVLGAAVAAG GDNNALAGAL SAGGSEAAAP
2251 YISKWLYGKE KGSDLTAEK ETVTAITNVL GTATGAAVGN SATDAAQGS
2301 NAQSAVENND TVEQVKFALR HPRIAIAGS VHKDPGSTLE PNISTIASTF
2351 QNLNFPNSEF GGEGGVGNF RHVLWQATIT REFGKDIAVK VGNSHESGEK
2401 INYSIRRLNS LDKADEMIDQ LNNEIGREIA LNTNRLNKE LVGLILETYK
2451 NNGFYQAERN SNGNYDVVRK RLSEKDYQNT SNILIHLDNT GAGFKIQRR
2501 KQIRAQISAR QWRR*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 563 shows 79.1% identity over a 2316 aa overlap with a predicted ORF (ORF 563.ng) from *N. gonorrhoeae*:

m563/g563

```

              10      20      30      40      50
g563.pep      MNKTLYRVIFNRKRGAVVAVAETTKREGKSCADSGSGSVYVKSVSFIPTH-----SKAFC
              |||||
m563.pep      MNKTLYRVIFNRKRGAVVAVAETTKREGKSCADSDSGSAHVKSVPFGTTHAPVCRSNIFS
              10      20      30      40      50      60

              60      70      80      90      100     110
g563.pep      FSALGFSLCLALGTVNIAFADGIIITDKAAPKTQQTILQTNIGIPQVNIQTPTSAGVSVN
              |||||
m563.pep      FSLGFSCLAVGTANIAFADGIIADKAAPKTQQTILQTNIGIPQVNIQTPTSAGVSVN
              70      80      90      100     110     120

              120     130     140     150     160     170
g563.pep      QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLTRGEARVVVNQINSSHPSQLNGYIE
              |||||
m563.pep      QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSSQMNGYIE
              130     140     150     160     170     180

              180     190     200     210     220     230
g563.pep      VGGRRAEVVIANPAGIAVNGGGFINASRATLTTCQPQYQAGDFSGFKIRQGNVIAHGHL
              |||||
m563.pep      VGGRRAEVVIANPAGIAVNGGGFINASRATLTTCQPQYQAGDLSGFKIRQGNVVIAGHGL
              190     200     210     220     230     240

              240
g563.pep      DARDTDFTRIL-----
              |||||
m563.pep      DARDTDFTRILSYHSKIDAPVWGQDVRVVGQNDVVATGNAHSPILNAAANTSNN'TANN
              250     260     270     280     290     300

              250     260     270     280     290
g563.pep      -----LYANKITLISTAEQAGIRNQGQLFASSGNVAIDANGRLVNSGTM
              :|||
m563.pep      GTHIPLFAIDTGKLGMYANKITLISTAEQAGIRNQGQLFASSGNVAIDANGRLVNSGTM
              310     320     330     340     350     360

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	300	310	320	330	340		
g563.pep	AAANVQDMNNTAEHKVNIRSQAFENSGTAVSQQGTQIHSQSIQNTGKLLSAGT-----						
	:: : : : : : : : :						
m563.pep	AAANAKDNTDNTAEHKVNIRSQGVENSGTAVSQQGTQIHSQSIQNTGTLSSGEILIHNSG						
	370	380	390	400	410	420	

g563.pep							
m563.pep	SLKNETSGTIEAARLAIDTDTLNNQGKLSQTGSQKLHIDAQGMNDRGRMGLQDTAPTAS						
	430	440	450	460	470	480	

g563.pep							
m563.pep	NGSSNOTGNSYNASFHSSTTTPTTATGTGTATVSISNITAPTTFADGTIRTHGALDNSGSI						
	490	500	510	520	530	540	

g563.pep							
m563.pep	IANGQTDVSAQQGLNNAQIDIHQLNAKGSAFDNHNGTIISDAVHIQAGSLNNQNGNITT						
	550	560	570	580	590	600	

g563.pep			350	360	370	380	
	-----		EDLAVSGSLNNQNGEIA TNQQLI	IHDGQQSTVVIDNT			
				:			
m563.pep	RQOLEIETDQLDNAHGKLLSAEIA DLAVSGSLNNQNGEIA TNQQLI						
	610	620	630	640	650	660	

g563.pep		390	400	410	420	430	440
	NGTIQSGRDVAIQAKSLSNNGTLAADNKLDIALQDDFYVERKIVAGNELSLSTRGSLKNS						
					:		
m563.pep	NGTIQSGRDVAIQAKSLSNNGTLAADNKLDIALQDDFYVERNIVAGNELSLSTRGSLKNS						
	670	680	690	700	710	720	

g563.pep		450	460	470	480	490	500
	HTLQAGKRIRIKANNLDNAVQGNIQSGGTTDIGTQHNLTNRGLIDGQQT KIQAGQMNNIG						
		:					
m563.pep	HTLQAGKRIRIKANNLDNAAQGNIQSGGTTDIGTQHNLTNRGLIDGQQT KIQAGQMNNIG						
	730	740	750	760	770	780	

g563.pep		510	520	530	540	550	560
	TGRIYGDNIAIAATRLDNQDENG TGAAIAARENLNLGIEQLNNREN SLIYSGNDMAVGGA						
m563.pep	TGRIYGDNIAIAATRLDNQDENG TGAAIAARENLNLGIEQLNNREN SLIYSGNDMAVGGA						
	790	800	810	820	830	840	

g563.pep		570	580	590	600	610	620
	LDTNQDQATGKAQRIHNAGAIIEAAGKMRLGVEKLHNTNEHLKTQLVETGRERIVDYEAFG						
m563.pep	LDTNQDQATGKAQRIHNAGATIEAAGKMRLGVEKLHNTNEHLKTQLVETGREHIVDYEAFG						
	850	860	870	880	890	900	

g563.pep		630	640	650	660	670	680
	RHELLREGTQHELGW FVYNNESDHLRTPDGVAHENWHKYDY EKVTQETQVTGTAPAKIIA						
							:
m563.pep	RHELLREGTQHELGWSVYNDES DHLRTPDGAAHENWHKYDY EKVTQKTQVTGTAPAKIIS						
	910	920	930	940	950	960	

	690	700	710	720	730	740	

—

858

m563 . pep	LMSAGIGFTIGSKTNTQENQSQSNEHTGSTVGS�KGDTTIVAGKHYEQIGSTVSSPEGNN
	1560 1570 1580 1590 1600 1610
g563 . pep	LISTQSMDIGAAQNQLNSKTTQTYEQKGLTVGIQFARYRFGTTSDCRSTQSSKQVGQSKN
	1350 1360 1370 1380 1390 1400
m563 . pep	TIYAQSIDIQAHNKLNSTTQTYEQKGLTVAFSSPVTDLAQQA- IAVAQSSKQVGQSKN
	1620 1630 1640 1650 1660
g563 . pep	DRVNAMAANAGWQAYQTGKGAQNLANGTTNAKQVSSITYGEQNRQTQVQANQAQAS
	1410 1420 1430 1440 1450 1460
m563 . pep	DRVNAMAANAGWQAYQTGKSAQNLANGTTNAKQVSSITYGEQNRQTQVQANQAQAS
	1670 1680 1690 1700 1710 1720
g563 . pep	QIQAGGKTTLYCRRCEQSNINITGSGVSGRAGTGLIADKQIHLQSAEQSNTERSQNKSA
	1470 1480 1490 1500 1510 1520
m563 . pep	QIQAGGKTTLIATGAEEQSNINIAGSDVAGKAGTILIADNDITLQSAEQSNTERGQNKSA
	1730 1740 1750 1760 1770 1780
g563 . pep	GWNAGAAVSFGQGGWSLGAAGGNVKGKGYSVTHRHSHIGDKGSQTLIQSGGDTTIK
	1530 1540 1550 1560 1570 1580
m563 . pep	GWNAGAAVSFGQGGWSLGVTAGGNVKGKGNGDSITHRHSHIGDKGSQTLIQSGGDTTIK
	1790 1800 1810 1820 1830 1840
g563 . pep	GAQVRGKGVQVNAKNLSIQSVQDRETYQSKQONAGAQTGVSAGSAGDYSQSKIRADHA
	1590 1600 1610 1620 1630 1640
m563 . pep	GAQVRGKGVQVNAKNLSIQSVQDRETYQSKQONASAGTQVVSAGSAGDYSQSKIRADHV
	1850 1860 1870 1880 1890 1900
g563 . pep	SVTEQSGIYAGEDGYQIKVGNHTGLKGGIITSSQSAKDKGNRFSTGTLAGSDIQNYSQY
	1650 1660 1670 1680 1690 1700
m563 . pep	SVTEQSGIYAGEDGYQIKVGNHTDLKGGIITSTQSAEDKGNRFQTATLTHSDIKNHSQY
	1910 1920 1930 1940 1950 1960
g563 . pep	EGKSFGLGASVAVSGKTLGQGAQKNPKQKHLTSIADKNGASSSVGYGSDSDSQSSITKSG
	1710 1720 1730 1740 1750 1760
m563 . pep	KGESFGLGASASISGKTLGQGAQKNPKQKHLTSVADKNSASSSVGYGSDSDSQSSITKSG
	1970 1980 1990 2000 2010 2020
g563 . pep	INTPKNIQITDEAAQIRLTGKIAAQTKADIDTNVTTDTAERHSGSLKNI FDKDRVQSELD
	1770 1780 1790 1800 1810 1820
m563 . pep	INT-RNIQITDEAAQIRLTGKTAAQTKADIDTNVTTDTAERHSGSLKNTFNKEAVQSELD
	2030 2040 2050 2060 2070 2080
g563 . pep	LQRTVSQDFSKNVQQTNTNTEINQHLDKLKADKEAAETAABALANGDMETAKRKAHEAQDA
	1830 1840 1850 1860 1870 1880
m563 . pep	LQRTVSQDFSKNVQQTNTNTEINQHLDKLKADKEAAETAABALANGDMETAKRKAHEAQDA
	2090 2100 2110 2120 2130 2140
g563 . pep	AAKADNWQOGKVILNMLASGLAEPQSGAGIAAATASPDVSYAIGQHFCDLAGQNAVGL
	1890 1900 1910 1920 1930 1940
m563 . pep	AAKADNWQOGKVILNMLASGLAEPQSGAGIAAATASPAVSYAIGQHFCDLAGQNAVGL
	2150 2160 2170 2180 2190 2200

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m564.seq
1 ATGAACCGCA CCTGTACAA AGTTGTATTT AACAAACATC GAAACTGCAT
51 GATAGCGGTT GCTGAAATTT CCAAAACGCGA GGGCAAAAAA ACAGCCGCACA
101 CCCAAGCTGT AGTGTATTTT CCAATAGATA TTGCGGGCTT TCGGGGTTT
151 ATCCATTCTA TCTCTGTTAT CTCATTCTCC CTTTCATTAC TGCTCGGTTT
201 TGCCCTTATC CTGACTTCTT CTTCTGCTAC TGCCCAAGGT ATCGTTGCCG
251 ACAAACTCCG ACCTGCACAG CCAACGCCTA CCATCCTGCA AACAGGTAAC
301 GGCATACCGA ACGTCAATAT TCAAACCCCT ACTTCGGGAG GAGTTTCTGT
351 TAATCAATAC GCCCAGTTTG ATGTGGGTAA TCGCGGGGCG ATTTTAAACA
401 ACAGTCGCAG CAACACCCAA ACACAGCTAG GCGGTTGGAT TCAAGGCAAT
451 CTTGTTGGTG CAAGGGGCGA AGCAGCTGTG GTTGTAAACC AAATCAACAG
501 CAGCAATTCT TCACAACCTGA ATGGCTATAT TGAAGTGGGC GGACGACGTG
551 CAGGAATCGT TATTGCCAAT CCGCGAGGGA TTGCAGTCAA TGCTGGTGGT
601 TTTATCAATG CTTCCCGTGC CACTTTGACG ACAGCCCAAC CGCAATATCA
651 AGCAGGAGAC CTTAGCGGCT TTAAGATAAG GCAAGGCAAT GTTGTAACTG
701 CCGGACACGG TTTGGATGCA CGTGATACCG ATTACACAG TATTTCTAGT
751 TATCATTTCCA AAATTGATGC ACCCGTATGG GGACAAGATG TTTCTGTCTG
801 CGCGGGACAA AACGATGTGG CCGCAACAGG TGATGCACTT TCGCCTATTC
851 TCAATAATCG TGCTGCCAAT ACGTCAAACA ATACAGCCAA CAACGGGACA
901 CATATCCCTT TATTTGCGAT TGATCAGGCG AAATTAGGAG GTATCTATGC
951 CAACAAAATC ACCTTGATCA GTACGGTCTGA GCAAGCAGGC ATTTCTGAATC
1001 AAGGGCAATG GTTTGCCCTCA GCCGGCAATG TGGCAGTGAA TGCTGAGGGT
1051 AAATCGGTCA ACACGGGCAT GATTGCACGG ACGGGAGAAA ATCATGCGGT
1101 TTCACTTTCAT GCCCGCAATG TTCATAATAG CGGTACGGTT GCCTCACAGG
1151 ATGATGCCAA TATTACACAGC CAGACGCTGG ACAATTCCAGG TACGGTCTTA
1201 TCCTCAGGTC GATTGACTGT TCGTAATTTA GGCCGTCTGA AAAACCAAAA
1251 CAACGGTACG ATCCAGGCTG CCCGCTTAGA TATGTCAACA GGTGGTTTGG
1301 ATAACACAGG TAATATTACT CAACACGGTT CACAAGCAAT GGAATTTGGTA
1351 TCTGCCGGCA AATTCGATAA CAGTGGCAAG ATTGGTGTA TGTACGTTCC
1401 ACAGACCGGT TTGAATCCCA ATCCATCAGT CATACCACAG ATTCCGAGTA
1451 CTGCAACAGG TTCAGGACGC AGCACTGTCT CGGTATCTFA GCCTGGTPCA
1501 AACAATCCCG TTTCACTCAT AGCACTTGCA AAAAACCATG CCGTAGGACG
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1601 GGCAAATTGA CATTGCCGCC CAAAACGGTT TGGGAAATTC GGGTAGTCTG
1651 AATGCGGCTA AACTACGAGT ATCAGGCGAT TCATTTAACA ATACGGTAAA
1701 AGGCAAACTC CAGGACACAG CATTGGCTGT TAACACTCAA ACTGCTAAAA
1751 ACAGCGGTCA CTTATTAACT AAACCGGCA AGATTGATA CCCTGAACCT
1801 CATAATGCCG GAGAAATTGC CGCCAAACAT CTGACACTCA TTTACTCGGG
1851 CCGCTTGAGC AATGATAAAA AAGGCAATAT TCGAGCTGCA CATTTACAGC
1901 TTGATACCGC CGGTTTACAT ATTCGAGGTA ACATTCTTGC CGATAGTTGA
1951 ACCGTTTACCA CCAAGAAATA TCTTCGAGTA ACAGGAAAAG TTTCTGTTGC
2001 ACGACTGAAT ACCGAAGGTC AGACTCTAGA TAATACGGCG GGACGTATAG
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2101 CATATTACTG CTACCGAACA ACTGACTATC AATGATCGAA ATGTAGACAA
2151 CCAAAACGGC AAATCCTCAT CTGCAAAACCA AGCACAATTA GCTGTTTACG
2201 ACGGCTTATA CAACCAACAT GGTGAAATTG CCACCAACCG CAGTTGTGTT
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 2301 GATTCAATCT GCCGTAATG TATCGCTACA AGCCAAATCA CTCGCCAACA
 2351 ATGGCACATT AACAGCCGGT AACAACTGG ATATTGCTTT GACGGACGAT
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 2451 AAAAGGCCGT CTGAAAAATA CCCATACCTT ACAAGCAGGC CATACGCTCA
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 2551 GGAGAACAAA CGGACATCAC ATCCGAACAG CATGTTGACA ACAGGGGCTT
 2601 GATCAACAGC GACGGTTTGA CCCACATCGG TGCAGTCAA ACCCTGACCA
 2651 ACACCGGGAC AGGCAAAATC TATGGCAACC ATATTGCCCT GGACGCGCAA
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 3251 AAAATTGGCT GAACAAAGAC AGCCGGATTG TAGTAGGCGG GCGTATTATC
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 3351 AGGTGCGACA GATGCTGTCT GCACACAGTG GGATTGAGT ACAAAAAAAG
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 3451 CTTTACCATG ATACCCAATC ATTTACCAC GACTTCGACA CGCTGTATC
 3501 CGTCATCCAA CAGAATGCCG CCTCCCTTC CTTTCAACCC GCCGCATCTG
 3551 CAATCAAATC GATTGACGGA GTATCCACGG CAGCCGTCOA TGGTCAGCGC
 3601 ATCCATACCG GTAATGTGGT CTCGTTAAAT AACGCTACTG TTAATCTGCC
 3651 TAACAGCAGC CTCTATACCA CCCATCCTGA CAATAAAGGC TGGTTGGTTG
 3701 AAACCGATCC TCAATTTGCA GACTACCGCC GCTGGTTGGG CAGCGACTAC
 3751 ATGTTGCAAC AACTGCAATT GGACACCAAT CATCTACACA AACGGCTTGG
 3801 CGACGGCTAC TACGAACAAA AACTTGTAA TGAACAAATC CATCAGTTAA
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 3951 AGGTATCGCC TTGAGTGCAG AGCAAGTTGC CCGCTTAACT TCAGATATCG
 4001 TTTGGATGGA AAATCAAACC GTCAACCTGT CTGACGGTTC GACTCAAACC
 4051 GTACTGGTTC CTAAAGTCTA TGCCCTGGCG CGCAAAGGTG ATCTCAATAC
 4101 CTCGGGTGGC CTGATTAGTG CCGAACAAGT CTTACTTAAA CTGCAAAACG
 4151 GCAACCTGAC TAACAGCGGT ACCATTGCGG GCGCAGAGGC CGTACTCATC
 4201 CAGGCACGGA ATATTAACAG CAACGGTAAC ATTCAAGCCG ACCAAATCGG
 4251 CTTAAAAGCT GAAAAAGTA TCAATATCGA CGGCGGGCAG GTACAAGCAG
 4301 GCGAGCTGCT GACTGCCCAA GCGCAAAATA TCAACCTTAA CGGTACAACC
 4351 CAACTTCCG GTAATGAACG TAACGGCAAT ACCGCCATCG ATCGTATGGC
 4401 CGGCATTAAAC GTGTCGGGAA GCCATACCTGA ACAAGTAGAT AACAGAACTT
 4451 CAGACGGCAT CCTATCCCTG CATGCCAGCA ACGATATCAA CCTCAATGCG
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 4551 CAATAATCTC AACCTCGGCA CCATCCGTAC CGAACATCGC GAAGCCTATG
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 4651 GGCAGCAGTA TCCGCACGCA AAACGGCGCA CTGCTTAGAG CCGGTAACGA
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 4901 TCGGCGGCGG CAAAATGATT GTTGCAGCGG GGCAGGATAT CAATGTACGC
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 5201 ACCGCTACCG ACAAAACGGC AGTACCGTCT CCAGCCCCGA GGGGCGCAAT
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 5301 CACTGACTAC GCCCATACCC AGGAACAAAA AGGCCTTACC GTGCCCTCA
 5351 ATTTCCCGGT GTCCAAAGCT GCACAAACT TCATACAAGC AGCCCAAAAT
 5401 GTGGGCAAAA GTAAAAATA ACGCGTTAAT GCCATGGCTG CAGCCAATGC
 5451 TGCATGGCAG AGTTATCAAG CAACCCAACA AATGCAACAA TTTGCTCCAA
 5501 GCAGCAGTGC GGGACAAGGT CAAAACAACA ATCAAAGCCC CAGTATCAGT

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5551 GTGTCCATTA CCTACGGCGA ACAGAAAAGT CGTAACGAGC AAAAAAGACA
5601 TTACACCGAA GCGGCAGCAA GTCAAATTAT CGGCAAAGGG CAAACCACAC
5651 TTGCGGCAAC AGGAAGTGGG GAGCAGTCCA ATATCAATAT TACAGGTTCC
5701 SATGTCATCG GCCATGCAGG TACTGCCCTC ATTGCCGACA ACCATATCAG
5751 ACTCCAATCT GCCAAACAGG ACGGCAGCGA GCAAAGCAAA AACAAAAGCA
5801 GTGGTTGGAA TGCAGGCGTA GCCGTCAAAA TAGGCAACGG CATCAGGTTT
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5901 TACTACCCAC CGCCACACCC ATGTCGGCAG CACAACCGGC AAAACTACCA
5951 TCCGAAGCGG CGGGGATACC ACCCTCAAAG GTGTGCAGCT CATCGGCAAA
6001 GGCATACAGG CAGATACGCG CAACCTGCAT ATAGAAAGTG TTCAAGATAC
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6101 GTTACGGATT CAGTGCAAGC GGCAGTTACC GCCAAAGCAA AGTCAAAGCA
6151 GACCATGCCT CCGTAACCGG GCAAAGCGGT ATTTATGCCG GAGAAGACGG
6201 CTATCAAATC AAAGTCAGAG ACAACACAGA CCTCAAGGGC GGTATCATCA
6251 CGTCTAGCCA AAGCGCAGAA GATAAGGGCA AAAACCTTTT TCAGACGGCC
6301 ACCCTTACTG CCAGCGACAT TCAAAACCAAC AGCCGCTACG AAGGCAGAAG
6351 CTTCCGCATA GCGGCGAGTT TCGACCTGAA CGGCGGTGCG GACGGCACGG
6401 TTACCGACAA ACAAGGCAGG CCTACCGACA GGATAAGCCC GGCAGCCGGC
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6501 CACCCACAAC ATACACATCA CCGACGAAGC GGGACAACCT GCCCGAACAG
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6601 GAAACTGCGG ATCAACACTC AGGCCATCTG AAAAAACAGT TCGACAAAGA
6651 CGCGGTGCGC AAAGAGATCA ACCTGCAAAG GGAAGTAACG AAGGAGTTCTG
6701 GCAGAAACGC CGCCCAAGCC GTAGCGGCGG TTGCCGACAA ACTCGGCAAT
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7201 AAGCGCGAAG TTGAAAAACG CGAAGGCAGA AAAATCAGCA GCCAAGAAGC
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7351 GAAGACAAAG CCTTGGGTTA TACTTGGGAC TACCGCGACT ACGGCGCAAG
7401 AAATCCGCAA ACCTACAACG ATCCGAAGCT GTTTGAGGAA TACCGCCGAC
7451 AGGACAAACC CGAATACCGC AACCTGACCT GGCTGCACAG CGGGACGAAA
7501 GACACCAAAA TCAGGCAGGG AGAGCGGAAA AACGAAGAGT TTGCACTGAA
7551 CGTTGCCGAA GGAATGACGA GCCTTGTCAA CCCCAATCCG AGGATAAAAG
7601 TCCCGATTCT TGCAGGCATC CGCAACCTGA AAAACATCAA GCCGACAGTT
7651 ACCGGCAGCG ATCCCTTAT TGGCGGTGCG GGAATATACC GTATCCCTGC
7701 AAACGGCAAT GTTCCGAAG GGGACAGGAT TCCGGATACG GCATTGGCTA
7751 GCAAGGGAAT CAAACATAAA GATCGTAAAG ATCAACTGGA GAAAAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1670; ORF 564>:

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m564.pep
1  MNRTLYKVVF NKHRNCMIIV AENAKREGKN TADTQAVGIL PNDIAGFAGF
51  IHSISVISFS LSLLLGSALI LTSSSATAQG IVADKSAPAQ QOPTILQTGN
101 GIPQVNIQTP TSAGVSVNQY AQFDVGNRGA ILNNSRSNTQ TQLGGWIQGN
151 PWLARGEARV VVNQINSSHS SQLNGYIEVG GRRAEVVIAN PAGIAVNGGG
201 FINASRATLT TAQPQYQAGD LSGFKIRQGN VVIAGHGLDA RDTDYTRILS
251 YHSKIDAPVW GQDVRVVAGQ NDVAATGDAH SPILNNAAN TSNNTANNGT
301 HIPLFAIDTG KLGGMYANKI TLISTVEQAG IRNQGWFAF AGNVAVNAEG
351 KLVNTGMIAA TGENHAVSLH ARNVHNSGTV ASQDDANIHS QTLNDSGTVL
401 SSGRLTVRNL GRLKNQNNGT IQAARLDMST GGLDNTGNIT QTGSQALDLV
451 SAGKFDNSGK IGVSDVPQTG LNPNSVPIQ IPSTATGSGS STVSVSKPGS
501 NNPVSPTAPA KNYAVGRIQT TGAFDNAGSI NAGGQIDIAA QNGLGNSGSL
551 NAAKLRVSCD SFNNTVKGKL QAHDLAVENTQ TAKNSGHLT QTGKIDNREL
601 HNAGEIAANN LTLHSGRLS NDKKGNIRAA HLQLDTAGLH NAGNILDGSG
651 TVTTKNNLRN TGKVSVARLN TEGQTLNTR GRIEAEVNI QSQQLTNQSG
701 HITATEQLTI NSRNVDNQNG KLLSANQAQL AVSDGLYNQH GEIATNRQLS
751 IHDKNQNTLA LNNADGTIQS AGNVSLQAKS LANNGTLTAG NKLDIALTDD
801 FVVERDLTAG KQLNLSIKGR LKNTHTLQAG HTLKLNAGNI DNQVTGKIIG
851 GEQTDITSEQ HVDNRGLINS DGLTHIGAGQ TLTNTGTGKI YGNHIALDAQ

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Homology with fha

SCORES Init1: 190 Initn: 524 Opt: 594
Smith-Waterman score: 866; 21.7% identity in 2427 aa overlap

		10	20	30	40	50	60
m564	.pep	MNRTLYKVVF	NKHRNC	MIAVAENAK	REGKNTAD	TQAVGILP	NDIAGFAGFIH
		: : : :	: : : :	: : :	: : : :	: : : :	: : : :
fhfab_borpe		MNTNLYRLV	FSHVRGML	VPVSEHCTV	-G-NTFCGR	TRG---QAR	SGARATSLSV
		10	20	30	40	50	
		70	80	90	100	110	119
m564	.pep	LSLLLG-SAL	ILTSSSATA	QGIVADKS	APAAQQOPT	ILQTGNGI	POVNIQTPTS
		: : : :	: : : :	:	:	:	:
fhfab_borpe		WALMLACTG	LPLVTH---	AQGLV----	P-QGQTQVL	QGGNKVPV	VNIADPNSGG
		60	70	80	90	100	
		120	130	140	150	160	179
m564	.pep	YAQFDVGNR	GAILNNSR	SNTQTQLG	GWIQGNPW	LARGEARV	VVNQINSSHSS
		: : : :	: : : :	: : : :	: : : :	: : : :	: : : :
fhfab_borpe		FQQFNVANP	GVVFNNG	LTDGVSRI	GALTKNPN	LR-QASAIL	AEVTDTPSP
		110	120	130	140	150	160

863

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      180      190      200      210      220      230      239
m564 .pep GGRRAEVVIANPAGIAVNGGGFINASRATLTTAQPQYQAGDLSGFKIRQGNVVIAGHGLD
      | : | : : | | | | | : : | | | | : : | : | : : | | : | : |
fhab_borpe YGKGADLIIANPNGISVNGSLTLNASNLTLTGRPSVNGGRI-GLDVQOGTVTIERGGVN
      170      180      190      200      210      220

      240      250      260      270      280      290
m564 .pep ARDTDYTRILSYHSKIDAPV---WGQ---DVRVVAGQNDVAATGDAHSPILNNAANTSN
      | : : : | : : : | : : | : | | | | : : | : | : : | : : :
fhab_borpe ATGLGYFDVVARLVKLQGA VSSKQ GKPLADI AVVAGANRYDHATRRATPI----AAGARG
      230      240      250      260      270      280

      300      310      320      330      340      350
m564 .pep NTANNGTHIPLFAIDTGKLGMYANKITLISTVEQAGIRNQGW FASAGNVAVNAEGKLV
      : | : : : | : | : : | : | : : | : | : : | : | : : | : | :
fhab_borpe AAAGA-----YAIDGTAAGAMYGKHITLVSSDSGLGVRQLGS-LSSPSAITVSSQGEIA
      290      300      310      320      330

      360      370      380      390      400      410
m564 .pep NTGMIAATGENHAVSLHARNVHNSGTVASQDDANIHSQTLDN SGTVLSSGRLTVRNIGRL
      : | : : : | : | : : | : | : : | : | : : | : | : : | : | :
fhab_borpe ---LGDATVQRGPLSLKAGVVSAGKLASGGGAV---NVAGGGAVKIA---SASSVGNL
      340      350      360      370      380

      420      430      440      450      460      470
m564 .pep KNQNGCTIQARLD MSTGGLDNTGNITQTGSQALDLVSAGKFDNSGKIGVSDVPQTGLNP
      | : | : | : | : : : | : : | : | : | : : : : : : : : : | :
fhab_borpe AVQGGGKVQATLLNAG-----GTLVSGRQAVQLGAASSRQALSVNAGGALKADKLSA
      390      400      410      420      430

      480      490      500      510      520      530
m564 .pep NPSV-IPQIPSTATGSGSSTVSVSKPGSNNPVSP TAPAKNYAVGRIQTTGAFD-NAGSIN
      : | : : : | : | : : : | : : : : | : | : : : | : | : : :
fhab_borpe TRRVVDVGKQAVALGSASSNALSVRAGGA-----LKAGKLSATGRLDVDGKQAVTLGSA
      440      450      460      470      480      490

      540      550      560      570      579
m564 .pep AGGQIDIAAQNLGNSGSLNAAKL RVSG-----DSFNNT-----VKGKLOAHD LAVNT
      : | : : : | : : : : | : : : : | : : : : | : : : : | : : :
fhab_borpe SDGALSVSAGGNLRANELVSSAQLEVRGQREVALDDASSARGMTVVAAGAL AARNLQSKG
      500      510      520      530      540      550

      580      590      600      610      620      630
m564 .pep QTAKNSGHLITQTGKIDNRELH--NAGEIAANNLTLI HSGRLSNDKKG NIRAHLQLDTA
      : : : : : : : : : | : : : : | : : : : | : : : : | : : :
fhab_borpe AIGVQGGAEVSVANANSDAELRVGRGQVDLHDL SAARGADISGEGRVNIGRARS DSDVK
      560      570      580      590      600      610

      640      650      660      670      680      690
m564 .pep GLHNAGNILADSGTVTTKNL RNTGKVSVARLNTEGQTL DNTRGRIEAE TVNIQSQQLTN
      : | : | : | : : : | : | : : : | : : : | : : : | : : : |
fhab_borpe -VSAHGALSIDSMTALGAIGVQAGGSVSAKDMRSRGAVTVSGGG-----AVNLGDVQ---
      620      630      640      650      660

      700      710      720      730      740      750
m564 .pep QSGHITATEQLTINSRNVDNQNGKLLSANQAQLAVSDGLYNQHGEIATNRQLSIHDKNQ
      : : : : | : : : | : | : : | : | : : | : | : : : : : :
fhab_borpe SDGQVRATSAGAMTVRDV-----AAAADLALQAGDALQAGFLKSAGAMTVNGRDAV
      670      680      690      700      710

```


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m564	.pep	760	770	780	790	800	810
		TLALNNADGTIQSAGNVSLQAKSLANNGTLTAGNKLDIALTEDFVVERDLTAGKQL-NLS					
fhab_borpe		RL-----DGA-HAGGQLRVSSDGAALGSLAAKGELTVSARAATVA-EL---KSLDNIS					
		720	730	740	750	760	
m564	.pep	820	830	840	850	860	870
		IKGRLLK-NHTTLQAGHTLKLNA-GNIDNQVTGKIIGGEQTDITSEQHVDNRGLINSGLT					
fhab_borpe		VTGGERVSVQSVNSASRVAISAHGALD---VGKV--SAKSGIGLE----GWGAVGADSL-					
		770	780	790	800	810	
m564	.pep	880	890	900	910	920	930
		HIGAGQTLTNTGTGKIYGNHIALDAQILLNREETEGSTKAGAIARLRDI-GAKEIHN					
fhab_borpe		--GSDGAISVSGRDVAVRDQARSLADISLG----AEGGATLGAVEAAGSIDVRGGSTV--					
		820	830	840	850	860	
m564	.pep	940	950	960	970	980	990
		QEGALLSSEGI FAVGNRLDEQHHAAGMADTFVNGSAGLEVQGDALMSVRNMQNINNHFKT					
fhab_borpe		AANSLHANRDVVRVSGK--DAVRVTAATSGGGLHVSSGRQLDLGAVQA-RGALALDGGAGV					
		870	880	890	900	910	920
m564	.pep	1000	1010	1020	1030	1040	1050
		ETYLAKAEK--QVRDYTVLQNTYYQAGKDGLFDNSQGGKQDTTATFHLKNGSRIEANK-					
fhab_borpe		ALQSAKASGTLHVQGGELDLGLTAAVGAVDV---NGTGDVVRVAKLVSDAGADLQAGRS					
		930	940	950	960	970	
m564	.pep	1060	1070	1080	1090	1100	
		--WHVRDYHIETYKERIENRPAHITVGGDLTASGQNWLKDSRIVVGGRIITDDLNOKE					
fhab_borpe		MTLGIVDTTGDQLQARAQQKLELGSVKSDGGLQAAAGGALSAAAEEVAGALELS---GQGV					
		980	990	1000	1010	1020	1030
m564	.pep	1110	1120	1130	1140	1150	1160
		ITNQSTTGKGRDVAVGTDQWDSVTKKGWY--SGRKRQRRTERNHTPYHDTQLFTHDFDTPV					
fhab_borpe		TVDRASASRARIDSTGSVIGALKAGAVEAASPRRARRALR-----QDFFTPG					
		1040	1050	1060	1070	1080	
m564	.pep	1170	1180	1190	1200	1210	1220
		SVI---QONAASPSFQPAASAIKLIDGVSTAAVNGQRIHTGNVVSNNATVTLPNSSLYT					
fhab_borpe		SVVVRAGNVTVGRGDPHQGVLAQGDIMDA--KGGTLLLRNDALTENGTVTISADSAVL					
		1090	1100	1110	1120	1130	1140
m564	.pep	1230	1240	1250	1260	1270	1280
		THPDNKGWLVED-PQFADYRRWLGS DYMLQQLQDLTNHLHKLRLGDGYEQKLVNEQIHQ					
fhab_borpe		EHSTIESKISQSVLAAGDKGKPAVSVKVAKKLFL--NGTLRAVNDN--NETMSGRIQIDV					
		1150	1160	1170	1180	1190	
m564	.pep	1290	1300	1310	1320	1330	1340
		LTGYRRLDGYRSDEEQFKALMDNGLTAAKTFGLTGP--IALSAEQVARLTSDIVWMENQTV					
fhab_borpe		VDGRPQI----TDAVTGEARKDES SVSDAALVADGGPIVVEAGELVSHAGGIGNGRNK--					
		1200	1210	1220	1230	1240	1250

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		1350	1360	1370	1380	1390	1400
m564	.pep	TLSDGSGTQTVLVPKVYALARKGDLNTSGGLISAEQVLLKLQNGNLNLSGTIAGRQAVLIQ					
		: : :	: : : : : :	: : :	: : :	: : :	: : :
fhab_borpe		--ENGASVTVRTT-----GNLVNKGYSAGKQGVLEV--GGALTNEFLVGSDDGTQRIE					
		1260		1270	1280	1290	1300
		1410	1420	1430	1440	1450	
m564	.pep	ARNINSNGNIQ-----ADQIGLKAESKINIDGGQVQAGRLLTAQ----AQININLNGTT					
		: : : :	: : : :	: : : :	: : : :	: : : :	: : : :
fhab_borpe		AQRIENRGTFQSQAPAGTAGALVVKAEEAI VHDGVMATKKGEMQIAGKGGGSPTVTAGAKA					
		1310	1320	1330	1340	1350	1360
		1460	1470	1480	1490	1500	
m564	.pep	QTSGNERNGNTAI--DRMAGINVV--GSHTEQVDNRTSD--GILSLHASNDINLNAATVSNQV					
		: : : :	: : : :	: : : :	: : : :	: : : :	: : : :
fhab_borpe		TTSANKLSVDVASWDNAGSLDIKKGGAQVTVAGRYAEHGEVSIQGDYTVSADAIALAAQV					
		1370	1380	1390	1400	1410	1420
		1510	1520	1530	1540	1550	
m564	.pep	--KDGTQTITAGNNLNLT--IRTE---HREAYGTLDDENHRHVRQST-----EVGS					
		: : : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
fhab_borpe		TQRGGAANLTSRHDRFSNKRILMGLPQVNAAGGPVSNNTGNLKVREGVTVTAASFNETGA					
		1430	1440	1450	1460	1470	1480
		1560	1570	1580	1590	1600	
m564	.pep	SIRTQNGALLRAGNDLKIRQGELEAEEGKTVLAAGRDV--TISEGRQITELDTS---VSG					
		: : : : : :	: : : : : : : : : : : : : : : : : : : : : : : :	: : : : : : : : : : : : : : : : : : : :	: : : : : : : : : : : : : : : : : : : :	: : : : : : : : : : : : : : : : : : : :	: : : : : : : : : : : : : : : : : : : :
fhab_borpe		EVMAKSATLTTSGAARN--AGKMVQKEAATIVAASVSNPGTFTAGKDITVTSRGGFDNEG					
		1490	1500	1510	1520	1530	
		1610	1620	1630	1640	1650	1660
m564	.pep	K---SKGILSSTKTHDRYF---SHDEAV--GSNIGGGKMIVAAGQDINVRGSNLISDKGI					
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :
fhab_borpe		KMESNKDIVIKTEQFSNGRVLDAKHDLTVTASGQADNRGSLKAGHDFTVQAQRI--DNSG					
		1540	1550	1560	1570	1580	1590
		1670	1680	1690	1700	1710	
m564	.pep	VLKAGHDIDISTAHNRYTG----NEYHESKKSGVMCTGGLGFTIGNRKTTDDTDRTNIV					
		: : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :
fhab_borpe		TMAAGHDATLKAHLRNTGQVVAGHDIHIINSAKLENTGRV--DARNIDIALDVAFTN--					
		1600	1610	1620	1630	1640	1650
		1720	1730	1740	1750	1760	1770
m564	.pep	HTGSIIGSLNGDTPVAGNRYQT---GSTVSSPEGRNTVTAKSIDVEFANNRYATDYA					
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :
fhab_borpe		-TGSLYAEHDA-TLTLAQGTQRDLVVDQDHILPVAECTLRVAKSLTTEIETGNPGSLIA					
		1660	1670	1680	1690	1700	1710
		1780	1790	1800	1810	1820	1830
m564	.pep	HTQEOKGLTVALNVPVQAAQNFIQAAQNVGKSKNKRNVNMAAANA--WQSYQATQOMQO					
		: : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :
fhab_borpe		EVQE-----NIDNKQA----IVVGKDLTSL--SAHGNVANEANALLWAAGELTVKAQN					
			1720	1730	1740	1750	
		1840	1850	1860	1870	1880	1890
m564	.pep	FAPSSSAGQGQNNNQSPSISVITYGEQKSRNEQKRHYTEAAASQIIGKGQTTLAATGSG					
		: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :
fhab_borpe		ITNKRAALIEAGGNARLTAAVALLNKLGRIRAGEDMHL--APRI----ENTAKLSGEV					
		1760	1770	1780	1790	1800	1810
		1900	1910	1920	1930	1940	1950
m564	.pep	EQSNINITGSDVIGHAGTALIADNHIRLQSAKQDGEQSKNKSSG					

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		1960	1970	1980	1990	2000	2010
m564	.pep	GITAGGNIGKGEQGGSTTHRHTHVGSTTGKTTIRSGGDTTLKGVQLIGKGIQADTRNLH					
fhab_borpe		GKDLYLNAGARKDE-----HRHL-----LNEGVIQAGGHGHIGG-----DVDNRSV-					
		1870	1880	1890	1900		

		2020	2030	2040	2050	2060
m564	.pep	IESVQDTETYSKQKQNGNVQTVGYGFSASGSYRQSKVKA-----DHASVTGQSGIYAGE				
fhab_borpe		VRTVSAMEYFKTFLPVSLTALDNRAGLSPATWNFQSTYELLDYLLDQNRYEYIWGLYPTY				
		1910	1920	1930	1940	1950

		2070	2080	2090	2100	2110	2120
m564	.pep	DGYQIKVRDNTDLKGGIITSSQSAEDKGNLFQTATLTASDIQNHS--RYEGRSFGIGGS					
fhab_borpe		TEWSVNTLKNLDL-GYQAKPAPTAPPMPKA-----FELDLRGHTLESAEGRKI-FGEY					
		1970	1980	1990	2000	2010	

		2130	2140	2150	2160	2170
m564	.pep	FDLNGGWDGT-----VTDKQGRPTDRISPAAGYSGDSDSKNSTTRSGVNTNHIHITDEAG				
fhab_borpe		KKLQGEYEKAKMAVQAVEAYGEATRRVHDQLG-----QRYGKALGGMDAETKEVDGIIQ				
		2020	2030	2040	2050	2060

		2180	2190	2200	2210	2220	2230
m564	.pep	QLARTGRTAKETEARIYTGIDTETADQHSGLKNSFDKDAVAKEINLQREVTKFEGRNAA					
fhab_borpe		EFAADLRTVYAKQADQAT-IDAET-DKVAQRYKSQID--AVRLQAIQPGRVT--LAKALS					
		2080	2090	2100	2110	2120	

		2240	2250	2260	2270	2280	2290
m564	.pep	QAVAAVADKLGNTQSYERYQEARTLLE-AELQNTDSEAEKAAFRASLGQVNAYL-----					
fhab_borpe		AALGADWRALGHSQLMQRWKDFKAGKRGAEIAFYPKQTVLAAGAGLTLSNGAIHNGENA					
		2130	2140	2150	2160	2170	2180

		2300	2310	2320	2330	2340	2350
m564	.pep	AENQSRDYTWKEGGIGRSILHGAAGGLTTGSLGGILAGGGTSLAAPYLDKAAENLGPAGK					
fhab_borpe		AQNRGRPEGLKIGAHSATSVSGSFDALRDVGLEKRLDIDDALAAVLVNPFIHTRIGAAQT					
		2190	2200	2210	2220	2230	2240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1671>:

```

g565.seq
1   atggacagca cattgtctaa aacgtgttgc gtttcgtgca tattgttgag
51  cgtaaccacc accattttcg cccgtcccag accggcggct tccaatactt
101 ccctgcgttt cgcacgccc aacgacacc gctcgcctgc acttctggct
151 acctgcacgc gtgcgatgtc caagtcgagc gcgaaatacg gaatatactc
201 ttggggcgaa gacgcgtccg accgtctgcc cgcccctgcc gaagccgaca
251 atcagcacat gatcagactt gctcagctgc tccaccaaca tgctgtgcag
301 atcgagcgac ttcattgtccc agcttgga

```

This corresponds to the amino acid sequence <SEQ ID 1672; ORF 565.ng>:

```

g565.pep
1   MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51  TCTRAMSKSS AKYGISSLGE DASDRLPAPA EADNQHMIRL AHRFHQHAVQ
101 IERLHVPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1673>:

```

m565.seq
1   ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
51  CGTAACCACC ACCATTTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCTGCCCC AAGCCGACAA

```

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```

251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGCGC
351 ATCGCTGCCG CCCAAGAGGA AGGCGCGGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTCGC CGCCTGTTCC CATTCTGGCG AAACCATATC AAGCTGCCCG
451 GCAATGGCCA GCATCACGAA GCCGAACGCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTTG AGGCTGTCGC CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT CAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1674; ORF 565>:

```

m565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
  51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
 101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSGETISSCP
 151 AMASITKPNS PPCARYKAVL RLSPTTEFIL KAMANTTSAP NTSSIAN SIN
 201 TCRQPPINA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m565/g565 100.0% identity in 67 aa overlap

```

                10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                |||
g565           MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                10      20      30      40      50      60

                70      80      90     100     110     120
m565.pep      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
                |||
g565           AKYGISSLGEDASDRLPAPAEADNQHMIRLAHRFHQHAVQIERLHVPA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1675>:

```

a565.seq
  1 ATGGACAGCA CATGTCTTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
  51 CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
 101 CCCTGCGTTF CGCATCGCCG AACGACACCG GTTCGCCCGC ACTTCTGGCA
 151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
 201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA
 251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
 301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGTGC
 351 ATCGCTGCCG CCCAAGAGGA AGGCGCGGAT AATCATCGAC AGCAGAACCG
 401 CCGCCGTCGC CGCCTGTTCC CATTCTAGCG AAACCATATC AAGCTGCCCG
 451 GCAATGGCCA GCATCACGAA GCCGAACGCG CCGCCCTGCG CGAGATACAA
 501 AGCCGTTTTG AGGCTGTCGC CGACCGAATG TTTCATTTTG AAGGCAATGG
 551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
 601 ACCTGCCGCC AGCCGCCGAT TAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1676; ORF 565.a>:

```

a565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
  51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
 101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSSETISSCP
 151 AMASITKPNS PPCARYKAVL RLSPTTEFIL KAMANTTSAP NTSSIAN SIN
 201 TCRQPPINA*

```

m565/a565 99.5% identity in 209 aa overlap

```

                10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                |||

```

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```

a565      MDSTLSKTCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS
           10      20      30      40      50      60
m565.pep  AKYGISSWARTRPTVCPLPKPTISTWSDLLMVSTSLCRSSDFMSQLDLTKRPTSASLP
           70      80      90      100     110     120
a565      AKYGISSWARTRPTVCPLPKPTISTWSDLLMVSTSLCRSSDFMSQLDLTKRPTSASLP
           70      80      90      100     110     120
m565.pep  PKRKGAIIDSRTAAVAACSHSGETISSCPAMASITKPNPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180
a565      PKRKGAIIDSRTAAVAACSHSSETISSCPAMASITKPNPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180
m565.pep  KAMANTTSAFNTSSIANSSINTCRQPPINAX
           190     200     210
a565      KAMANTTSAFNTSSIANSSINTCRQPPINAX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1677>:

```

g566.seq..
1  atgccgtctg aacaatatct tttcagacgg cattttgtat ggggggtaac
51 ggttggttcag cccgagtagc tcctgcatat cgtacaaacc cgttttgccg
101 tttacccaaa ctgcggcgcg gacggcaccg gcggcaaagg tcatgcggct
151 gccggctttg tgggtgattt ccacgcgttc gccgtcgggt gcgaagaggg
201 cgggtgtggtc gccgactatg tcgcctgcgc ggacggtggc aaagccgatg
251 gtggaaggat cgcgcgacc agtgtggcct tcgcggccgt aaacggcgca
301 ttgtttgagg tcgcggccga gcgcgccggc gatgacttcg cccattcgta
351 a

```

This corresponds to the amino acid sequence <SEQ ID 1678; ORF 566.ng>:

```

g566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVYPNCGA DGTGGKGHAA
51 AGFVGDFHAF AVGGEEGGVV ADYVACADGG KADGGRIART SVAFAAVNGA
101 LFEVAAERAG DDFAHSA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1679>:

```

m566.seq..
1  ATGCCGTCCTG AACAAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51 GGTGTGTTTCA CCGAGTAGC TCCTGCATAT CGTACAAACC CGTTTGTCCG
101 TTGACCCAAA CTGCGGCGCG GACGGCACC GCGGCAAAGG TCATGCGGCT
151 GCTGGCCTTG TGGGTGATT CCACGCCTC GCCGTCGGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCTGCGC GGACGGTGGC AAAGCCGATG
251 GTCGACGGAT CGCGCGGACC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1680; ORF 566>:

```

m566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT REAVDPNCGA DGTGGKGHAA
51 AGLVGDFHAL AVGGEEGGVV ADDVACADGG KADGRRART GVAFAAVNGA
101 LFEVSAERAG DDFAHSA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m566/g566 93.1% identity in 116 aa overlap

```

           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||

```

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```

g566      MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFAVYPNCGADGTGGKGHAAAGFVGDFHAF
           10      20      30      40      50      60

           70      80      90      100     110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g566      AVGGEEGGVVADYVACADGGKADGGRIARTSVAFAAVNGALFEVAAERAGDDFAHSX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1681>:

```

a566.seq
1  ATGCCGCTCTG  AACAAATATCT  TTTCAGACGG  CATTTTGTAT  GGGGGTTAAC
51  GGTGTGTTACG  CCCGAGTACG  TCCTGCATAT  CGTACAAACC  CGTTTTACCG
101 TTTACCCAAA  CTGCGGCGCG  GACGGCGCCG  GCGGCAAAGG  TCATGCGGCT
151 GCTTGCCTTG  TGGGTGATT  CCACGCGCTC  GCCGTCGGTG  GCGAAGAGGG
201 CGGTGTGGTC  GCCGACGATG  TCGCCCGCGC  GGACGGTGGC  AAAGCCGATG
251 GTGGACGGAT  CGCGCGGGCC  GGTGTGGCCT  TCGCGGCCGT  AAACGGCGCA
301 TTGTTGAGG  TCTCTGCCGA  GCGCGCCGGC  GATGACTTCG  CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1682; ORF 566.a>:

```

a566.pep
1  MPSEQYLFRH  HFVWGLTVVQ  PEYVLHIVQ  RFTVYPNCGA  DGAGGKGHAA
51  ACLVGDFFAL  AVGGEEGGVV  ADDVARADGG  KADGGRIARA  GVAFAAVNGA
101 LFEVSAERAG  DDFAHAX*

m566/a566  94.0% identity in 116 aa overlap

           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a566      MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFTVYPNCGADGAGGKGHAAACLVGDFHAL
           10      20      30      40      50      60

           70      80      90      100     110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a566      AVGGEEGGVVADDVARADGGKADGGRIARAGVAFAAVNGALFEVSAERAGDDFAHAX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1683>:

```

g567.seq..
1  atcgacgac  gggcagcggc  atcgacaagg  cgggtttgca  gtccggcggt
51  tatcaggtct  tattgggcga  tgcggacgtg  cagtcggcgg  cggtacgcag
101 caaagagggc  ggatacggcg  tgttggtgca  gaacgcgcgc  gcttgccggc
151 gcggaaatcg  agctgggtgca  ggaaatcgcc  cgggaagtgc  gtttgaaaaa
201 cgcgtcaag  gcagtggcgg  aagattacga  cttatcctg  atcgactgtc
251 cgcttcgct  gacgtgttg  acgcttaacg  gcttggtggc  ggcgggcggc
301 gtgattgtgc  cgatgtgtg  cgaatattac  gcgctggaag  ggatttcgga
351 ttgattgctg  accgtgcgca  aaatccgtca  ggcggtcaat  cccgatttgg
401 acatcacggg  catcgtgcgt  acgatgtacg  acagccgcag  caggctggtt
451 gccgaagtca  gcgaacagtt  gcgcagccat  ttcggggatt  tgctttttga
501 aaccgccatc  ccgcgcaata  tccgccttgc  ggaagcgccg  agccacggta
551 ccgcggtgat  ggcttacgac  gcgcaggcaa  aggggtgcaa  ggcgtatctt
601 gccttgccgg  acgaacggc  ggcgaggggt  tcggggaaat  ag

```

This corresponds to the amino acid sequence <SEQ ID 1684; ORF 567.ng>:

```

g567.pep
1  MRRRAAATR  RVCSPAFIRS  YWAMRTCSRR  RYAAKRADTA  CWVRTRALAG
51  AEIELVQEIA  REVRLKNALK  AVAEDYDFIL  IDCPPSLTLL  TLNGLVAAGG
101 VIVPMLCEYY  ALEGISDLIA  TVRKIRQAVN  PDLDITGIVR  TMYDSRSRLV
151 AEVSEQLRSH  FGDLLFETAI  PRNIRLAEAP  SHGMPVMAYD  AQAKGAKAYL
201 ALADELAARV  SGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1685>:

```
m567.seq..
1  ATGAGTGC GA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101 GCGTGCTGGT GGTGATTTTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151 GGCATCGACA AGGCGGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201 CGATGCGGAC GTGCAGTCGG CGGCGGTACG CAGCAAAGAG GCGGATACG
251 CTGTGTTGGG TGCGAACCGC GCGCTGGCCG GCGCGGAAAT CGAACTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTGAAA AACGCGCTCA AGGCAGTGGA
351 AGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCCTCG CTGACGCTGT
401 TGACGCTTAA CGGGCTGGTG GCGGCGGGCG GCGTGATTGT GCCGATGTTG
451 TGCGAATATT ACGCGCTGGA AGGGATTTCG GATTTCATTG CGACCGTGCG
501 CAGAAATCCG CAGGCGGTCA ATCCCGATTG GGACATCAGC GGCATCGTGC
551 GCACGATGTA CGACAGCCGC AGCAGGCTGG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTTCGGGA TTTGCTTTT GAAACCGTCA TCCGCGCAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTACG
701 ACGCGCAGG AAGGGTACC AAGCGTATC TTGCCTTGGC GGACGAGCTG
751 GCGGCGAGG TGTCGGGGA ATAG
```

This corresponds to the amino acid sequence <SEQ ID 1686; ORF 567>:

```
m567.pep..
1  MSANILAIA N QXGGVGKTTT TVNLAASLAS RGKRIVVVDL DPQGNATTGS
51  GIDKAGLQSG VYQVLLGDAD VQSAAVRSKE GGYAVIGANR ALAGAEIELV
101 QEIAREVRLK NALKAVEEDY DFILDCPPS LTLLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLDT GIVRTMYDSR SRLVAEVSEQ
201 LRSFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGT KAYLALADEL
251 AARVSGK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```
m567/g567 98.2% identity in 168 aa overlap

60      70      80      90      100      110      119
m567.pep  GYVQVLLGDADVQSAAVRSKEGGYAVLGNRALAGAEIELVQEIAREVRLKNALKAVEED
g567      AFIRSYWAMRTCSRRRYAAKRDTACWVRTRALAGAEIELVQEIAREVRLKNALKAVEED
           20      30      40      50      60      70

120      130      140      150      160      170      179
m567.pep  YDFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDT
g567      YDFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDT
           80      90      100      110      120      130

180      190      200      210      220      230      239
m567.pep  TGIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKG
g567      TGIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETAIPRNIRLAEAPSHGMPVMAYDAQAKG
           140      150      160      170      180      190

240      250
m567.pep  TKAYLALADELAARVSGKX
g567      AKAYLALADELAARVSGKX
           200      210
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1687>:

```
a567.seq
1  ATGAGTGC GA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101 GCGTGCTGGT GGTGATTTTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151 GGCATCGACA AGGCGAGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201 CGATGCGGAC GTGAAATCGG CGGCGGTACG CAGCAAAGAG GCGGATACG
```

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```

251 GCGTGTGGG TCGGAACCGC GCGCTGGCCG GCGCGGAAAT CGAGCTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTTGAAA AACGCGCTCA AGGCAGTGGC
351 GGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CGGCTTGGTG GCGGCAGGCG GCGTGATGT GCCGATGTTG
451 TGCGAATATT ACGCGCTGGA AGGGATTTCG GATTTGATTG CGACCGTGCG
501 CAAAATCCGT CAGGCGGTCA ATCCCGATTG GGATATCACG GGCATCGTGC
551 GTACGATGTA CGACAGCCGC AGCAGGCTAG TTGCCGAAGT CAGCGAACAG
601 TTGGCGAGCC ATTTCCGGGA TTTGCTGTTT GAAACCGTCA TCCCGCGCAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTATG
701 ATGCGCAGGC AAGGGTGCC AAGCGTATC TTGCCTTGGC GGACGAGCTG
751 ATGGCGAGGG TETCGGGGAA ATAG

```

This corresponds to the amino acid sequence <SEQ ID 1688; ORF 567.a>:

```

a567.pep
1 MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
51 GIDKASLQSG VYQVLLGDAD VKSAAVRSKE GYGVLGANR ALAGAEIELV
101 QEIAREVRLK NALKAVAEDY DFILIDCPPS LTLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLDT GIVRTMYDSR SRLVAEVSEQ
201 LRSHFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGA KAYLALADEL
251 MARVSGK*

m567/a567 97.7% identity in 257 aa overlap

              10      20      30      40      50      60
m567.pep      MSANILAIANQKGGVGKTTTTVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKAGLQSG
a567           MSANILAIANQKGGVGKTTTTVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG
              10      20      30      40      50      60

              70      80      90      100     110     120
m567.pep      VYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAVEEDY
a567           VYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAVEEDY
              70      80      90      100     110     120

              130     140     150     160     170     180
m567.pep      DFILIDCPPSLTLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDT
a567           DFILIDCPPSLTLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDT
              130     140     150     160     170     180

              190     200     210     220     230     240
m567.pep      GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGT
a567           GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGA
              190     200     210     220     230     240

              250
m567.pep      KAYLALADELAARVSGKX
a567           KAYLALADELMARVSGKX
              250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1689>:

```

g568.seq
1 atgctcaggg tcagaccggt attatttgcc gtcaaggctt ccgcctcttc
51 gataccttgc agaattctgcc gattaaagcg ttcgcggtcg cccaatattt
101 tcagcgcat attgttttcg tgcaggcggc gtacctgttt ttgcaaagcc
151 tgtaaaaaaca gcccatcag gaacgaaact tcgtcttcgg ggcgacgcca
201 gttttcgtt gaaaaggcaa acacggtcag atattgcacg cccagtttg
251 cgcaatgctt caccatattt tccaacgcgt ccaagccgct tttgtgtccc
301 attatacgcg ggagaaacg ttttttcgcc caacggcgtg tgccgtccat
351 aattacggcg atgtgcctcg ggatggcggt gtgttccaaa atggtctgcg

```


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401 tgctgctctt catatctgcc ttctcgcggtt cggcggtcaa atgccgtctg
451 aacgcgcgcg cgtga

This corresponds to the amino acid sequence <SEQ ID 1690; ORF 568.ng>:

g568.pep
1 MLRVRPVLFA VKASASSIPC RICRLKRSRL PNIFRRILFS CRRRTCFCCKA
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IIRGRKRFFA QRPLPSIITA MCLGMAVCSK MVCVLLFISA FRGSAFKCRL
151 NAAP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1691>:

m568.seq
1 ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAACGCTT CCGCCTCTTC
51 GATGCCTTGC AGAATCTGCC GGTGAAGCG TTCGCGGCTG CCAATATCT
101 TCAGGCGCAT ATTGTTTTCG TGCAGGCGGC GTACCTSTT TTGCAAAGCC
151 TGTAATAACA GCGCCATCAG GAACGAACT TCGTCTTCGG GCGGCGCGCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACGCG TTTGTGTCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCGGT TGCCGTCCAT
351 AATCAGGCG ATATGCTTGG GAATGGCGGT GTGTCCAAA ACGCCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTTCGGTT CCGCATTCAA ATGCCGCTG
451 AACGCCGAAC CGTGCAGGTT AAATGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCCGCTTCG GTAATGTATT TGTCCGTCAG TTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTTGAG
601 GAGTTTTCG ATGTGTCGT TGGCATCGCG GCGCACGTTG CGGATAGAGA
651 CGCGGCCTTC TTCCGCTTCG CCGGTACGA CTTAATCAG GTCTTTGCGG
701 CGTTCCTCG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTT AGTCCCAAGT TTGA

This corresponds to the amino acid sequence <SEQ ID 1692; ORF 568>:

m568.pep..
1 MLRVRPVLFA VNASASSMPC RICRLKRSRL PNIFRRILFS CRRRTCFCCKA
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL
151 NAEPCLRNCH QIFFFGSQEF VGFNMFVVGQ FLNRFFAATC LVFGNFFVFE
201 EFFDVVVGIA AHVADRDAAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m568/g568 94.8% identity in 154 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
g568	MLRVRPVLFAVKASASSIPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
g568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIIRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m568.pep	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCRLNCHQIFFFGSQEFVGFNMFVVGQ					
g568	MCLGMVCSKMVCVLLFISAFRGSFAFKCRLNAAPX					
	130	140	150			
	190	200	210	220	230	240
m568.pep	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADRDAAFRFAAYDFNQVFAAFLGQHG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1693>:

```
a568.seq
1   ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAAGGCTT CCGCCTCTTC
51  GATGCCCTTC AGGATTGAC  GGTGAAGCG TTCGCGGCTG CCCAGTATTT
101 TCAGGCGCAT ATTGTTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC
151 TGTA AAAACA GCCCATCAG GAACGAACT TCGTCTTCGG GCGGCGGCCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT
351 AATCAGCGCG ATATGCTTGG GAATGGCGGT GTGTCCAAA ACGGCCTGCG
401 TGCTGCTTTT CATGCTGCC TTTTCGGGT CCGCATTCAA ATGCCGCTCTG
451 AACGCCGAAC CGTGCAAGTT AAATGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTGGTCAG TTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTTGAG
601 GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATGGAGA
651 CGCGGCCTTC TTCCGCTTCG CCGCGTACGA CTTAATCAG GTCTTTGCCG
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTT AGTCCCAAGT TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1694; ORF 568.a>:

```
a568.pep
1   MLRVRPVLFA VKASASSMPF RI*RLKRSRL PSIFRRILFS CRRRTCFCCKA
51  CKNSPIRNET SSSGRROFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL
151 NAEPCRLNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVEE
201 EFFDVVVGIA AHVADGDAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*
```

m568/a568 98.1% identity in 257 aa overlap

m568.pep	10	20	30	40	50	60
	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
a568	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
m568.pep	70	80	90	100	110	120
	SSSGRROFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
a568	SSSGRROFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
m568.pep	130	140	150	160	170	180
	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
a568	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
	130	140	150	160	170	180
m568.pep	190	200	210	220	230	240
	FLNRFFAATCLVFGNFFVEEFDVVVGIAAHVADRDAAFFRFAAYDFNQVFAAFLGQHG					
a568	FLNRFFAATCLVFGNFFVEEFDVVVGIAAHVADGDAAFFRFAAYDFNQVFAAFLGQHG					
	190	200	210	220	230	240
m568.pep	250					
	HRHADQVADSCRVSQVX					
a568	HRHADQVADSCRVSQVX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1695>:

```
g569.seq..
1   atgctgaaac aacgggtaat aaccgctatg tggctgctgc cgctgatgct
51  gggcatgctg ttttacgcgc cgcaatggct gtgggctgca ttttgcgggc
101 tgattgccct gaccgccttg tgggagtatg cccgatggc cggtttgtgc
```

874

```

151 aaaaccgaaa ccaaccatta cctcgccgca accttggttt tcggcgtagt
201 tgectatgcg ggcggctgga tgetgcctaa tttggtttgg tatgttggtt
251 tggcattttg gctcgccgtt atgcctttgt ggttgagatt caaatggagg
301 ctcaacggcg gttggcaggt ttatgccgtc ggctgggttt tgctcatgcc
351 gttttggttc gcgctcgat ccctggcgcc cgcatccga tga

```

This corresponds to the amino acid sequence <SEQ ID 1696; ORF 569.ng>:

g569.pep

```

1 MLKQKVITAM WLLPLMLGML FYAPQWLWAA FCGLIALTAL WEYARMAGLC
51 KTETNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LGGWQVYAV GWLLMPFWF ALVSLAPASR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1697>:

m569.seq..

```

1 ATGCTGAAAC AACGGGTAAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGCGGAC
101 TGATTGCCCT GATTGCCCTG TGGGAATATG CCCGTATGGG CGGTTTGTGC
151 AAAATTAATA CCAACCATTA CCTCGCCGCA ACCTIGGTTT TCGGCGTGGT
201 TGCCTATGCG GCGGGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCTTTAT GGTGAGATT CAAATGGAGG
301 CTCACGCGG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCTGCGGCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCGCCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGCGCG CGCGGTTTGC GTGGCAGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCGA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGTCT ACCGTTGTCA GCGTATCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAACACAGCA
701 GCAAGCTGCT GCCCGGACAC GCGGCGGTGT TCGACCGTAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGCTTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1698; ORF 569>:

m569.pep..

```

1 MLKQKVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51 KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAIKPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
201 FDTVLIGLVL TVSVCGDLL ESWLKRAAGI KDSSKLLPGH GGVFDRDTSI
251 IAVISVYAM MSVLN*

```

m569/g569 95.3% identity in 127 aa overlap

	10	20	30	40	50	60
m569.pep	MLKQKVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA					
g569	MLKQKVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALTALWEYARMAGLCKTETNHYLAA					
	10	20	30	40	50	60
m569.pep	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLGGWQVYAVGWLLVMPFWF					
g569	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLGGWQVYAVGWLLMPFWF					
	70	80	90	100	110	120
m569.pep	ALVSLRPHPD DALPLAVMGLVWVADICAYFSGKAFGKHKIAPAIKPGKSWEGAIGGAVC					
g569	ALVSLAPASRX					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1699>:

a569.seq

```

1 ATGCTGAAAC AACGGGTGAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGCGGAC
101 TGATTGCCCT GATTGCCCTG TGGGAATATG CCCGTATGGG CGGTTTGTGC

```

875

```

151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGGTTT TCGGCGTGGT
201 TGCCTATGCG GCGCGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCCTTAT GGTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTTCGG CAAACACAAA ATCGCACCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCCGTGT
551 ACATGACCCG CGTACGAAGT GCCGGCTGGC TGGCATTCTGA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGTG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAACCTGCT GCCCGGACAC GCGGCGGTGT TCGACCGCAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGICTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1700; ORF 569.a>:

```

a569.pep
1  MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALLIAL WEYARMGGLC
51  KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
201 FDTVLIGLVL TVVSVCGDLL ESWLKRAAGI KDSSNLLPGH GGVFDRDTS
251 IAVISVYAAM MSVLN*

```

m569/a569 99.6% identity in 265 aa overlap

```

              10      20      30      40      50      60
m569.pep      MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALLIALWEYARMGGLCIKTNHYLAA
              |||||||
a569           MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALLIALWEYARMGGLCIKTNHYLAA
              10      20      30      40      50      60

              70      80      90      100     110     120
m569.pep      TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF
              |||||||
a569           TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF
              70      80      90      100     110     120

              130     140     150     160     170     180
m569.pep      ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC
              |||||||
a569           ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC
              130     140     150     160     170     180

              190     200     210     220     230     240
m569.pep      VAVYMTAVRSAGWLAFDTGWFDTVLIGLVLTVVSVCGDLLESWLKRAAGIKDSSKLLPGH
              |||||||
a569           VAVYMTAVRSAGWLAFDTGWFDTVLIGLVLTVVSVCGDLLESWLKRAAGIKDSSNLLPGH
              190     200     210     220     230     240

              250     260
m569.pep      GGVFDRDTSLIAVISVYAAMMSVLNX
              |||||||
a569           GGVFDRDTSLIAVISVYAAMMSVLNX
              250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1701>:

g570.seq..

```

1  atgatccgtt tgaccgcgcg gtttgccgcc gccctgatcg gtttatgetg
51  caccacaggc gcgcacgcgc acaccttcca aaaaatcggc tttatcaaca
101 cggagcgcat ctacctcgaa tccaagcagg cgcgcaacat ccaaaaaacg
151 ctggacggcg aattttccgc cgtcaggac gaattgcaaa aactgcaacg
201 cgaaggtctg gatattgaaa ggcagctcgc cggcggcaaa cttaaggacg
251 caaaaaaggc gcaagccgaa gaaaaatggc gcgggctggc cgaagcgctc
301 cgcaaaaaac aggcgcagtt tgaagaagac tacaacctcc gccgcaacga
351 agagtttgcc tccctccagc aaaaacgcaa ccgcgtcatc gtcaaatcgg

```

876

401 ccaaacagga aggttacgat gtcattttgc aggacgtgat ttacgtcaac
 451 acccaatcag acgttaccga cagcgtcatt aaagaaatga acgcccgcgtg
 501 a

This corresponds to the amino acid sequence <SEQ ID 1702; ORF 570.ng>:

g570.pep..

1 MRLTRAFAA ALIGLCCTTG AHADTFQKIG FINTERIYLE SKQARNIQKT
 51 LDGEFSARQD ELQKLQREGL DLERQLAGGK LKDAKKAQAE EKWRGLVEAF
 101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
 151 TQYDVTDSVI KEMNAR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1703>:

m570.seq..

1 ATGACCCGTT TGACCCGCGC GTTGGCCGCG GCTCTGATCG GTTGTGCTG
 51 CACCGCAGGC GCGCAGCCCG ACACCTTCCA AAAAATCGGC TTTATCAACA
 101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAACG
 151 CTGGACAGCG AATTTCCGCG TCGTCAGGAC GAATTGCAAA AACTGCAACG
 201 CGAAGGTCTG GATTGGAAA GGCAGCTTGC CGAAGGCAAA CTCAGAAACG
 251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGC GCGGGCTGGT CGCAGCGTTC
 301 CGCAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
 351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
 401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGAACGTGAT TTACGTCAAC
 451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG
 501 A

This corresponds to the amino acid sequence <SEQ ID 1704; ORF 570>:

m570.pep

1 MRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
 51 LDSEFSARQD ELQKLQREGL DLERQLAEGK LRNAKKAQAE EKWRGLVAAF
 101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQNVIIYN
 151 TQYDVTDSVI KEMNAR*

m570/g570 94.6% identity in 166 aa overlap

	10	20	30	40	50	60
m570.pep	MRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD					
g570	MIRLTRAFAAALIGLCCTTAGAHADTFQKIGFINTERIYLESKQARNIQKTLDBFSARQD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA					
g570	ELQKLQREGLDLERQLAGGKLRNAKKAQAEKWRGLVEAFRKKQAQFEEDYNLRNNEEFA					
	70	80	90	100	110	120
	130	140	150	160		
m570.pep	SLQQNANRVIVKIAKQEGYDVILQNVIIYNTQYDVTDSVIKEMNARX					
g570	SLQQNANRVIVKIAKQEGYDVILQDVIYNTQYDVTDSVIKEMNARX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1705>:

a570.seq

1 ATGACCCGTT TGACCCGCGC GTTGGCCGCG GCTCTGATCG GTTGTGCTG
 51 CACCGCAGGC GCGCAGCCCG ACACCTTCCA AAAAATCGGC TTTATCAACA
 101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAACG
 151 CTGGACAGCG AATTTCCGCG CCGCCAGGAC GAATTGCAAA AACTGCAACG
 201 CGAAGGTCTG GATTGGAAA GGCAGCTTGC CGAAGGCAAA CTCAGAAACG
 251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGT GCGGGCTGGT CGCAGCGTTC
 301 CGCAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
 351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
 401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGGACGTGAT TTACGTCAAC
 451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG

877

501 A

This corresponds to the amino acid sequence <SEQ ID 1706; ORF 570.a>:

```

a570.pep
1  MTRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
51  LDSEFSARQD ELQKLQREGL DLERQLAEGK LKDAKKAQAE EKWCGLVAAF
101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
151 TQYDVTDSVI KEMNAR*

m570/a570 97.6% identity in 166 aa overlap

              10      20      30      40      50      60
m570.pep  MTRLTRAFAAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD
              |||
a570       MTRLTRAFAAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD
              10      20      30      40      50      60

              70      80      90     100     110     120
m570.pep  ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA
              |||
a570       ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA
              70      80      90     100     110     120

              130     140     150     160
m570.pep  SLQQNANRVIVKIAKQEGYDVILQNVIVNTQYDVTDSVIKEMNARX
              |||
a570       SLQQNANRVIVKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1707>:

```

g571.seq (partial)
1  atgcgcggtt tccgagtaaa cegatttgtt gttaccgttt tcggcggcgg
51  tataggttct gccgtcccac acgctgcctg cgtcggaaaa caggctcagg
101 cggacggtgc gtgcgtcttt cgcacggggc atcggaaaga gcagctcggc
151 ggagacggtg gcttttttgt tgcgcgcgta gctgattttt tcgcggtatt
201 cgtcatacac ttccgggccc agcgtgcgcg ttctgtagcc gcgcaccgaa
251 cccaggccgc cgcgtagaa gttttcaaag aaggggattt ctttggttct
301 gccgtagccg cccgcaatgc cgacttcgcc gccgagcatc agcgtgaagg
351 ttttgc...

```

This corresponds to the amino acid sequence <SEQ ID 1708; ORF 571.ng>:

```

g571.pep (partial)
1  MRVFRVNRFV VTVFGGGIGS AVPHAACVGK QAQADGACVF RTGHRBEEQLG
51  GDVGGFFVAAV ADFFAVFVIH FRAERAAFVA AHRTQAAAVE VFKEGDPFGS
101 AVAARNADFA AEHQREGFA...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1709>:

```

m571.seq
1  ATGGGTATTG CCGGCGCCGT AAATGTTTGG AACCTGCGG CCGGTCGCGG
51  AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACACGCT GCCTGCGTCG
101 GCAAACAGGC TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGGCATCGG
151 GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCGG CCGTAGCTGA
201 TTTTTCGCC GTATTCTGTA TAGACTTTCG GACCGAGCGT GCCGCTTTCG
251 TATCCGCGCA CCGAACCCAG GCCGCGCGCG TAGAAGTTT CAAAGAAGGG
301 GATTTCCTTG GTTCTGCCGT AGCGGCCCGC AATGCCGACT TCGCGCCGGA
351 GCATCAGCGT GAAGGTTTGG CTCAGGGGGA AGAACCGAGT TTGTTGTGG
401 GTGGCGGAGT AGTATTGCAG TTTGCTGCCA GGCAGGGCGA TTTGCGCGTT
451 CACGCCCGTC AGGTAGCCGC GCGTCGCCA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1710; ORF 571>:

```

m571.pep
1  MGIAGAVNVL NPAAGRGTAV VVVGFAVPHA ACVGKQAQAD GARVFRAGHR
51  EEQLGGDVGF FVAAVADFFA VFVIDFRTER AAFVSAHRTQ AAAVEVFKEG
101 DFFGSAVAAR NADFAAEHQR EGFAQGEEPG LVVGGGVVLQ FAARQGDPGV
151 HARQVAARRP *

```

878

m571/g571 93.1% identity in 102 aa cverlap

```

      10      20      30      40      50      60
m571.pep  MGIAGAVNVNLPAAAGRGTA VVVVGFAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
           :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g571      MRVFRVNRFFVTVFGGGIGSAVPHAACVKGQAQADGACVFRTGHREEQLGGDVGF
           10      20      30      40      50

      70      80      90      100     110     120
m571.pep  FVAAVADFFAVFVIDFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g571      FVAAVADFFAVFVIHFRAERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
           60      70      80      90      100     110

      130     140     150     160
m571.pep  EGFAQGGEPLVVGGVVLQFAARQGD FGVHARQVAARRPX
           ||||
g571      EGFA
           119

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1711>:

```

a571.seq
1  ATGGGTATTG CCGGCGCCGT AAATGTTTGT AACCTGCCG CCGGTCGCGG
51  AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACAGCT GCCTGCGTCG
101 GCAAACAGGC TCAGGCGGAC GGTGCGCGC TCTTTCGCGC CGGGCATCGG
151 GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CCGTAGCTGA
201 TTTTTCGCC GTATTCGTCA TACACTTTCG GACCGAGCGT GCCGCTTCG
251 TATCGCGCGA CCGAAGCCAG GCCGCCGCCG TAGAAGTTT CAAAGAAGGG
301 GATTTCTTTG GTTCTGCCGT AGCCGCCCGC AATGCCGACT TCGCCGCCGA
351 GCATCAGCGT GAAGTTTGT CTTAAGGGGA AGAACCAGG TTGGTTGTGG
401 GTGGCGGAGT AGTATTGCAG TTGCTGCCG GGCAGGCGA TTTCGGCGTT
451 CACGCCCGTC AGGTAGCCGC GCGTCGGCCA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1712; ORF 571.a>:

```

a571.pep
1  MGIAGAVNVL NPAAGRGTA VVVVGFAVPHA ACVKGQAQAD GARVFRAGHR
51  EEQLGGDVGF FVAAVADFFA VFVIHFRTER AAFVSAHRTQ AAAVEVFKEG
101 DFFGSAVAAR NADFAAEHQ EGFA*GEEPG LVVGGGVVLQ FAAGQGD FGV
151 HARQVAARRP *

```

m571/a571 98.1% identity in 160 aa overlap

```

      10      20      30      40      50      60
m571.pep  MGIAGAVNVNLPAAAGRGTA VVVVGFAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a571      MGIAGAVNVNLPAAAGRGTA VVVVGFAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
           10      20      30      40      50      60

      70      80      90      100     110     120
m571.pep  FVAAVADFFAVFVIDFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a571      FVAAVADFFAVFVIHFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
           70      80      90      100     110     120

      130     140     150     160
m571.pep  EGFAQGGEPLVVGGVVLQFAARQGD FGVHARQVAARRPX
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a571      EGFAQGGEPLVVGGVVLQFAAGQGD FGVHARQVAARRPX
           130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1713>:

g572.seq.

q572.pnp.

1	MCAIVGAAGL	PSALAAAKQG	KTIYLANKET	LTVSGALFME	TARANGAAYL
51	PVDSEHNAIF	QVLPRDYTR	LNWEGIDSII	LTASGGFFLT	TDLSTFDSIT
101	PEQAVKPNW	RMGRKISVDS	ATMANKGLAL	IEAHLWFNCP	POKLEVV1HP
151	QSVIHSVMRY	RDGSVLAQY	NPDMRTPIEL	CLGLPWRIDS	GVGKLDLFGAL
201	SALTPOKDFE	GRFPCCLKFQ	ETINAGGAAP	CVLNAANETA	VAAFLDGOGL

m572.seq..

1	ATGTGCGCCA	TGTCGCGGGC	GGTGGGCGTG	CCTTCGCGCG	TGCGAGCGGC
51	GCAAAAAGCG	AAAACCATTT	ATCTGCGCAA	CAAGAGAACG	CTGGTGGTIT
101	CCGCGCGCTT	GTTTATGGAA	ACCGCCCGTG	CAACCGGCGC	GGCAGTGCCT
151	CCCGCTCGACA	GCGAACACAA	CGCCGTTTTC	TTCAGTTTTCG	CGCGCGATTAA
201	CGCCGGCGCGT	CTGAACGAAC	ACGGCATTCG	TTCGATTATC	CTGACCGCTT
251	CGCGCGCGCCC	GTTTCTGCC	GCGGATTTAA	ACACGTTTCG	CCGCATTACG
301	CCCGGCCAAG	CGGTCAAACA	CCCCAATTGG	CGTATGGGAC	GCAAAATCTC
351	CGTCGATTCC	GCCACCATGA	TGAACAAAGG	TTTGGAGCTG	ATTGAAGCGC
401	ATTGCGTGT	CAACTGTCCG	CCGCGACAAAC	TGCAAGTCGT	CATCCATCAT
451	CAATCCGTGA	TACACAGCAT	TGTGCGCTAC	CGGACGGGCT	CCGTGCTGGC
501	GCAACTGGGC	AATCCCGATA	TGCGAAGCGC	CATCGCTTAT	TGTTTGGGTT
551	TGCCCGAGCG	CATCGATTCC	GGTGTGCGCG	ACCTGGATT	CGACGCATTG
601	TCCGCGCTGA	CCTTCCAAAA	GCCCGCATTT	GACCGCTTCC	CCTGCTGTAG
651	GCTCGCCTAT	GAAAGCATGA	ACGCAGCGCG	AGCCGCGCCT	TGCGTATTGA
701	AGCCGCGCAA	CGAAGCCGCC	GTGCGCGCCT	TTTTGGACGG	ACAGATTAA
751	TTTACCGACA	TTGCCAAAAAC	CGTCGCCCAC	TGCTTCAAGC	AAGACTTTTC
801	AGACGGCATA	GGGCATATAG	GGGGGCTCTT	GGCGCAAGAT	GCCCGGCAC
851	GCGACAACG	GCGAGCATTT	ATTCGGCACAC	TGCGCTGA	

m572.pcp..

1	MCAIVGAVGL	PSALAAQKG	KTIYLANKET	LVVSGALFME	TARANGAVVL
51	PQVSEHNNAV	QVLRPRDYGAR	LNHEGLASII	LTASGGFNPL	ADLNTDFDRI
101	PAADAKHNW	RMKRISVDS	ATMMNGLESL	IEAHLWFNCP	PKDLKVTHPT
151	QSVIHSVMRY	RDGSVLAQLG	NPDMRTPIAY	CLGLPERIDS	GVGDLDFDAL
201	SALTQPKQFD	DRDFCLRLAR	EDMMAGTAAP	CVLNAANEAA	VAAFLDGGCIK
251	FTDIAKTVAH	CLAQDFSDGI	DGIGGLLAQD	ARTRQAARFA	IGTLR*

m572/q572 92.9% identity in 295 aa overlap

	10	20	30	40	50	60
m572 . pep	MCAIVGAVGLPSALAAAKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAV					
	: : : : :					
g572	MCAIVGAAGLPSALAAAKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNATF					
	: : : : :					
	10	20	30	40	50	60
	70	80	90	100	110	120
m572 . pep	QVLPRDYAGRLENEHGIASIILTASGGPFLTDLTNFTDRITPAQAVKHPNWRMGRKISVDS					
	: : : : :					
g572	QVLPRDYLTRLNEHGIDSIILTASGGPFLTDLSTFDLSITPEQAVKHPNWRMGRKISVDS					

880

	70	80	90	100	110	120
m572 . pep	130	140	150	160	170	180
	ATMMNKGLELEIAHWLFNCP	PPDKLEVVIHPQSVIHS	MVRYRDGSLAQLGNPDM	RTPAIY		
g572	ATMANKGLELEIAHWLFNCP	PPDKLEVVIHPQSVIHS	MVRYRDGSLAQLGNPDM	RTPAIY		
	130	140	150	160	170	180
m572 . pep	190	200	210	220	230	240
	CLGLPERIDSGVGLDFDALS	ALTFOKPDFRFPCLRLAYE	AMNAGGAAPCVLNAANEA			
g572	CLGLPERIDSGVGLDFGALS	ALTFOKPDFRFPCLKFAYE	TINAGGAAPCVLNAANETA			
	190	200	210	220	230	240
m572 . pep	250	260	270	280	290	
	VAAFLDGQIKFTDIAKTVAH	CLAQDFSDGIGDIGLLAQD	ARTRAQARAFIGTLRX			
g572	VAAFLDGQIKFTDIAKTVAH	CLAQDFSDGIGDIGLLAQD	ARTRAQARAFIGTLRX			
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1717>:

```
a572 . seq
1   ATGTGCGCCA TCGTCGGGGC GGTGGGGCTG CCTTCCGCGC TCGCAGCGGC
51  GCAAAAAGGC AAAACCATTT ATCTGGCGAA CAAAGAGACG CTGGTGGTTT
101 CCGGCGCGTT GTTTATGGAA ACCGCCCGTG CAAACGGCGC GGCAGTGC TG
151 CCCGTCGACA GCGAACACAA CGCCGTTTTC CAAGTTTTCG CGCGCGATTA
201 CACAGGTCGC CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGGCGGCCC GTTTC'TGACC GCCGATTTAA ACACGTTTGA CAGCATTACG
301 CCCGACCAAG CCGTCAAACA CCCCAATTGG CGTATGGGAC GCAAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGGAGCTG ATTGAAGCGC
401 ATTGCTGTT CAACTGTCCG CCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCTGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTGTGGGC
501 GCAACTGGGC AATCCCGATA TCGGAACGCC TATCGCTTAT TGTTTGGGTT
551 TGCCCGAGCG CATCGATTCC GGTGTCGGCG ACCTGGATT TCGACGCATTG
601 TCCGCGCTGA CCTTCCAAAA GCCCGACTTT GACCGCTTCC CTGCCTGAA
651 GCTCGCCTAT GAAGCCATGA ACGCAGGCGG AGCCGCGCCC TCGGTATTGA
701 ACGCCGCCAA CGAAGCCGCC GTCGCCGCTT TTTGGACGG ACAGATTAAG
751 TTTACCGACA TTGCCAAAAC CGTCGCCCAT TGTCTTTCAC AAGACTTTC
801 AGACGGCATA GCGGACATAG GGGGGCTCTT GCGCAAGAT GCCCGGACAC
851 GCGCACAAAG GCGGGCATT ATCGGCACAC TCGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1718; ORF 572.a>:

```
a572 . pep
1   MCAIVGAVGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAAVL
51  PVDSEHNAVF QVLPDYTGRLNEHGIASII LTASGGPFLT ADLNTFDSIT
101 PDQAVKHPNW RMGRKISVDS ATMMNKGLELEIAHWLFNCP PDKLEVVIHP
151 QSVIHSMVRY RDGSLAQLG NPD MRTPIAY CLGLPERIDS VGDGLDFDAL
201 SALTFOKPDF DRFPCLKLAY EAMNAGGAAP CVLNAANEA VAAFLDGQIK
251 FTDIAKTVAH CLSQDFSDGI GDIGLLAQD ARTRAQARAF IGTLR*

m572/a572 98.3% identity in 295 aa overlap

10      20      30      40      50      60
m572 . pep MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAVF
a572       MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAVF
10      20      30      40      50      60

70      80      90      100     110     120
m572 . pep QVLPDYAGRLNEHGIASII LTASGGPFLTADLNTFDRITFAQAVKHPNWRMGRKISVDS
a572       QVLPDYTGRLNEHGIASII LTASGGPFLTADLNTFDSITFDQAVKHPNWRMGRKISVDS
70      80      90      100     110     120
```

881

	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPDKLEVVIHPQSVIHSMVRYRDGSLAQLGNPDMRTPIAY					
a572	ATMMNKGLELIEAHWLFNCPDKLEVVIHPQSVIHSMVRYRDGSLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGLDFDALSALTFOKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
a572	CLGLPERIDSGVGLDFDALSALTFOKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDQGIKFTDIAKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
a572	VAAFLDQGIKFTDIAKTVAHCLSQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1719>:

g573.seq..

```

1  atgcctgtt tgtgcgcct taatcgcaat atcggcagtt tccaaatcac
51  gaatctcacc gaccataatg atgtccgggt cctgacgcag gaaagacttc
101 aaagcagcgg caaaagtcag accctgttta tcattgacgt taacctgatt
151 gatgccccgc aggttaatct cggcagggtc ttccgcggtt gcaatattta
201 ccgactccgt attcaaaata ttcaaacagg tatagagcga caccgtctta
251 ccgaaccggc tcggaccggg taccagcacc atcccgtaag gacggtgaat
301 cgcttccaac aacaattttt tctggaacgg ctcaaaaccg agctggtcga
351 tgttcaaaaga cgcggcatcg gaattcaaaa tccgcatcac gaccttttcg
401 ccaaacagcg tcggcaatgt gctgacacgg aaatcgacag gcttgccggc
451 cttttgaaag gtcagctgca tcctaccgtc ctgcggtatc cgtttttcgg
501 aaatgtccaa acgcgacatt accttaatcc ggaagcaag ctgccccctt
551 accgcaatgg gcggctgaac cacctcgcgg agctgccgtt ccacacggaa
601 acggatacgc gcattgtgtt cgtaaaactc gaaatggatg tcggatgccc
651 cgctacgcaa ggcacccgac aaagttttat ggataaacct cggaacaggg
701 cgtctctctg cctcctcgtc gtcgatatac aggggtgggc ttctctcttc
751 ctcttgcccc tccccaaagt cctgaagcag cgatgtcgaa cgcgaacca
801 cccaatcgag caaacccgcc aactggtcat cctcgacaat gaccaactca
851 accgcaatcc ctgcggcaga aaccgttttc tgaatttgcg gcatctgggt
901 cggatcgaaa accgcaaaaa atactttgtc gcccccacgg aaaaccggca
951 cacagtggaa ctccaccatc tgcctctcgg tcaacacccc catcagcacc
1001 ctgtggcgcg gataatgacg caaatcaaga atcgataaac tgaacaccct
1051 cgcaatcaat gccgcaagcg acttgggcga aatgacaccg tctga

```

This corresponds to the amino acid sequence <SEQ ID 1720; ORF 573.ng>:

g573.pep..

```

1  MPCLRLNRN IGSFQITNLT DHNDVRVLTQ BRLQSSGKSQ TLLIIDVNL
51  DARQVNLGRV FRRCNLYRLR IQNIQTGIER HRLTRTRRTG YQHHPVRTVN
101 RFQQQFFLER LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPTV LRYPPFFGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTRIVFVKL EMDVGCPATQ GIRQSFMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNRNPGCR NRFLNLRHLG
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1721>:

m573.seq..

```

1  ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51  GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG GCCTGCTTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAACAGG TATAGAGCGA CACCGTCTTA
251 CCGAACCCTG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGCTACCAAC aCaw.TTTT TCTGAAACGG CTCAAACCG AGCTGGTCTGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAACAGCGC TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTTGAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GTGAAGCAAG CTGCCCCCTT

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882

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551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCGT CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCCTCTTC
751 CTCTGCCCC TCCCAAGCT CCTGAAGCAG CGATGTGAA CGCGAACCCA
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTTGCG GCATCTGTGT
901 CCGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1722; ORF 573>:

m573.pep..

```

1  MPCLCRLNRN IGSFQITNLT DHNDVRLTQ ERLQSSGKSQ ALLIIDVNLI
51  DARQVNLGRV FRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RYQHXFFLKR LKTELVDVQR RGIGIQNPBH DLPKQRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPFPGNVQ TRHYLNP*SK LPPYRNGRLN HLAELPVHTE
201 TDTGIVPVKL EMDVRCPPAQ GIRQSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/g573 95.9% identity in 364 aa overlap

m573.pep	10	20	30	40	50	60
	MPCLCRLNRNIGSFQITNLTDHNDVRLTQERLQSSGKSQALLIIDVNLIIDARQVNLGRV					
g573	MPCLCRLNRNIGSFQITNLTDHNDVRLTQERLQSSGKSQTLIIIDVNLIIDARQVNLGRV					
	10	20	30	40	50	60
m573.pep	70	80	90	100	110	120
	FRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVMRYQHXFFLKRKTELVDVQR					
g573	FRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVMRFQQFFLERLKTTELVDVQR					
	70	80	90	100	110	120
m573.pep	130	140	150	160	170	180
	RGIGIQNPBHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPFPGNVQTRHYLNPXSK					
g573	RGIGIQNPBHDLFAKQRRQCADTEIDRLAALLKGQLHPTVLRYPFGNVQTRHYLNPXSK					
	130	140	150	160	170	180
m573.pep	190	200	210	220	230	240
	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPPAQGIRQSLMDKPRNRAVFCLLV					
g573	LPPYRNGRLNHLAELPVHTETDTRIVFVKLEMDVGCPTAQGIRQSFMDKPRNRAVFCLLV					
	190	200	210	220	230	240
m573.pep	250	260	270	280	290	300
	VDIQGVAFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
g573	VDIQGVAFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNRNPGCRNRFNLRHLG					
	250	260	270	280	290	300
m573.pep	310	320	330	340	350	360
	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
g573	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360
m573.pep	NDTVX					
g573	NDTVX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1723>:

883

a573.seq

```

1 ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51 GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG ACCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAATA TTCAAACAGG TATAGAGCGA CACCSTCTTA
251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGCTTCCAAC AACAATTTTT TCTGAAACGG CTCAAACCG AGCTGGTCGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTTGAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GGAAGCAAG CTGCCCCCTT
551 CCGCAATGGG GCGCTGAAC CACCTCGCG AGCTGCCCGT CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCCTCTTC
751 CTCCTGCCCC TCCCAAGCT CCTGAAGCAG CGATGTCGAA CGGAACCCA
801 CCAATCGAG CAAACCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTT TGAATTTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCGACGG AAAACCGGCA
951 CACAGTGGA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCTT
1051 CGCAATCAAT GCCGAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1724; ORF 573.a>:

a573.pep

```

1 MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI
51 DARQVNLGRV FRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHHFVGTVN
101 RFQQQFFLKR LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPPFGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCFAAQ GIROSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKRYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/a573 98.6% identity in 364 aa overlap

	10	20	30	40	50	60
m573.pep	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQALLIIDVNLI DARQVNLGRV					
a573	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI DARQVNLGRV					
	10	20	30	40	50	60
m573.pep	FRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHXXFLKRLKTELVDVQR					
a573	FRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRFQQQFFLKRLKTELVDVQR					
	70	80	90	100	110	120
m573.pep	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPGSK					
a573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPGSK					
	130	140	150	160	170	180
m573.pep	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCFAAQGIROSLMDKPRNRAVFCLLV					
a573	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCFAAQGIROSLMDKPRNRAVFCLLV					
	190	200	210	220	230	240
m573.pep	VDIQGVAFLELLPLPKLLKQRCRTTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
a573	VDIQGVAFLELLPLPKLLKQRCRTTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
	250	260	270	280	290	300

884

	310	320	330	340	350	360
m573.pep	RIGNRK	KYFVAPT	ENRHTVELH	HLRLRQHP	QHPVARIM	TQIKNRITEHPRNQCRKRLGR
a573	RIGNRK	KYFVAPT	ENRHTVELH	HLRLRQHP	QHPVARIM	TQIKNRITEHPRNQCRKRLGR
	310	320	330	340	350	360

m573.pep	NDTVX
a573	NDTVX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1725>:

g574.seq

```

1  atgctgccga atctgccaaa cagccttaag aaagccgata tggacaacga
51  attgtggatt atcctgctgc cgattatcct tttgcccgtc ttcttcacga
101 tgggtcggtt tgcgcgccgc gtggatatga aaaccgtatt gaagcaggca
151 aaaagcatcc cttcgggatt ttataaaagc ctggacgctt tggtcgaccc
201 caacagcggg cgcgcggcaa gggagttggc ggaagtcgtc gacggccggc
251 cgcaatcgta tgatttgaa cttaccctcg gcaaaactta ccgtcagcgc
301 ggcgaaaacg acaaagccat caacatacac cggacaatgc tcgattctcc
351 cgatacggtc ggcgaaaagc gcgcgcgcgt cctgtttgaa ttggcgcaaa
401 actaccasag cgcgggtttg gtcgatcggt ccgaacagat ttttttgggg
451 ctgcaagacg gtgaatggc gcgtgaagcc agacagcacc tgcacaatat
501 ctaccagcag gacagggatt gggaaaaagc ggttgaaacc gcccaacttc
551 ttagtccaga cgaacagaca tatcagtttg agattgcaca gttttattgc
601 gaacttgccc aagccgcgct gttcaagtcc aatttcgatg ccgcgcggtt
651 caatgtcgcc aaggcaactc aagccaacaa aaaatgcacc cgcgccaaaca
701 tgattttggg cgacattgaa caccgacaag gcaatttccc tgcgcgcgtc
751 gaagcctatg ccgccatcga gcagcaaaac catgcatact tgagcatggg
801 cggcgagaag ctttacgaag cctatgccgc gcagggaaaa cctgaagaag
851 gcttgaaccg tctgacagga tatatgcaga cgtttccgca acttgacctg
901 atcaatgtcg tgtacgagaa atccctgctg ctttaaggcg agaaaagaagc
951 cgcgcaaaac gccgtcgagc ttgtccgcgc caagcccgac cttaacggcg
1001 tgtaccgcct gctcggtttg aaactcagcg atttggatcc ggcttggaag
1051 gccgatgccg acatgatgcg ttccggtatc ggacggcagc tccagcgagc
1101 cgtgatgtac cgttgccgca actgccactt caaatcccaa gtctttttct
1151 ggcactgtcc cgcctgcaac aaatggcaga cgtttacgcc gaataaaatc
1201 gaagttaa
```

This corresponds to the amino acid sequence <SEQ ID 1726; ORF 574.ng>:

g574.pep..

```

1  MLNPLNSILK KADMDNELWI ILLPIILLPV FFTMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAENV DGRPQSYDLN LTLGKLYRQR
101  GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151  LQDGSMAREA RQHLLNIYQQ DRDWEKAVET AQLLSHDEQT YQFETQFYC
201  BLAQALPKS NFDAARFNVG KALBANKKCT RANMILGDIE HRQGNFPAAV
251  BAYAAIEQQN HAYLSMVGEK LYEAYAAQCK PEBGLNRLTG YMQTFPELDL
301  INVVEKSLI LKGBKEAAQT AVELVRRKPD LNGVYRLGL KLSLDLPAWK
351  ADADMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQFTTPNKI
401  EV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1727>:

m574.seq..

```

1  ATGCGCCCGA ATCTACCAA CAGCCTTAAG AAAGCCGATA TGGACAACGA
51  ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTC TTCTTCGCGA
101  TGGGCTGGTT TGCCGCCCGC GTGGATATGA AAACCGTATT GAAGCAGGCA
151  AAAAGCATCC CTTGGGATT TTATAAAAGC TTGGACGCTT TGGTCGACCG
201  CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251  CGCAATCGTA TGATTGAAC CTCACCTCG GCAAACTTTA CCGCCAGCGT
301  GGCAGAAAAG ACAAAGCCAT CAACATACAC CGGACAATGC TCGATTCTCC
351  CGATACGGTC GGCAGAAAAG CCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401  ACTACCAAGG TCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTTCGGG
451  CTGCAAGACC GTAAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501  CTACCAACAG GACAGGGATT GGGAAAAAGC GGTGAAAACC GCCCGGCTGC
551  TCAGCCATGA CGATCAGACC TATCASTTTG AAATCGCCCA GTTTTATATG
601  GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTTCGATG TCGCGCGTTT
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885

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651 CAATGTCCGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCCGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGCATGGT
801 CGCGGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCTG TGTACGAGAA ATCCCTGCTG CTTAAGTGGC AGAAAGAAGC
951 CGCGCAAAAC GCGTCTGAGC TTGTCCGCGC CAAGCCCAC CTTAACGGCG
1001 TGTACCGCCT GCTCGGTTTG AAACCTCAGCG ATATGAATCC GGCTTGGAAA
1051 GCCGATGCCG ACATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGTTGCCGCA ACTGCCACTT CAAATCCCAA GTCTTTTCT
1151 GGCACGTGCC CGCCTGCAAC AAATGGCAGA CGTTTACCCC GAATAAATCT
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1728; ORF 574>:

m574.pep..

```
1 MRPNLPNSLK KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51 KSTPSGFYKS LDALVDRNSG RAARELAEVVDGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGKMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 BLAQAAALFKNFDVARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 BAYAAIEQQN HAYLSMVGEK LYEAYAAQCK PEEGLNRLTG YMQTFPELDL
301 INVVEKSLLL KCEKEAAQT AVELVRRKPD LNGVYRLGL KLSDMNPAWK
351 ADADMMSVI GRQLQSRVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
401 EV*
```

m573/g573 97.8% identity in 402 aa overlap

	10	20	30	40	50	60
m574.pep	MRPNLPNSLKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS					
g574	MLPNLPNSLKKADMDNELWIILLPIILLPVFTMGWFAARVDMKTVLKQAKSIPSGFYKS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m574.pep	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGLKLYRQRGENDKAINIHRTMLDSPDTV					
g574	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGLKLYRQRGENDKAINIHRTMLDSPDTV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m574.pep	GEKRARVLPFELAQNYQSAGLVDRAEQIFLGLQDGKMAREARQHLLNIYQQDRDWEKAVET					
g574	GEKRARVLPFELAQNYQSAGLVDRAEQIFLGLQDGKMAREARQHLLNIYQQDRDWEKAVET					
	130	140	150	160	170	180
	190	200	210	220	230	240
m574.pep	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDVARFNVGKALEANKKCTRANMILGDIE					
g574	AQLSHDEQTYQFEIAQFYCELAQAALFKSNFDAARFNVGKALEANKKCTRANMILGDIE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m574.pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQCKPEEGLNRLTGYMQTFPELDL					
g574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQCKPEEGLNRLTGYMQTFPELDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m574.pep	INVVEKSLLLKCEKEAAQTAVELVRRKPD LNGVYRLGLKLSDMNPAWKADADMMSVI					
g574	INVVEKSLLLKCEKEAAQTAVELVRRKPD LNGVYRLGLKLSDLPAWKADADMMSVI					
	310	320	330	340	350	360
	370	380	390	400		
m574.pep	GRQLQSRVMYRCRNCHFKSQVFFWHCPACNWKQTFTPNKIEVX					
g574	GRQLQSRVMYRCRNCHFKSQVFFWHCPACNWKQTFTPNKIEVX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1729>:

```
a574.seq
1   ATGCGCCCGA ATCTGCCAAA CAGCCTTGAG AAAGCCGATA TGGACAATGA
51  ATTGTGGATT ATCCTGCTGC CGATTATCCT TTGCCCCGTT TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AGACTGTATT AAAGCAGGCA
151 AAAAGCATAC CGTCGGGATT TTATAAAAGT CTGGATGCCT TGGTTGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTTGAAC CTCACCCTCG GCAAACCTTA CCGCCAGCGT
301 GCGGAAAACG ACAAAGCCAT CAATATGCAC CAAACATTGC TTGACTCTCC
351 CGATACAACC GGAGCCAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TGCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTGTGGG
451 CTGCAAGACG GTGAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACCTGCCC AAGCCGCGCT GTTCAAGTCC AATTTCGATG CCGCGCGTTT
651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCGGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGTATGGT
801 CGGCGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGTACGAGAA ATCCCTGCTG CTTAAGTGGC AGAAAGAAGC
951 CGCGCAAACC GCCGTCGAGC TTGTCCGCCG CAAGCCCGAC CTCAACGGCG
1001 TGTACCGCCT GCTTGGTTTG AAATCAGCGC ATTTGGATCC GGCTTGGAAA
1051 GCCGATGCCG ATATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGGTGCCGAA ACTGCCACTT CAAATCACA GTCTTTTCT
1151 GGCATTGTCC TGCCTGCAAC AAATGGCAGA CGTTTACGCC AAACAAAATC
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1730; ORF 574.a>:

```
a574.pep
1   MRPNLPNSLE KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINMH QTLDSPDTT SAKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LDQGEMAREA RQHLNLIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQAAALFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQSK PEEGLNRLTG YMQTFPELDL
301 INVVYEKSL LKCEKEAAQT AVELVRRKPD LNGVYRLGL KLSDLDPAWK
351 ADADMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
401 EV*
```

m574/a574 97.5% identity in 402 aa overlap

	10	20	30	40	50	60
m574.pep	MRPNLPNSL	KADMDNELWI	ILLPIILLPV	FFAMGWFAAR	VDMKTVLKQA	KSIPSGFYKS
a574	MRPNLPNSLE	KADMDNELWI	ILLPIILLPV	FFAMGWFAAR	VDMKTVLKQA	KSIPSGFYKS
	70	80	90	100	110	120
m574.pep	LDALVDRNSG	RAARELAEVV	DGRPQSYDLN	LTLGKLYRQR	GENDKAINIH	RTMLDSPDTV
a574	LDALVDRNSG	RAARELAEVV	DGRPQSYDLN	LTLGKLYRQR	GENDKAINMH	QTLDSPDTT
	130	140	150	160	170	180
m574.pep	GEKRARVLFE	LAQNYQSAGL	VDRAEQIFLG	LQDGKMAREA	RQHLNLIYQQ	DRDWEKAVET
a574	GAKRARVLFE	LAQNYQSAGL	VDRAEQIFLG	LQDGEMAREA	RQHLNLIYQQ	DRDWEKAVET
	190	200	210	220	230	240
m574.pep	ARLLSHDDQT	YQFEIAQFYC	ELAQAAALFKS	NFDAARFNVG	KALEANKKCT	RANMILGDIE
a574	ARLLSHDDQT	YQFEIAQFYC	ELAQAAALFKS	NFDAARFNVG	KALEANKKCT	RANMILGDIE

887

	190	200	210	220	230	240
	250	260	270	280	290	300
m574.pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQKGPEEGLNRLTGVMQTFPELDL					
a574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQKGPEEGLNRLTGVMQTFPELDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m574.pep	INVVYEKSLLLKCEKAAQTAVELVRRKPDINGVYRLLGLKLSDMNPAWKADADMMRSVI					
a574	INVVYEKSLLLKCEKAAQTAVELVRRKPDINGVYRLLGLKLSDLPAWKADADMMRSVI					
	310	320	330	340	350	360
	370	380	390	400		
m574.pep	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFTPNKIEVX					
a574	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFTPNKIEVX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1731>:

```

g575.seq (partial)
1  ..atgccgtgcc tccgccggca agcagcaagg tgtaacgaacc gccgaacaga
51  ccgtcaaaca gtcgcgttcc ggtttcttct tcggcagaaa cctgttcgac
101 aggttcggca acgggttcgg cggcaacttc actggctgtt tccgcaacag
151 gttcggaaac ggtgttaccg gtttcgtcgg tcggcgtgtc gatggcagaa
201 gcggcggttt cttggggggg cggattcggc agcgggttcc gatgcggcag
251 tatttcgacg ggttacaggt cgggttggc gttctgtcgc cgaagccgga
301 gtttcggaca ctgcgggttt ggggttcggg cgaacggccg gtttttcgcg
351 ttttgcttcg ggcgcggcaa cttttgcttc aggtttttca accggttttt
401 cgacaggttt ctctatcggt ttctccacag ttgcctgttt ggacgggtta
451 gacggcatgg atgcagtttc ggccttgggt ttgcgcgttt gcggttggg
501 ttggtccgct ttgatttttt tgggtgctgc cgcttgatc ctgttcagat
551 tcggaatgtg a*

```

This corresponds to the amino acid sequence <SEQ ID 1732; ORF 575.ng>:

```

g575.pep (partial)
1  ..MPCLRRQAAR CTNRRTDROT VRFRELLRQK PVRQVRQVR RQLHNLFPQO
51  VRKRCYRFRR SACRWQKRRL LGGADSAVS DAAVFAAGTG PGWRSVAEAG
101 VSDTAGLGSG RTAGFSAFAS GAATFASGFS TGFSTGFSIG FSTVACLDS
151 DGMDAVSALG FAVCGLGCSA LIPLGAAALI LRFPM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1733>:

```

m575.seq..
1  ATGGTTTCGG GCGAGGAAGC CTTACGGAAG CCTGCCAGTC CGGAGGGTGA
51  GGCAGGTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
101 GCAGGTTGTC GGAGAAATCG GTATCGACGG TTTCCGGTTT GTTTTCGGCA
151 GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTCGACAGG
201 GTTGTTACGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGATTTCGA
251 TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
301 AGTGCGCCGG ATAAAATGCC GTTTTGCGCG GCTGCCAGGC TGTGAAATC
351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGTT
401 TTGCGGATAA CTCTTCTTCA GATTCCCAT CTAAGGCAAG TGTGCTGTTT
451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCCGAGTTT CGACTTCGSC
501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT
551 CCTCAGGAC GGATTCTTCG GTACGGCGCG CGGTTTGGA TTGGGCAAGG
601 CGCAAAAGCA GCAGCAGGGC GATTAATGCC GCGCCTCCGC CGGCAAGCAG
651 CAAGGTGTAC GAACCGCGA ACAGACCGTC AAACAGTCG CTTTCGGTTT
701 CTTCTTCGCG AGAAACCTGT TCGACAGGTT CGGAAACGGC GTTACCGGTT
751 TCGTCGGTCG GCGTGTGAT GGCAGAACGG GCGGCTTCTT GGGGGCGGSA
801 TTCGGCAGCG GTTTCGATG CCGCAGTATT TGCAGCGGGT ACAGGTTTCG
851 CTCGAACGCG CGGTTTTTCC GCTTTTGCTT CGGCGCGGCG AACTTTTGCT
901 TCAGGTTTTT CAACCGGTTT CTCTACCGTT GCCTGTTTGG ACGGTTTCGSA
951 CGGCATGGAT GCGGTTTCGG CTTTGGGTTT CGCGGTTTGC GGTTCGGGTT
1001 GTTCCGCTTT GATCCTGTTT AGATTGGA TGTGA

```


888

This corresponds to the amino acid sequence <SEQ ID 1734; ORF 575>:

m575.pep
 1 MVSGEAEFRK PASPEGEAGF AEAVSSVPIW LFEGRLESEK VSTVSGLFSA
 51 VWATDSGSGV SMTISTGLYG LKVGSGYTLS VDSMAFQSAS ARFWVSSSCV
 101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSS DSPSKASVSF
 151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
 201 RKSSSRAINA APPPASSKVY EPPNRPNSNP LSVSSSAETC STGSETALPV
 251 SSVGVSMABA AASWGADSA VSDAAVFAAG TGSORTAGFS AFASGAATFA
 301 SGFSTGFTV ACLDGSQMD AVSALGFAVC GLGCSALILF RFGM*

m575/g575 70.2% identity in 114 aa overlap

	240	250	260	270	280	
m575.pep	SSAETCSTGSETALPVSSVGVSMAEAAASWGADSAVSDAAVFAAGTG	-----				
g575	LHWLFPPQVRKRCYRPRRSACRWQKRLLGGADSAVSDAAVFAAGTGPWRSVAEAGVS					
	50	60	70	80	90	100

	290	300	309	310	320	
m575.pep	-----SORTAGFSAFASGAATFASGFSTGFST-----	VACLDGSDGMDAVSALGFA				
g575	DTAGLGSGRTAGFSAFASGAATFASGFSTGFSTGFSIGFSTVACLDGSDGMDAVSALGFA					
	110	120	130	140	150	160

	330	340	
m575.pep	VCGLGCSALI-----LFRFGMX		
g575	VCGLGCSALIFLGAALILFRFGMX		
	170	180	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1735>:

a575.seq
 1 ATGTTTTCGG GCGAGGAAGC CTTGAGGAAG CCTGCCAGTC CGGAGGGTGA
 51 GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTGAGG
 101 GCAGGTTGTC GGAGAAATCG GTATCGACGG TTTCCGGTTT GTTTTCGGCA
 151 GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTCGACAGG
 201 GTTGTACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTGA
 251 TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCTGCGTA
 301 AGTGGCGCGG ATAAATGCC GTTTTGGCGG GCTGCCAGGC TGTGAAATC
 351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGTT
 401 TTGCCGACAA CTCTTCTTCA GATTCCCAT CTAAGGCAAG TGTGTCGTTT
 451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGGAGTTT CGACTTCGGC
 501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAGG TCAGGCTCTT
 551 CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGA TTGGGCAAGG
 601 CGCAAAGCA GCAGCAGGGC GATCAATGCC GCGCTCCGC CGGCAAGCAG
 651 CAAGGTGTAC GAACGCGCA ACAGTCCGCT TTCGGTTTCT TCTTCGGCAG
 701 AAACCTGTTT GACAGGTTTC GAAACGGCGT TACCGGTTTC GTCGGTCGGC
 751 TGTCGATGG CAGAAGCGGC GGCTTCTTGG GGGGCGGATT CGGCAGCGGT
 801 TTCCGATGCG CAGTATTTG CAGCGGTAC AGGTCGGGT CGAACGCGCG
 851 GTTTTCCGC TTTTGCTTCG GCGCGGCA CTTTGTCTC AGGTTTTCTA
 901 ACCGGTTTCT CTACCGTTGC CTGTTTGGAC GGTTCGGAC GCATGGATGC
 951 GGTTCGGCT TTGGGTTTCG CCGTTGCGG TTTGGGTTGT TCCGCTTTGA
 1001 TCCTGTTTCA ATTCGGAATG TGA

This corresponds to the amino acid sequence <SEQ ID 1736; ORF 575.a>:

a575.pep
 1 MVSGEAEFRK PASPEGEAGF AEAVSSVPIW LFEGRLESEK VSTVSGLFSA
 51 VWATDSGSGV SMTISTGLYG LKVGSGYTLS VDSMAFQSAS ARFWVSSSCV
 101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSS DSPSKASVSF
 151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
 201 RKSSSRAINA APPPASSKVY EPPNSPLSVS SSAETCSTGS ETALPVSSVG
 251 VSMAEAAASW GADSAVSDA AVFAAGTGS RTAGFSAFAS GAATFASGFS
 301 TGFSTVACLD GSDGMDAVSA LGFAVCGLGC SALILFRFGM *

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m575/a575 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
m575.pep	MVSGEEAFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV					
a575	MVSGEEAFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV					
	70	80	90	100	110	120
m575.pep	SMTISTGLYGLKVGSYTSLVDSMAFQASARFWVSSSCVSAPOKMPFCAAARLSKSKSM					
a575	SMTISTGLYGLKVGSYTSLVDSMAFQASARFWVSSSCVSAPOKMPFCAAARLSKSKSM					
	130	140	150	160	170	180
m575.pep	RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSAASSR					
a575	RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSAASSR					
	190	200	210	220	230	240
m575.pep	SGSSSGTDSSVRRARLDWARRKSSSRINAAPPPASSKVYEPNRPNSPLSVSSSAETC					
a575	SGSSSGTDSSVRRARLDWARRKSSSRINAAPPPASSKVYEPN----SPLSVSSSAETC					
	250	260	270	280	290	300
m575.pep	STGSETALPVSSVGVSMAEAAASWGADSAAVDAVFAAGTSGSRTAGFSAFASGAATFA					
a575	STGSETALPVSSVGVSMAEAAASWGADSAAVDAVFAAGTSGSRTAGFSAFASGAATFA					
	310	320	330	340		
m575.pep	SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLGCSALILFRFGMX					
a575	SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLGCSALILFRFGMX					
	300	310	320	330	340	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1737>:

g576.seq.. (partial)

```

1 ..atgggcgtgg acatcggacg ctccctgaaa caaatgaagg aacaggcgcg
51 ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaagaaat caaatgacc gaagagcagg cccaggaagt gatgatgaaa
151 ttctctgcagg agcagcaggc taaagccgta gaaaaacaca aggcggatgc
201 gaagcccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgcccgcg
251 aagacggcgt gaagaccact gttccgggtc tgcagtacaa aatcaccaaa
301 cagggtgaag gcaaacagcc gacaaaagac gacatcgta ccgtggaata
351 cgaaggccgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcggcccgcc caccctccct ttgagccaag tgattccggg ttggaccgaa
451 ggcgtagcgc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggtgacggg cgaaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactgggtc aaatcgggcg acccgaaaaac
601 gcgcccgcca agcagccgga tcaagtcgac atcaaaaaag taaattaa

```

This corresponds to the amino acid sequence <SEQ ID 1738; ORF 576.ng>:

g576.pep.. (partial)

```

1 ..MGVDIGRSLK QMKEQGAIED LKVFTDAMQA VYDGKEIKMT EEQAQEVNMK
51 FLQEQQAKAV EKHKADAKAN KEKGEAFLKE NAAEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIVTVEYEGR LIDGTVFDSS KANGGPATFP LSOVIPGWTE
151 GVRLLKEGGE ATFFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKVN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1739>:

m576.seq.. (partial)

```

1 ..ATGCAGCAGG CAAGCTATGC GATGGCGGTG GACATCGGAC GCTCCCTGAA

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51   GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
101  CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
151  GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
201  AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251  TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
301  CTGCAATACA AAATACCCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
351  CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
401  TCGACAGCAG CAAAGCCAAC GCGGCCCCGG TCACCTTCCC TTTGAGCCAA
451  GTGATTCGGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGCGCA
501  AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
551  GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
601  AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
651  CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1740; ORF 576>:

m576.pep... (partial)

```

1   ..MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
51  AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLEKNA KDGVKTTASG
101 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVDVKLV
201 KIGAPENAPA KQPAQVDIKK VN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 97.2% identity in 215 aa overlap

	10	20	30	40	50	60
m576.pep	MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ A QEVMMKFLQ					
g576	:					
	10	20	30	40	50	
	70	80	90	100	110	120
m576.pep	EQQAKAVEKH KADAKANKEK GEAFLEKNA KDGVKTTASGLQYKITKQEGKQPTKDDIV					
g576	EQQAKAVEKH KADAKANKEK GEAFLEKNA EDGVTASGLQYKITKQEGKQPTKDDIV					
	60	70	80	90	100	110
	130	140	150	160	170	180
m576.pep	TVEYEGRLID GTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLKEGGEATFYIPSNLAYRE					
g576	TVEYEGRLID GTVFDSSKANGGPATFPLSQVIPGWTEGVRLLEKGEATFYIPSNLAYRE					
	120	130	140	150	160	170
	190	200	210	220		
m576.pep	QGAGDKIGPNATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
g576	QGAGEKIGPNATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN					
	180	190	200	210		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1741>:

a576.seq

```

1   ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTCCG CCGCTTTGGC
51  ACTTTCGCCG TGCGCAAAA AAGAAGCCGC CCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTCCGCG CAGGGCGACA CCTCTCGAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC GATGGCGGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATACCCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GCGGCCCCGG TCACCTTCCC TTTGAGCCAA

```

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```

601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTGTATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1742; ORF 576.a>:

```

a576.pep
1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEFAAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLEKNAE KDGVKTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

m576/a576 99.5% identity in 222 aa overlap

m576.pep
10 20 30
MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
|||||
a576 CGKKEAAPAS ASEFAAASSA QGDTSSIGST MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
30 40 50 60 70 80

40 50 60 70 80 90
m576.pep FTEAMQAVYD GKEIKMTEEQ AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLEKNAE
|||||
a576 FTEAMQAVYD GKEIKMTEEQ AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLEKNAE
90 100 110 120 130 140

100 110 120 130 140 150
m576.pep KDGVKTTASGL QYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
|||||
a576 KDGVKTTASGL QYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
150 160 170 180 190 200

160 170 180 190 200 210
m576.pep VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV KIGAPENAPA
|| |||||
a576 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV KIGAPENAPA
210 220 230 240 250 260

220
m576.pep KQPAQVDIKK VN*
|||||
a576 KQPAQVDIKK VN*
270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1743>:

g576-1.seq

```

1 ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51 ACTTTCCGCC TGCAGCAAAA AAGAAGCCGC CCCCAGCATCT GCATCCGAAC
101 CTGCCCAGCG TTCTGCCGCG CAGGCGGACA CCTCTTCAAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC AATGGCGGTG GACATCGGAC GCTCCCTGAA
201 ACAAATGAAG GAACAGGGCG CGGAATCGA TTTGAAAGTC TTTACCGATG
251 CCATGCAGGC AGTGTATGAC GGCAAGAGAA TCARAATGAC CGAAGAGCAG
301 GCCCAGGAAG TGATGATGAA ATTCCTGCAG GAGCAGCAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT
401 TCCTGAAGGA AATGCGCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGT
451 CTGCAGTACA AATCACCAA ACAGGCTGAA GGCAACAGC CGACAAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGCCCGCG CCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACGG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTGACGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1744; ORF 576-1.ng>:

```
g576-1.pep
1  MNTIFKISAL TLSAALALSA CGKKEAPAS ASEPAASAA QGDTSSIGST
51  MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKOPTKDDIV TVEYEGRLID GTVFDSSKAN GGPATFPLSQ
201 VIPGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPDQVDIKK VN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1745>:

```
m576-1.seq
1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTCCG CCGCTTTGGC
51  ACTTTCGCCG TCGCGCAAAA AAGAAGCCGC CCCCAGCATCT GCATCCGAAC
101 CTGCGGCGCG TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTTCTGAAAG AAATCCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAACACAG CGACCAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GCGGCGCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCGGG GTTGGACCGA AGCGGTACAG CTTCTGAAAG AAGGCGGCCG
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCSACAAAT CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAGTCCGA
801 CATCAAAAAA GTAAATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1746; ORF 576-1>:

```
m576-1.pep
1  MNTIFKISAL TLSAALALSA CGKKEAPAS ASEPAASAA QGDTSSIGST
51  MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKOPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*
```

g576-1/m576-1 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISAL	TLSAALALS	SACGKKEA	PASASEPA	ASAAQGD	TSSIGSTM
m576-1	MNTIFKISAL	TLSAALALS	SACGKKEA	PASASEPA	ASAAQGD	TSSIGSTM
	70	80	90	100	110	120
g576-1.pep	DIGRSLQMK	EQGAEIDL	KVFTDAM	QAVYDGE	KIKMTEE	QAQEVMM
m576-1	DIGRSLQMK	EQGAEIDL	KVFTDAM	QAVYDGE	KIKMTEE	QAQEVMM
	130	140	150	160	170	180
g576-1.pep	KADAKANKE	KGAEFLK	ENAAKDG	VKTASGL	QYKITKQ	GEGKOPT
m576-1	KADAKANKE	KGAEFLK	ENAAKDG	VKTASGL	QYKITKQ	GEGKOPT
	190	200	210	220	230	240
g576-1.pep	GTVFDSSK	ANGGPAT	FPLSQVI	PGWTEGV	RLLEKGE	ATFYIPS
m576-1	GTVFDSSK	ANGGPAT	FPLSQVI	PGWTEGV	RLLEKGE	ATFYIPS
	250	260	270			
g576-1.pep	ATLVFDVK	LKIGAPEN	APAKQPD	QVDIKK	VNX	
m576-1	ATLVFDVK	LKIGAPEN	APAKQPD	QVDIKK	VNX	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1747>:

a576-1.seq

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```

1  ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCGG CCGCTTTGGC
51  ACTTTCCCCC TCGCGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCCGC CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGCGGTG GACATCGGAC GCTCCCTGAA
201 GCAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GCGGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAG ACAGGGCGAA GGCACACAGC CGACCAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GCGCGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGTTGCGG
701 GCGACAAAT CCGGCCGAAC GCCACTTTGG TATTGTATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCGCC AAGCAGCCGG CTCAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1748; ORF 576-1.a>:

a576-1.pep

```

1  MNTIFKISAL TSLAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKOMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

a576-1/m576-1 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISALTSLAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTSLAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a576-1.pep	DIGRSLKOMKEQGAIEDLVFTEAMQAVYDQKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKOMKEQGAIEDLVFTEAMQAVYDQKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
	130	140	150	160	170	180
a576-1.pep	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
	190	200	210	220	230	240
a576-1.pep	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
	250	260	270			
a576-1.pep	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

Expression of ORF 576

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. ORF 576 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 3A shows the results of affinity purification and Figure 3B shows the expression in E.coli. Purified His-fusion protein was used to immunize mice, whose sera were used for ELISA (positive result), FACS analysis (Figure 3C), western blot (Figure 3D). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The

hydrophilicity plots, antigenic index, and amphipatic regions of ORF 576 are provided in Figure 7. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1749>:

```
g577.seq..
1   atggaagga gcggtgtatt tggtaaaatt gtcggcaatc gcatactccg
51  tatgccgtcc gaacacgctg ccgcattcta tccgaaaccg tgcaaatcgt
101 ttaactaac gcaatcttgg ttcagagtgc gaagctgtcc gtgcggcggtt
151 tttatttacg gagcaaacat gaaacttata tataccgtca tcaaaatcat
201 tatcctgctg ctcttctgcg tgcttgccgt cattaatatg gatgccgtta
251 ccttttcccta tcttcggggg cagagtgtca atctgccgct gattgtcgta
301 ttgttcggcg cgtttgcgtg cggcatcgtg ttcggaatgt ttgccctggt
351 cgggcggctg ctgtccttgc gcggcgaaaa cagccgcctg cgtgcggaag
401 tgaagaaaag tgcgcgcttg agcggacaga aattgactgc accgccgata
451 caaaatgctg ccgaatctgc caaacagcct taa
```

This corresponds to the amino acid sequence <SEQ ID 1750; ORF 577.ng>:

```
g577.pep
1   MERSGVFGKI VGNRILRMPS EHAAAFYPKP CKSFKLTQSW FRVRSPCGV
51  FIYGANMKLI YTVIKIIILL LFLLLAVINM DAVTFSYLPG QSVNEPLIVV
101 LFGAFVVGIV FGMFALFGRL LSLRGENSRL RAEVKKSARL SGQKLTAPPI
151 QNAAESAKQP *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1751>:

```
m577.seq..
1   ATGGAAAGGA ACGGTGTATT TGGTAAATTT GTCGGCAATC GCATACTCCG
51  TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAATCGT
101 TTAAGTACG GCAATCTTGG TTCAGAGTGC GAAGCTGTCT GGGCGGCGTT
151 TTTATTTACG GAGCAAACAT GAACTTATC TATACCGTCA TCAAAATCAT
201 TATCCTGCTG CTCTTCCTGC TGCTTGCCGT CATTAAATACG GATGCCGTTA
251 CCTTTTCCTA CCTGCGGGG CAAAATTCG ATTGCGCGCT GATTGTGCTA
301 TTGTCGGCG CATTGTAGT CGGTATTATT TTTGGAATGT TTGCCTTGT
351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTG CGTGCCGAAG
401 TAAAGAAAAA TCGCGTTTG ACGGGGAAG AGCTGACCGC ACCACCGCG
451 CAAAATGCGC CCGAATCTAC CAAACAGCCT TAA
```

This corresponds to the amino acid sequence <SEQ ID 1752; ORF 577>:

```
m577.pep..
1   MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSFKLAQSW FRVRSCLGGV
51  FIYGANMKLI YTVIKIIILL LFLLLAVINT DAVTFSYLPG QKFDPLIVV
101 LFGAFVVGII FGMFALFGRL LSLRGENGRL RAEVKKNARL TGKELTAPPA
151 QNAPESTKQP *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m577/g577 88.1% identity in 160 aa overlap

	10	20	30	40	50	60
m577.pep	MERN	GVFGKIVGNRILRMSS	EHAAASYPKP	CKSFKLAQSW	FRVRSCLGGV	FIYGANMKLI
g577	MERS	GVFGKIVGNRILRMPS	EHAAAFYPKP	CKSFKLTQSW	FRVRSPCPGV	FIYGANMKLI
	10	20	30	40	50	60
	70	80	90	100	110	120
m577.pep	YTVIKIIILL	LFLLLAVINT	DAVTFSYLPG	QKFDLPLIVV	LFGAFVVGII	FGMFALFGRL

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```

|||||
g577  YTVIKIIILLFLLAVINMDAVTFSYLPQSVNPLIVVLFGAFVVGIVFGMFALFGR
      70      80      90      100     110     120

      130     140     150     160
m577.ppep LSLRGENGRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
|||||
g577  LSLRGENSRLRAEVKKSARLSGQKLTAPPIQNAESAQKQPX
      130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1753>:

```

a577.seq
1  ATGGAAAGGA  ACGGTGTATT  TGGTAAAATT  GTCGGCAATC  GCATACTCCG
51  TATGTCGTCC  GAACACGCTG  CCGCATCCTA  TCCGAAACCG  TGCAAATCGT
101 TTAAACTAGC  GCAATCTTGG  TTCAGAGTGC  GAAGCTGTCC  GGGCGGCGTT
151 TTTATTTACG  GAGCAAACAT  GAAACTTATC  TATACCGTCA  TCAAATCAT
201 TATCCTGCTG  CTCTTCCTGC  TGCTTGCTGT  CATTAAATACG  GATGCCGTTA
251 CCTTTTCCTA  CCTGCCGGGG  CAAAATTTCG  ATTTGCCGCT  GATTGTCGTA
301 TTGTTGCGCG  CGTTTGTCTG  CGGCATCGTG  TTCGGAATGT  TTGCCTTGTT
351 CGGACGGTTG  TTGTCGTTAC  GTGGCGAGAA  CGGCAGGTTG  CGTGCCGAAG
401 TAAAGAAAAA  TCGCGGTTTG  ACGGGGAAGG  AGCTGACCGC  ACCACCGGCG
451 CAAATGCGC  CCGAATCTGC  CAAACAGCCT  TGA

```

This corresponds to the amino acid sequence <SEQ ID 1754; ORF 577.a>:

```

a577.ppep
1  MERNGVFGKI  VGNRILRMSS  EHAAASYPKP  CKSFKLAQSW  FRVRSPPGGV
51  FIYGANMKLI  YTVIKIIILL  LFLLLAVINT  DAVTFSYLPQ  QKFDLPLIVV
101 LFGAFVVGIV  FGMFALFGR  LSLRGENGRL  RAEVKKNARL  TGKELTAPPA
151 QNAPESAKQP  *

```

m577/a577 98.1% identity in 160 aa overlap

```

      10      20      30      40      50      60
m577.ppep MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSFKLAQSWFRVRSCLGGVFIYGANMKLI
|||||
a577  MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSFKLAQSWFRVRSPPGGVFIYGANMKLI
      10      20      30      40      50      60

      70      80      90      100     110     120
m577.ppep YTVIKIIILLFLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIIIFGMFALFGR
|||||
a577  YTVIKIIILLFLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIVFGMFALFGR
      70      80      90      100     110     120

      130     140     150     160
m577.ppep LSLRGENGRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
|||||
a577  LSLRGENGRLRAEVKKNARLTGKELTAPPAQNAPESAKQPX
      130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1755>:

```

g578.seq..
1  atgggaaagc  tcgacatcgg  gatattgttt  gcgattttct  tcaaagattt
51  cgcgccacag  ttcggtggtt  tccaaaacgt  tggctttgce  tacggagcag
101 acttttttgc  tgcgtttttg  ggcgatttgg  aaggccacgt  gggcgatgcg
151 ggcgatttcg  cttecgctgt  atttcattgt  gttgtagcct  tcgtgttcgc
201 cgttttccaa  aacacggatg  ccgcgcggtt  cgccgaaata  aatatcgccg
251 gtaagtctgc  gcacaatcaa  aatatccaaa  ccggcaacga  ttccaggctt
301 gagcgtggag  gcgttggtta  a

```

This corresponds to the amino acid sequence <SEQ ID 1756; ORF 578.ng>:

```

g578.ppep
1  MGKLDIGILF  ADFFKDFAPQ  FGGFQNVGFA  YGADFFAAFL  GGLEGHVGDA
51  ADFAFAVFHG  VVAFVFAVFQ  NTDAARFAEI  NIAGKFAHNQ  NIQTGNDFRL

```


896

101 ERGGVG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1757>:

```
m578.seq..
1  ATGGGAAAGC TCGACATCAG GGTACTCTTT GCCGATTCTT TCAAAGATTT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAACAG
101 ACTTTTTTGC TGCCTTTTTC GCGGATTGG  AAGCAACAT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTTCATGGT GTTGTAGCCT TCGCGTTCCG
201 CGTTTTCAG AACCGGATG CCGCGCGTT CGCCGAAATA GATGTCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCGCAACGA TTTCAGGCTT
```

This corresponds to the amino acid sequence <SEQ ID 1758; ORF 578>:

```
m578.pep..
1  MGKLDIRVLF ADFFKDFAPQ FGGFQNVGFA YGTDFFAFL GGLEGNMGNT
51  ADFAFAVFHG VVAFAFAVFQ NADAARFAEI DVAGEFAHNQ NIQTGNDFRL
101 QRGGVG*
```

m578/g578 87.7% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAFLGGLEGNMGNTADFAFAVFHG					
	: :					
g578	MGKLDIGILFADFFKDFAPQFGGFQNVGFAYGADFFAFLGGLEGHVGDAADFAFAVFHG					
	10	20	30	40	50	60

	70	80	90	100
m578.pep	VVAFAFAVFQ NADAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX			
	: :			
g578	VVAFAFAVFQNTDAARFAEINIAGKFAHNQNIQTGNDFRLERGGVGX			
	70	80	90	100

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1759>:

```
a578.seq
1  ATGGGAAAGC TCGACATCAG GGTATTCTTT GCCGATTCTT TCAAAGATTT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAGCAG
101 ACTTTTTTGC TGCCTTTTTC GCGGATTGG  AAGGCGACGT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTTCATGGT GTTGTAGCCT TCGCGTTCCG
201 CGTTTTCCAG AACACGGATG CCGCGCGTT CGCCGAAATA AATATCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCCGCAACGA TTTCAGACTT
301 GAGCGTGGAG GCGTTGGCTA G
```

This corresponds to the amino acid sequence <SEQ ID 1760; ORF 578.a>:

```
a578.pep
1  MGKLDIRVFF ADFFKDFAPQ FGGFQNVGFA YGADFFAFL GGLEGDVGNT
51  ADFAFAVFHG VVAFAFAVFQ NTDAARFAEI NIAGEFAHNQ NIQTRNDFRL
101 ERGGVG*
```

m578/a578 91.5% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAFLGGLEGNMGNTADFAFAVFHG					
	: :					
a578	MGKLDIRVFFADFFKDFAPQFGGFQNVGFAYGADFFAFLGGLEGDVGNTADFAFAVFHG					
	10	20	30	40	50	60

	70	80	90	100
m578.pep	VVAFAFAVFQ NADAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX			
	: :			
a578	VVAFAFAVFQNTDAARFAEINIAGEFAHNQNIQTRNDFRLERGGVGX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1761>:

```
g579.seq..
1  ATGAGGCGCG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
```

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```

51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGACG GTTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GCGCGGGGTT TGGCGGTGGC GTTGTCTTA AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCGCTGATTA TCCTGTTCG CCCGTTCAAA GTCGGCGACT
251 TTATCCGTGT CGGCGGTTT GAAGGATATG TCCGGGAAAT CAAAATGGTG
301 CAGACTTCTT TCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCAGCTG CCGCTTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATT GAAAGTGGCG
451 AAAGAGGCGG TGTGAAAGC CGCCGCGAA CACCCCTGA GCGTTCAAAA
501 CGAAGAGCGG CAGCCCGCGC CTACATCAC CGCCTTGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1762; ORF 579.ng>:

g579.pep..

```

1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAAE HPLSVQNEER QPAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1763>:

m579.seq..

```

1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGCAG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GCGCGGGGTT TGGCGGTGGC GTTGTCTTA AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCACTGATTA TCCTGTTCG CCCGTTCAAA GTCGGCGACT
251 TTATCCGTGT CGGCGGTTT GAAGGATATG TCCGAGAGAT TAAAATGGTG
301 CAGACTTCTT TCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATT GAAAGTGGCG
451 AAAGAGGCGG TGTGAAAGC CGCCGTCGAA CACCCCTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCTGCCG CTACATCAC CGCCTTGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1764; ORF 579>:

m579.pep..

```

1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAAE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m579/g579 98.7% identity in 231 aa overlap

	10	20	30	40	50	60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
g579	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m579.pep	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
g579	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	: : : : : :					
g579	GNSIVNRSSLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAAEHPLSVQNEERQPAAYITALG					
	130	140	150	160	170	180

	190	200	210	220	230
m579.pep	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX				
	: : : : :				
g579	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX				
	190	200	210	220	230

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1765>:

```
a579.seq
1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTGGTG ATTATGCCG
101 CATTGGGCAG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GCGCGCGGGT TGGCGGTGGC GTTGTCTTG AAAGACCAGC TGTCCAATTT
201 TGCCGCGGGC GCGCTGATTA TCCTGTCCG CCCGTTCAAA GTCGGCGATT
251 TTATCCGCGT CGGCGGTTTT GAAGGATATG TCCGAGAGAT TAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATT T GAAAGTGGCG
451 AAAGAGGCGG TGTTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCCGCGC CCTACATCAC CGCCTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1766; ORF 579.a>:

```
a579.pep
1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSTL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*
```

m579/a579 100.0% identity in 231 aa overlap

	10	20	30	40	50	60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
	: : : : :					
a579	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60

	70	80	90	100	110	120
m579.pep	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
	: : : : :					
a579	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
	70	80	90	100	110	120

	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	: : : : :					
a579	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	130	140	150	160	170	180

	190	200	210	220	230
m579.pep	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX				
	: : : : :				
a579	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX				
	190	200	210	220	230

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1767>:

g579-1.seq

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```

1  ATGGA CTTC AACAATTGA TTTTACAC CTGATCAGT TTTCCGGTTG
51  GCGGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTCTTGGTC GGGAAATGGG CGGCGAAACG CATTGTCGCC
151 GTAATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTTGGG ACGGTTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGGCGCGG GTTGGCGGT GCGTTGTCC TTAAGAGACC AGCTGTCCAA
351 TTTTCCGCC GCGCGCTGA TTATCTGTT CCGCCCGTTC AAAGTCGGCG
401 ACTTTATCCG TGTGCGCGGT TTTGAAGGAT ATGTCGGGGA AATCAAPATG
451 GTGCAGACTT CTTTGGGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCAGC CTGCCGCTTT
551 GCGCGCCCCA AGTGATAGTC GCGTCGATT ACAATGCGA TTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCCGCGCC GAACACCCCT TGAGCGTTCA
651 AACGAAGAG CCGCAGCCCG CCGCTACAT CACCGCCTTG GCGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAACCTCC GCAAGTCAA
801 TATCAACATC CCGTCCCGC AACGCGACAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1768; ORF 008.ng>:

g579-1.pep

```

1  MDFKQDFDLH LISVSGWHL AEKAWAFGLN LAAALLIFLV GKWAARKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLRTDN EEVLPNSV MGNSIVNRSS LPLCRAQVIV GVDYNCDELK
201 AKEAVLKAAE EHPLSVQNEE RQAAAYITAL GDNAIETLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQDIHII NS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1769>:

m579-1.seq

```

1  ATGGA CTTC AACAATTGA TTTTACAC CTGATCAGT TTTCCGGTTG
51  GGAGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTTGTGGTC GGGAAATGGG CGGCGAAACG CATTGTCGCT
151 GTGATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTTGGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGGCGCGG GTTGGCGGT GCGTTGTCC CTGAAAGACC AGCTGTCCAA
351 TTTTCCGCC GCGCGACTGA TTATCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTATCCG CTGCGCGGT TTTGAAGGAT ATGTCGGAGA GATTAATGATG
451 GTGCAGACTT CTTTGGGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCACA CTGCCGCTGT
551 GCGCGCCCCA AGTGATAGTC GCGTCGATT ACAATGCGA TTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCCGCGTC GAACACCCCT TGAGCGTTCA
651 AACGAAGAG CCGCAGGCTG CCGCTACAT CACCGCCTTG GCGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAACCTCC GCAAGTCAA
801 TATCAACATC CCGTCCCGC AACGCGACAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1770; ORF 579-1>:

m579-1.pep

```

1  MDFKQDFDLH LISVSGWEHL AEKAWAFGLN LAAALLIFLV GKWAARKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLRTDN EEVLPNSV MGNSIVNRST LPLCRAQVIV GVDYNCDELK
201 AKEAVLKAAE EHPLSVQNEE RQAAAYITAL GDNAIETLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQDIHII NS*

```

m579-1/g579-1 98.6% identity in 282 aa overlap

	10	20	30	40	50	60
m579-1.pep	MDFKQDFDLH	LISVSGWEHL	AEKAWAFGLN	LAAALLIFLV	GKWAARKRIVA	VMRAAMTRAQ
g579-1	MDFKQDFDLH	LISVSGWEHL	AEKAWAFGLN	LAAALLIFLV	GKWAARKRIVA	VMRAAMTRAQ
	70	80	90	100	110	120
m579-1.pep	VDATLISFLC	NVANIGLLIL	VIIAALGRLG	GVSTTSVTALI	GGAGLAVALS	LKDQLSNFAA
g579-1	VDATLISFLC	NVANIGLLIL	VIIAALGRLG	GVSTTSVTALI	GGAGLAVALS	LKDQLSNFAA
	130	140	150	160	170	180
m579-1.pep	GALIILFRPF	KVGDFIRVGG	FEGYVREIKM	VQTSRLRTDN	EEVLPNSV	MGNSIVNRST

900

```

|||||
g579-1  GALIILFRPFKVGDFIRVGGFESYVREIKMVQTSRLTTDNEEVVLPNSVVMGNSIVNRSS
          130      140      150      160      170      180
          190      200      210      220      230      240
m579-1.pep LPLCRAQVIIVGVNDYNDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIETTLW
          |||||
g579-1  LPLCRAQVIIVGVNDYNDLKVAKEAVLKAAEHPLSVQNEERQPAAYITALGDNAIETTLW
          190      200      210      220      230      240
          250      260      270      280
m579-1.pep AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX
          |||||
g579-1  AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1771>:

```

a579-1.seq
1  ATGGACTTCA AACAAATTTGA TTTTTCAC CTGATAAGTG CTTCCGGCTG
51  GGAGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCGG
101 CGCTGCTTAT TTTTTCGTC GGAATAAGG CGGCGAAACG CATTGTCGCC
151 GTGATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTTCGTCG AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTTGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 CGCGGCGCGG GTTGGCGGCT GCGCGTGTCC TTGAAAGACC AGCTGTCCAA
351 TTTTCCCGCC GCGCGCGCTG TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTCGGCGGT TTTGAAGGAT ATGTCCGAGA GATTAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTCCACA CTGCCGCTGT
551 CCGCGCGCCA AGTGATAGTC GCGCTCGATT ACAACTGCGA TTTGAAAGTG
601 CCGAAAGAGG CGGTGTTGAA AGCGCGCGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGGCGC CCGCTACAT CACCGCCTTG GCGGACAATG
701 CCATCGAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTCCCGC AACGCGACAT ACACATCATC AATCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1772; ORF 579-1.a>:

```

a579-1.pep
1  MDFKQDFDLH LISASGWEHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLTTDN EEVVLPSVSV MGNSIVNRST LPLCRAQVIV GVDYNDLKV
201 AKEAVLKAAV EHPLSVQNEE RQAAAYITAL GDNAIETLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQRDIHII NS*

```

a579-1/m579-1 99.6% identity in 282 aa overlap

```

          10      20      30      40      50      60
a579-1.pep MDFKQDFDLHLISASGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ
          |||||
m579-1  MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ
          10      20      30      40      50      60
          70      80      90      100     110     120
a579-1.pep VDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          |||||
m579-1  VDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          70      80      90      100     110     120
          130     140     150     160     170     180
a579-1.pep GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPNSVVMGNSIVNRST
          |||||
m579-1  GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPNSVVMGNSIVNRST
          130     140     150     160     170     180
          190     200     210     220     230     240
a579-1.pep LPLCRAQVIIVGVNDYNDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIETLW
          |||||
m579-1  LPLCRAQVIIVGVNDYNDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIETLW
          190     200     210     220     230     240
          250     260     270     280
a579-1.pep AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX

```

901

m579-1 |||||
 AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQDIHIINSX
 250 260 270 280

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1773>:

g580.seq
 1 atggattcgc ccaaggtcgg gtgcgggtgg atggttttgc cgatgtctgc
 51 cgcgtcgcag ccatttcga tggcaaggca gacttcgccg atcatgtcgc
 101 caccgttcgg accgacaatg ccgccgccga tgatgcggcc ggtttcggca
 151 tcgaaaatca gcttggtaaa gccgtgtcgc caaccgttgg caatcgcacg
 201 accggaagcc gcccatggga agttggcttt ggttaattttg cggcctgatg
 251 ctttggcaga caattcggtt tcaccgaccc atgccacttc gggggaagtg
 301 tag

This corresponds to the amino acid sequence <SEQ ID 1774; ORF 580.ng>:

g580.pep..
 1 MDSPKVGCGW MVLPMASASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
 51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPDALADNSV SPTHATSGEV
 101 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1775>:

m580.seq..
 1 ATGGATTTCG CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
 51 CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATATCGC
 101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTCGGCA
 151 TCAAAAATCA GCTTGGTAAA GCCGTGTGCG CAACCGTTGG CAATCGCACG
 201 GCCGGAAGCC GCCACGCGGA AGTTGGCTTT GGTGATTTTG CGGCCGAGG
 251 CTTTGGCGGA CAGTTCGGTT TCGCCACCCC ACGCCACTTC GGGGGAAGTG
 301 TAG

This corresponds to the amino acid sequence <SEQ ID 1776; ORF 580>:

m580.pep..
 1 MDSPKVGCGW MVLPMASASQ PISMARQTSP IISPPFGPTM PPPMMRPVSA
 51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADSSV SPTHATSGEV
 101 *

m580/g580 97.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCGWMVLPMASASQPISMARQTSP IISPPFGPTMPPPMRPVSASKISLVKPLS					
	10	20	30	40	50	60
g580	MDSPKVGCGWMVLPMASASQPISMARQTSPIMSPPFGPTMPPPMRPVSASKISLVKPLS					
	70	80	90	100		
m580.pep	QPLAIARPEAAHGKLALVILRPEALADSSVSPTHATSGEVX					
	70	80	90	100		
g580	QPLAIARPEAAHGKLALVILRPDALADNSVSPTHATSGEVX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1777>:

a580.seq
 1 ATGGATTTCG CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
 51 CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATGTCCG
 101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTCAGCA
 151 TCAAAAATCA GCTTGGTAAA ACCATTGTGCG CAACCGTTGG CAATCGCACG
 201 GCCGGAAGCA GCCCATG3GA AGTTGGCTTT GGTGATTTTG CGGCCGAGG
 251 CTTTGGCAGA CAATTCG3TT TCGCCACCCC ATGCCACTTC AGGAGAAGTG
 301 TAA

This corresponds to the amino acid sequence <SEQ ID 1778; ORF 580.a>:

a580.pep
 1 MDSPKVGCGW MVLPMASASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
 51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADNSV SPTHATSGEV

902

101 *

m580/a580 98.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCGWMVLPMSAASQPISMARQTSPIISPPFGPTMPPPMRPPVSASKISLVKPLS					
a580	MDSPKVGCGWMVLPMSAASQPISMARQTSPIISPPFGPTMPPPMRPPVSASKISLVKPLS					
	10	20	30	40	50	60

	70	80	90	100
m580.pep	QPLAIARPEAAHGKLALVILRPEALADSSVSPHATSGEVX			
a580	QPLAIARPEAAHGKLALVILRPEALADNSVSPHATSGEVX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1779>:

g581.seq..

```

1 atgcacttcg cccagcttgt gggcacaacc ggtatagaac aaaatacgtt
51 ctgtcgtcgt ggttttaccg gcatcgatat gggcggaaat accgatgttg
101 cgggtacaggc tgatcggggt cttacgagcc attttattag cctttcaaaa
151 ttgaaaacgg aagtggagaga atgctttgtt ggcttcagcc atacgggtga
201 cttcttcacg ttttttcaac gcaccgccac ggcttcggga cgcatacaatc
251 aactcgccctg ccaaacgcag atccatggat ttctcaccac gtttgcgggc
301 cgcgtcgcca acccaacgca ttgccaaagc cagacggcgt ga

```

This corresponds to the amino acid sequence <SEQ ID 1780; ORF 581.ng>:

g581.pep..

```

1 MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVAVQADRG LSHFISLSK
51 LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQLACQTQ IHGFLTTFAG
101 RVANPTHCS QTA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1781>:

m581.seq..

```

1 ATGCACTTCG CCCAGCTTGT GGTCAAACC GGTATAGAAC AAAATACGTT
51 CTGTCGTCGT GGTTTTACCC GCGTCAATAT GGGCGGAAAT ACCGATGTTA
101 CCGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGGTGA
201 CTTCTTCACG TTTTTTCAAC GCACCGCCAC GGCTTCGGGA CGCATCAATC
251 AATTCGCCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTCGGGGC
301 CGCATCGCGA ACCCAGCGCA TTGCCAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1782; ORF 581>:

m581.pep..

```

1 MHFAQLVGQT GIEQNTFCRR GFTRVNMGGN TDVTQADRG LSHFISLSK
51 LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RIANPAHCQS QTA*

```

m581 / g581 93.8% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTQADRG LSHFISLSKLETEVRECFV					
g581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVTQADRG LSHFISLSKLETEVRECFV					
	10	20	30	40	50	60

	70	80	90	100	110
m581.pep	GFSHTVYFFTFFQRTATAFGRINQFACQTQVHGFLLTFAGRANPAHCQSQTAX				
g581	GFSHTVYFFTFFQRTATAFGRINQLACQTQIHGFLTTFAGRANPTHCSQTAX				
	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1783>:

903

```

a581.seq
1  ATGCACTTCG CCCAGCTTGT GGTCAAAACC GGTATAGAAC AAAATACGTT
51  CTGTCTGTCGT GGTTTTACCC GCATCGATAT GGGCGGAAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CTTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201 CTTCTTCACG TTTTTC AAC GCACCGCCAC GGCCTTCGGA CGCATCAATC
251 AATTCGCCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTCGGGGC
301 CGCATCGCGA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1784; ORF 581.a>:

```

a581.pep
1  MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVTVQADRC LTSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RINPAHCQS QTA*

```

m581/a581 98.2% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTVQADRG	LTSHFISLSKLETEVRECFV				
a581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVTVQADRG	LTSHFISLSKLETEVRECFV				
	10	20	30	40	50	60
	70	80	90	100	110	
m581.pep	GFSHTVYFFTFQRTATAFGRINQFACQTQVHGFLTTFAGRIANPAHCQSQTAX					
a581	GFSHTVYFFTFQRTATAFGRINQFACQTQVHGFLTTFAGRIANPAHCQSQTAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1785>:

```

g582.seq..
1  atgcgctata ttcttttgac aggactgttg ccgacggcat ccgcttttgg
51  agagaccgcg ctgcaatgcg ccgctttgac ggacaatgtt acgcgtttgg
101 cgtgttacga caggattttt gcggcacagc ttccgtcttc ggcagggcag
151 gaagggcagg agtcgaaagc cgtactcaat ctgacggaaa ccgtccgcag
201 cagcttgatg aagggcgagg cggtcattgt tgttgaaaaa ggcggggatg
251 cgcttcctgc cgacagtgcg ggcgaaacgc ccgatatac tacgccttgc
301 agcctgatgt acgacttggc caaaaacgat ttgcgggggc tgttggcggt
351 acgcgaaac aatccgatgt accttatgcc gttttggtat aacaattcgc
401 ccaactatgc cccgagttcg ccgacgcgcg gtacgactgt acaggaaaaa
451 ttccggacagc agaaacgtgc ggaaaccaaa ttgcaggttt cgttcaaaag
501 caaaattgcc gaaaatttgc ttaaaaccgc cgcgatctg tggttcggct
551 acaccctaaag atccgattgg cagatttaca accaaggcag gaaatccgcg
601 ccgttcgcga atacggatta caaacctgaa atttccctga cccagcctgt
651 gaaggcgatg ttgccgttcg gcggcaggct gcgtatgctc ggtgcggggt
701 ttgtccacca gtccaacgga cagagccgtc ccgaatcgcg ttcgtggaac
751 aggatttatg coactggcagg catggaatgg ggcaaatgta cggtgattcc
801 gcgcgtgtgg gtgcgtgcgt tcgatcagag cggcgataaa aacgacaatc
851 ccgatattgc cgactatatg gggtatggcg acgtgaagct gcagtaccgc
901 ctgaacgaca ggcagaatgt gtattccgta ttgcgtaca accccaaaac
951 gggctacggc gcgattgaag ccgcctacac gtttccgatt aaggggcaaac
1001 tcaaaaggcg ggtacgcgga ttccacggtt acggcgagag cctgatcgac
1051 tacaaccaca agcagaacgg tatcggtatc gggttgatgt tcaacgactg
1101 ggacggcatc tga

```

This corresponds to the amino acid sequence <SEQ ID 1786; ORF 582.ng>:

```

g582.pep ..
1  MRYILLTGLL PTASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EQQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLGVRH NPMYLMFPWY NNSPNYAPSS PTRGTTVQEK
151 PQQOKRAETK LQVSFKSKIA ENLPKTRADL WFGYTQSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVI PRVW VRAFQSGDK NDNPDADYD GYGDVVKLYR
301 LNDRONVYSV LRYNPKTYG AIEAAYTPPI KGKLGKVVVRG FHGYGESLID
351 YNHKQNGIGI GLMPNDWDGI *

```


The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1787>:

```
m582.seq ..
  1 ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
 51 AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTTCACG CAGGATTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGAAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CCGTCATGTG TGTGAAAAA GGCGGGGATG
251 CGCTTCCTGC CGACAGTGGC GGCGAAACCG CCGACATCTA TACGCCTTGG
301 AGCCTGATGT ACGACTTGGG CAAAAACGAT TTGCGCGGGC TGTGGGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATCGC
401 CCAACTATGC CCCGGGTTCC CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGGACAGC AGAAACGTGC GGAACCAAA TTGCAGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTGT TTAACCCG CGCGGATCTG TGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCGCGA ATACGGATTA CAAACCTGAA ATTTCTCTGA CCCAGCCTGT
651 GAAGGCGGAT TTGCGGTTCC GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CGGTGATTCC
801 GCGCGTGTGG GTGCGTGCCT TCATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CGACTATATG GGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAATGT GTATTCCGTA TTGCGCTACA ACCCCAAAAC
951 GGGCTACGGC GCGATTGAAG CCGCCTACAC GTTCCGATT AAGGGCAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA
```

This corresponds to the amino acid sequence <SEQ ID 1788; ORF 582>:

```
m582.pep
  1 MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
 51 EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRLLGVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW KCLTVIPRVW VRAFDQSGDK NDNPDADYM GYGDVKLQYR
301 LNDQNVYSV LRYNPKTGYG AIEAAYTFPI KGKLGVVVRG PHGYGESLID
351 YNHKQNGIGI GLMFNDLOGI *
```

m582 / g582 98.6% identity in 370 aa overlap

```

      10      20      30      40      50      60
m582.pep MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
      |||
g582      MRYILLTGLLPTASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
      |||

      70      80      90     100     110     120
m582.pep LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRLLGVREH
      |||
g582      LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRLLGVREH
      |||

      130     140     150     160     170     180
m582.pep NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL
      |||
g582      NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAENLFKTRADL
      |||

      190     200     210     220     230     240
m582.pep WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
      |||
g582      WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
      |||

      250     260     270     280     290     300
m582.pep QSRPESRSWNRIYAMAGMEWGLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR
      |||
g582      QSRPESRSWNRIYAMAGMEWGLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR
      |||

      310     320     330     340     350     360
```

905

```

m582.pep  LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
g582      LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
          310          320          330          340          350          360

          370
m582.pep  GLMFNDLDGIX
          ||||| |||
g582      GLMFNDWDGIX
          370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1789>:

```

a582.seq
1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTACGA CAGGATTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CGGTCATTGT TGTGAAAAA GGCGGGGATG
251 CGCTTCCTGC CGACAGTGCG GCGGAAACCG CCGACATCTA TACGCCTTTG
301 AGCCTGATGT ACGACTTGA CAAAAACGAT TTGCGCGGGC TGTGGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAATTCCG
401 CCAACTATGC CCCGGGTTCG CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGGACAGC AGAAACGTGC GGAACCAAA TTGCAGGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTGT TAAAACCCG CGCGGATCTG TGGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCCGCA ATACGGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
651 GAAGGCGGAT TTGCCGTTTC GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CCGTGATTCC
801 GCGCGTGTGG GTGCGTGCCT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CGACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAATGT ETATTCCGTA TTGCGCTACA ATCCCAAAAC
951 GGGCTACGCG GCGATTGAAG CCGCTACAC GTTTCGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1790; ORF 582.a>:

```

a582.pep
1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLGVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQQKRAETK LQVSFKSKIA EDLEKTRADL WFGYTQRSW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFQSGDK NDNPDADYM CYGDVKLQYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGLKGVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *

```

m582/a582 100.0% identity in 370 aa overlap

```

          10          20          30          40          50          60
m582.pep  MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582      MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          10          20          30          40          50          60

          70          80          90          100         110         120
m582.pep  LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVREH
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582      LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVREH
          70          80          90          100         110         120

          130         140         150         160         170         180

```

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```

m582.pep      NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL
               ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
a582          NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL
               13C      140      150      160      170      180

               190      200      210      220      230      240
m582.pep      WFGYTQSRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSN
               ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
a582          WFGYTQSRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSN
               190      200      210      220      230      240

               250      260      270      280      290      300
m582.pep      QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDIADYMGYGDVKLQYR
               ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
a582          QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDIADYMGYGDVKLQYR
               250      260      270      280      290      300

               310      320      330      340      350      360
m582.pep      LNDQRNVYSVLRYPNKTGYGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKGQNGIGI
               ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
a582          LNDQRNVYSVLRYPNKTGYGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKGQNGIGI
               310      320      330      340      350      360

               370
m582.pep      GLMFNDLDGIX
               |||||||||||
a582          GLMFNDLDGIX
               370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1791>:

g583.seq..

```

1  atgataattg accaaagcca aatatttacc catcttgccct tctgtgcctt
51  ttgcgggatt ggagccgtaa ctgccggcaa tcgactgcat aatcggatgt
101 ataatgccgc cgccgcgcgc ggtattggaa ggggtaacgg gagccagcag
151 cagttcggaa agagcgagac tgtaaccgat gccagcgtt tttcttccaa
201 aaacggcgat aaacaaatat ccgatacgca tccccagccc tgttttgagc
251 aaaccgcgct aaatcataac tgcgatggca atcagccaaa tcaacggatt
301 ggcgaacgca ctcaacgcat cgctcatcgc cgcgccgggt ttgtcggcgg
351 ttacgcccgt tactgagacc aaccgcgagg caataatcga cagcgcgccc
401 aacggcataa ccttgccgat aatggcgcca atcacaccga caaacatagc
451 cagcagcgtc caagcctgag gcttgacccc gtcgggtacg ggcagtgcca
501 aaaccagggc gcacaatact gcggcaatgg cgaggggtat cggtttgaaa
551 cccaatttca tcatattgac ctccgtaaaa aagaccgtcc cgaaaaatcg
601 gaaaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1792; ORF 583.ng>:

g583.pep..

```

1  MIIDQSIFT HLAFCAPCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ
51  QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIHR RARFVGGYAG YCDQPDGNNR QRAQRHNLAD NGGNHTDKHS
151 QQRPSLRLLP VGYGQCQNGG AQYCGNGEGY RFETQPHHID LRKKDRPEKS
201 EK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1793>:

m583.seq..

```

1  ATGATAGITG ACCAAAGCCA AATATTTACC CATCTTGCCT TCTGTGCCTT
51  TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT
101 ATATATGCCG CGCCGCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTCGGAA AGAGCGAGAC TGTAACCGAT GCCCAGCGTT TTTCTTCCAA
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACGGCGCG AAATCATAAC TGCGATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCGCCCGGT TTGTCGGCGG
351 TTACGCCGGT TACTGCGACC AACCAGCGG CAATAATCGA CAGCGCGCCC
401 AACGGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA CAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACAGGGC GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA

```

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551 CCCAATTTC A TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1794; ORF 583>:

m583.pep..

1 MIVDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAAARGIGRNGSQQ
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIHR RARFVGGYAG YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG
151 QQRPSLRLDP VGYGQCQNQG AQYCGNGEGY RFETQFHHID LRKKDRPEKS
201 EK*

m583 / g583 98.5% identity in 202 aa overlap

	10	20	30	40	50	60
m583.pep	MIVDQSQIFT	HLAFCAFCGI	GAVTAGNRLH	NRMYNAAAAA	ARGIGRNGSQQ	QFGKSETVTD
g583	MIIDQSQIFT	HLAFCAFCGI	GAVTAGNRLH	NRMYNAAAAA	ARGIGRNGSQQ	QFGKSETVTD
	10	20	30	40	50	60
	70	80	90	100	110	120
m583.pep	AQRFSKNGDKQ	ISDTHPQPCFEQ	TARNHNC	DGNQPNQRI	GERTQRIHR	RARFVGGYAG
g583	AQRFSKNGDKQ	ISDTHPQPCFEQ	TARNHNC	DGNQPNQRI	GERTQRIHR	RARFVGGYAG
	70	80	90	100	110	120
	130	140	150	160	170	180
m583.pep	YCDQPDGNNR	QRAQRHGLAD	NGGNHTDKHG	QQRPSLRLDP	VGYGQCQNQG	AQYCGNGEGY
g583	YCDQPDGNNR	QRAQRHGLAD	NGGNHTDKHG	QQRPSLRLDP	VGYGQCQNQG	AQYCGNGEGY
	130	140	150	160	170	180
	190	200				
m583.pep	RFETQFHHID	LRKKDRPEKSEKX				
g583	RFETQFHHID	LRKKDRPEKSEKX				
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1795>:

a583.seq

1 ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTTGCCCT TCTGTGCCTT
51 TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCGCGC GGTATTGGAA GGGTAACGG GAGCCAGCAG
151 CAGTTCGGAA AGAGCGAGAC TGTAAACGAT GCCCAGCGTT TTTCTTCCAA
201 AAACGCGCAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACGCGCGC AAATCATAAC TCGATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCACCCGGT TTGTCGCGCG
351 TTACGCCGGT TACTGCGACC AACCCGACGG CAATAATCGA CAGCGCACCC
401 AACGCGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA TAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACCAAGGC GCACAATACT GCGCAATGG CGAGGGGTAT CGGTTTGAAA
551 CCCAATTTC A TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1796; ORF 583.a>:

a583.pep

1 MIVDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAAARGIGRNGSQQ
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIHR RTRFVGGYAG YCDQPDGNNR QRTQRHGLAD NGGNHTDKHG
151 QQRPSLRLDP VGYGQCQNQG AQYCGNGEGY RFETQFHHID LRKKDRPEKS
201 EK*

m583/a583 99.0% identity in 202 aa overlap

	10	20	30	40	50	60
m583.pep	MIVDQSQIFT	HLAFCAFCGI	GAVTAGNRLH	NRMYNAAAAA	ARGIGRNGSQQ	QFGKSETVTD

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```

a583      MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRNGSQQFQKSETVTD
           10      20      30      40      50      60
           70      80      90      100     110     120
m583.pep  AQRFSKNGDKQISDTHPQPCFEQTARNHNCNQPQNRIGERTQRIAHRRARFVGGYAG
           |||||
a583      AQRFSKNGDKQISDTHPQPCFEQTARNHNCNQPQNRIGERTQRIAHRRTRFVGGYAG
           70      80      90      100     110     120
           130     140     150     160     170     180
m583.pep  YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
           |||||
a583      YCDQPDGNNRQRTQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
           130     140     150     160     170     180
           190     200
m583.pep  RFETQFHHIDLKKDRPEKSEKX
           |||||
a583      RFETQFHHIDLKKDRPEKSEKX
           190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1797>:

g584.seq..

```

1  atgtctgcgtt ctattttggc ggcttccctg ctggcggtat cttttccggc
51  ggcggctgag gcattgaatt acaatattgt cgaattttcc gaatcggcgg
101 gtatcgaggt ggctcaggat acaatgtccg cgcgtttcca ggtggcggcg
151 gaaggacggg acaaaaatgc cgtcaatgcc gagtttgta aaaaattcaa
201 caatttcacc agaaaatcga aaaatggtag ctttaaaacc gaattggtat
251 cgcgcagtcg gatgccgcgc tatcaatata ccaacggcag acgcattcaa
301 acaggctggg aggagcgtgc ggaatttaag gcggaggcca gggattttga
351 tgccttaaac cgttttattg ctgatgttca gacggatgct tcgcttgaag
401 ataccgattt cagcgtgtcg cgcgaacgcc gaaacgaggt catcgatcag
451 gtcagcaagg atgccgtttt gcgtttcaag gcgcgtgccg aaaaactggc
501 gggcgcttcg ggtgcgtccg gttataaaat cgtcaaatg aattttgggc
551 aaatcggcag ccatattgcg ggcgatgggg ctgttcgggc aaaaatgctg
601 cgcgcgatgc cgatggcggc aagcgtcaat atgaagggt aegattcagc
651 cgcacgggt gtggaggaaa tcagcatcag catcaatggg acggttcagt
701 tctaa

```

This corresponds to the amino acid sequence <SEQ ID 1798; ORF 584.ng>:

g584.pep Length:..

```

1  MLRSILAASL LAVSFPAAS ALNYNIVEFS ESAGIEVAQD TMSARFQVAA
51  BGRDKNVNA EFKKFNFT RSKNGSFKT ELVSRSAMPR YQYNGRRRIQ
101 TGWEERAEFK AGRDFDALN RFIADVQTD SLEDTDFSVS RERNREVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NFGQIGSHIA GDGAVRAKML
201 RAMPMAASVN MKGTDAAFG VEEISISING TVQF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1799>:

m584.seq..

```

1  ATGTTCGCTC TTGTTTGGC GGCTTGGCTG TCGGCGGTAT CTTTTCCGGC
51  AGCGGCTGAA GCATTGAATT ACAATATTGT CGAATTTTCC GAATCGGCGG
101 GTGTCGAGGT GGCTCAGGAT ACAATGTCCG CAGTTTCCA AGTGACGGCG
151 GAAGGACGGG AAAAAATGC CGTCAATGCT GAGTTTGTTA AAAAAATCAA
201 CAAGTTCATC AGAAAAATCGA AAAATGGTAG CTTTAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGCTGGG AGGAGCGTGC GGAATTTAAG GTCGAAGGTA GAGATTTTGA
351 TGAGTTAAAC CGTTTATTG CCGATATTCA AGCAGATGCC GCGTTGGMAT
401 ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCkATCAG
451 GTCAGCAAGG ATGCCGTTT GCGTTTCAAG GCGCGTCCG AAAAGTTGGC
501 GGGCGTTTTG GGTGCGTCCG GTTATAAAAT CGTCAAATG AATTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGAG CTGCTCAGGC AAAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCCGC
651 CGCGCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTCACT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1800; ORF 584>:

909

m584.pep..

```

1  MLRLVLAASL SAVSFPAAAE ALNYNIVEFS ESAGVEVAQD TMSARFQVTA
51  EGRDKNVNA EFVKKFNKFI RKSKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRDFDELN RFIADIQADA ALXYTDFHVS RERRNEVIXQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584 / g584 89.7% identity in 234 aa overlap

```

              10      20      30      40      50      60
m584.pep      MLRLVLAASLSAVSFPAAAEALNYNIVEFS ESAGVEVAQDTMSARFQVTABGRDKNVNA
              ||| :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584           MLRSILAASLLAVSFPAAAEALNYNIVEFS ESAGIEVAQDTMSARFQVAEGRDKNVNA
              10      20      30      40      50      60

              70      80      90      100     110     120
m584.pep      EFVKKFNKFIKRSKNGSFKTELVSRSAMPRIYQYTNRRRIQTGWEEERAEFKVEGRDFDELN
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584           EFVKKFNKFTRKSKNGSFKTELVSRSAMPRIYQYTNRRRIQTGWEEERAEFKAEGRDFDALN
              70      80      90      100     110     120

              130     140     150     160     170     180
m584.pep      RFIADIQADAALXYTDFHVSRRERRNEVIXQVSKDAVLRFKARA EKLAVLGASGYKIVKL
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584           RFIADVQTDASLEDTFVSRRERRNEVIDQVSKDAVLRFKARA EKLAVLGASGYKIVKL
              130     140     150     160     170     180

              190     200     210     220     230
m584.pep      NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGV EEEISISVNGTVQFX
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g584           NFGQIGSHIAGDGAVRAKMLRAMPMAASVNMKGTD SAAPGV EEEISISVNGTVQFX
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1801>:

```

a584.seq
1  ATGTTGCGTT CTATTTTGGC GGCTTCCCTG CTG.....
51  .....ATTGT CGAATTTTCT GAATCGGCGG
101 GTGTCGAGGC GGTTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG AAAAAATGC CGTCAATGCC GAGTTTGTTA AAAAATTCAA
201 CAATTTCAAC AGAAAATCAA AAAATGGTAG CTTTAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGTTGGG AGGAGCGTGC GGAATTTAAG GTCGAGGGTA GGAATTTTGA
351 TCGGTTGAAC CGTTTTATG CCGATGTTCA GGCAGATGCC GCGTTGGAAT
401 ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCGATCAG
451 GTACGCAAGG ATGCCGTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTGG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCGCG
651 CGGCCTGCT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTCACT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1802; ORF 584.a>:

```

a584.pep
1  MLRSILAASL L..... IVEFS ESAGVEAVQD TMSARFQVTA
51  EGRDKNVNA EFVKKFNKFI RKSKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRNFDALN RFIADVQADA ALEYTDFHVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584/a584 88.9% identity in 234 aa overlap

```

              10      20      30      40      50      60
m584.pep      MLRLVLAASLSAVSFPAAAEALNYNIVEFS ESAGVEVAQDTMSARFQVTAEGRDKNVNA
              ||| :||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a584           MLRSILAASL-----IVEFS ESAGVEAVQDTMSARFQVTAEGRDKNVNA
              10      20      30      40

```

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	70	80	90	100	110	120
m584.pep	EFVKKFNKFIRKSKNGSFKTELVSRSAMPYQYTNGRRIQTGWEERAEFKVEGRDFDELN					
a584	EFVKKFNNFTRKSKNGSFKTELVSRSAMPYQYTNGRRIQTGWEERAEFKVEGRNFDALN					
	50	60	70	80	90	100
	130	140	150	160	170	180
m584.pep	RFIADIQADAALXYTDFHVSRRERNEVIXQVSKDAVLRFKARAELAGVLGASGYKIVKL					
a584	RFIADVQADAALXYTDFHVSRRERNEVIDQVSKDAVLRFKARAELAGVLGASGYKIVKL					
	110	120	130	140	150	160
	190	200	210	220	230	
m584.pep	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
a584	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1803>:

g585.seq..

```

1  atgaaactgt  tccaacgcat  tttegccaca  ttttgcgcg  ttatcgctcg
51  cgcaatcttt  gtggcgagtt  tttctttttg  gctgggtgcag  aacacccttg
101  ccgaaaacca  attcaaccaa  cgccgcacca  tcgaaaccac  attgatgggc
151  agcattatgt  ccgcattcaa  gacacggggc  gacaacggcg  cgcgcgaaat
201  cctgaccgaa  tggaaaaaca  gcccgctctc  atccgcgctt  tacgtcatac
251  agggcgacga  gaaaaaagac  atcttaaaac  gctatatcga  caattacacc
301  atagaacgcg  cccggctgtt  tgccgccaac  aacccccatt  ccaaccttgt
351  ccgcacgcaa  tacgaccggt  tcggcgaaga  atacctgttc  ttcattaaag
401  gctgggacaa  ccaccaggca  caacgcctgc  ccagcccgct  gtttatcccg
451  ggctcgccgc  ttgcccgat  ttggcacgaa  ttcacatccc  tctccttcat
501  catcattgtc  ggactgctga  tggcatatat  ccttgccggc  aacattgccg
551  aacccatcag  aatcttaggc  aacgcatggt  acagggtggc  agaacgagaa
601  ctggaagacc  gcgtttgcca  acaggttcgc  gaccgcgacg  acgaattggc
651  cgatgttgcc  atgcaattcg  acacaatggt  ggaaaaactg  gaataa

```

This corresponds to the amino acid sequence <SEQ ID 1804; ORF 585.ng>:

g585.pep..

```

1  MKLFORIFAT  FCAVIVCAIF  VASFSFWLVQ  NTLAENQFNQ  RRTIETTLMG
51  SIISAFKTRG  DNGAREILTE  WKNSPVSSAV  YVIQDEKED  ILNRYIDNYT
101  IERARLFAAN  NPHSNLVRIE  YDRFGEEYLF  PIKGDNDHQA  QRLPSPLFIP
151  GLPLAPIWHE  FIILSFIIIV  GLLMAYILAG  NIAKPIRILG  NGMDRVAERE
201  LEDRVCCQVR  DRDELADVA  MQPDTMVEKL  E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1805>:

m585.seq..

```

1  ATGAAACTGT  TCCAACGCAT  TTTCGCCACA  TTTTGCGCGG  TTATCGTCTG
51  TGCAATCTTT  GTGGCGAGTT  TTTCTTTCTG  GCTGGTGCAG  AACACCCCTG
101  CCGAAAACCA  GTTCAACCAA  CGCCGCACCA  TCGAAACCAC  TTTGATGGGC
151  AGCATCATTT  CCGCATTCCG  GGCACGCGGG  GACGCGGGTG  CGCGCGAAAT
201  CCGACGGGAA  TGGAAAGACA  GCCCGCTCTC  ATCGGGCGTG  TACGTTATAC
251  AGGGCGACGA  GAAAAAGAT  ATCCTGAACC  GGTATATCGA  CAGCTATACC
301  ATCGAACGCG  CCGGCTTTT  CGCCGCCGGA  CACCCGCATT  CCAACCTCGT
351  CCATATCGAA  TACGACGCT  TCGGCGAAGA  ATACCTGTTC  TTCACCAAAG
401  ACTGGGACAA  ACTCCAAGCC  CGCCGCTGCG  CCAGCCCCCT  GTTGATCCCC
451  GCGCTGCCGC  TCGCCCGAT  TTGGCACGAA  CTCATCATAT  TGTCTTCAT
501  CATCATGCTC  GGAATGCTGA  TGGCATATAT  CCTCGCCGGC  AACATTGCCA
551  AACCCATCAG  AATCTTAGGC  AACGGCATGG  ACAGGCTGGC  AAACGGAGAA
601  CTTGAAACCC  GTATCTCCCA  ACAGGTCGAC  GACCGCGACG  ACGAATTGTC
651  CCATCTTGCC  ATCCAATTGC  ACAAATGGT  GGAAAACTC  GAAAACTCG
701  TTGCCAAGA  ACGCCACCTG  CTCCATCAG  TCTCCATGA  AATGCGTCT
751  CCCCTTGCGC  GCATGCAGGC  AATTGTCGGA  CTGATTACAG  CGCAGCCCA
801  AAAAAAGGAG  CAATATCTCA  AACGGCTGGA  AGGCGAACTG  ACCCGCATGG
851  ATACGCTGGC  CGGGGAAGT  TTAACCTGT  CCCGTCTCGA  AACTTCCAAT
901  ATGGCTTTGG  AAAAAAGAA  CCTGAACTC  CTGCCCTTCC  TGGGCAACCT
951  GGTAAGAGCA  AATCAAAGCA  TTGCCAGAA  AAACGGACAA  ACGTTACCC
1001  TGTCTGCCGA  CGGAAAAATC  CCCGAAAAA  CAACCATCCT  TGCCAACGAA

```

m585.pap..

1	MKLFORIFAT	FCATIVCAIF	VASPSFWLQV	NTLAENQFNQ	RRTIETTLMG
51	SIISAFRARG	DAGAREILITE	WKDPSVSSGV	YVIQDQDKKD	ILNRYIDSYT
101	IERARLPAAG	HPHNSLVITE	YDRFGEYBLF	FTKDQWKLKL	RLRPSLLPII
151	GLPLAPIWHE	LILLSFIIIV	GLLMAYILAG	NIAPKPIRIIG	NGMDRVANGE
201	LETRISQQVD	DRDDELSHLA	IQFDKMWLEL	EKLVAKERHL	LHHVSHBMSR
251	PLARMQAIVG	LIIQAQPOKQE	QYLKRLBEGK	TRMDTLAGEL	LITLSRLETSN
301	MALEKESLKL	PLFGLNVLVD	NQSTAQKNGQ	TVTILSADGKI	PENTTILANE
351	SYLYRAFDNV	IRNAVNYSPE	GSTILINIQG	DHKHMI IDVT	DNGPCVDEMQ
401	LPHEPTAFYR	ADSSANKPGT	GLGLALTQHI	IEQHCGKIITA	ENIKPNGLRM
451	RFLIPKMKTG	SKTEKSAN*			

	10	20	30	40	50	60
m585.pep	MKLFQRI FATFC AVIVCAIFVASFSFWL VQNTLAENQFNQRRTIETTLMGSIISAFRRAG					
g585	MKLFQRI FATFC AVIVCAIFVASFSFWL VQNTLAENQFNQRRTIETTLMGSIISAFKTRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m585.pep	DAGARBILTEWKDSPVSSGVVYIQGDEKKDILNRYIDSYTTIERARLFAAGHPHNSLNVHIE					
g585	DNGAREILTEWKNSPVSSAVVYIQGDEKKDILNRYIDNYTTIERARLFAANNPHNSLNVRIE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m585.pep	YDRFGEEYLFFTKWDNKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG					
g585	YDRFGEEYLFPIKGWDNHQARLPSPLPFIPGLPLAPIWHEFIILSFIIIVGLLMAYILAG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m585.pep	NIAPKPIRILGN GMDRVANGELETRISQQVDDRDEL SHLAIQFDKMKVEKLEKLVAKERHL					
g585	NIAPKPIRILGN GMDRVAERELED RVCCQVRDRDELADVAMQFDIMVEKLEX					
	190	200	210	220	230	
	250	260	270	280	290	300
m585.pep	LHHVSHENRSPLARMAOIVGLIQAOQKQEQYLKRLLEGELTRMDTLAGELLTSLRLETS					

a585.seq

1	ATGAAACTGT	TCCAACGCAT	CTTCGCCACA	TTTTGCGCGG	TTATCGTCTG
51	TGCAATCTTT	GTGGCGAGTT	TTTCTTTCTG	GCTGGTGCAG	AACACCTTTG
101	CCGAAAACCA	GTTCACCAA	CGCCGCGCCA	TCGAAACCA	TTTGATGGGC
151	AGCATCTATT	CCGCATTCCG	GGCAGCGGGA	GACGCGGGTG	CGCGCGAAAT
201	CCTGACGGAA	TGGAAAGACA	GCCCCGTCTC	ATCGGGCGTG	TACGTTATAC
251	AGGGCGACGA	GAAAAAAGAT	ATCCTGCACC	GGTATATCGA	CAGCTACACC
301	ATCGAACCGC	CCCGGCTTTT	CGCCGCGCGA	CACCCGCATT	CCAACCTCGT
351	CCATATCGAA	TACGACCGCT	TCGGCGAAGA	ATACCTGTTT	TTCAACCAAAG
401	ACTGGGACAA	ATCTCAAGCC	CGCGCGCTGC	CCAGCCCCCT	GTTGATCCCC
451	GGCCTGCCGC	TCGCCCCGAT	TTGGCACGAA	CTCATCATAT	TGTCTTTCAT
501	CATCATCTGC	GGACTCTGTA	TGGCGTACAT	CCTCGCCCGC	AACATTTGCCA
551	AACCCATCAG	AATCTTAGGC	ACAGGCATGG	ACAGGGTGGC	AACCGGAGAA
601	CTTGAAACCC	GTATCTCCCA	ACAGGTCGAC	GACCGCGACG	ACGAATTGTC

912

```

651 CCATCTTGCC ATCCAATTCG ACAAATGGT GGAAAACTC GAAAACTCG
701 TTGCCAAGA ACGCCACCTG CTCCATCACG TCTCCATGA AATGCGTTCT
751 CCCCTTGCGC GCATGCAGGC AATTGTCGGA CTGATTCAGG CGCAGCCCCA
801 AAAACAGGAG CAATATCTCA AACGGCTGGA AGGCGAACTG ACCCGCATGG
851 ATACGCTGGC CGGGGAACCTG TTAACCCCTGT CCCGTCTCGA AACTTCCAAT
901 ATGGCTTTGG AAAAAGAAAG CCTGAAACTC CTGCCCTTCC TGGGCAACCT
951 GGTAGAAGAC AATCAAAGCA TTGCCAGAA AAACGGACAA ACGGTTACCC
1001 TGTCTGCCGA CGGAAAAATC CCGGAAACA CAACCATCCT TGCCAACGAA
1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGGCC CCGGCGTGGG CGAAATGCAG
1201 CTCCGCACCA TCTTCACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGAAGTGGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTCGGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCGGT TCCAAACAG AAAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1808; ORF 585.a>:

```

a585.pep
1  MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51  SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGDEKKD ILHRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRI,PSLLIP
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQVDD DRDDELSHLA IQFDKMVEKL EKLVAKEERHL LHHVSHEMRS
251 PLARMQAIIVG LIQAQPQKQE QYLKRLEGEL TRMDTLAGEL LTLSRLETNS
301 MALEKESLKL LPFLGNLVED NQSIAQKNGQ TVTLSADGKI PENTTILANE
351 SYLYRAFNDV IRNAVNSYPE GSTILINIQ DHKHWIIDVT DNGPGVDEMQ
401 LPHIFTAFYR ADSANKPGT GLGLALTQHI IEQHCCKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*

m585/a585 99.8% identity in 468 aa overlap

10      20      30      40      50      60
m585.pep MKLFQRI FATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRRTIETTLMGSIISAFRARG
a585      MKLFQRI FATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRRTIETTLMGSIISAFRARG
10      20      30      40      50      60

70      80      90      100     110     120
m585.pep DAGAREILTEWKDSPVSSGVYVIQGDEKKDILNRYIDSYTIERARLFAAGHPHSNLVHIE
a585      DAGAREILTEWKDSPVSSGVYVIQGDEKKDILHRYIDSYTIERARLFAAGHPHSNLVHIE
70      80      90      100     110     120

130     140     150     160     170     180
m585.pep YDRFGEEYLF FTKDWDKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG
a585      YDRFGEEYLF FTKDWDKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG
130     140     150     160     170     180

190     200     210     220     230     240
m585.pep NIAKPIRILGNMGMDRVANGELETRISQVDDRDDELSHLAIQFDKMVEKLEKLVAKEERHL
a585      NIAKPIRILGNMGMDRVANGELETRISQVDDRDDELSHLAIQFDKMVEKLEKLVAKEERHL
190     200     210     220     230     240

250     260     270     280     290     300
m585.pep LHHVSHEMRSP LARMQAIIVGLIQAQPQKQEYQLKRLEGELTRMDTLAGELLTSLRLETNS
a585      LHHVSHEMRSP LARMQAIIVGLIQAQPQKQEYQLKRLEGELTRMDTLAGELLTSLRLETNS
250     260     270     280     290     300

310     320     330     340     350     360
m585.pep MALEKESLKL LPFLGNLVEDNQSIAQKNGQTVTLSADGKIPENTTILANESYLYRAFNDV
a585      MALEKESLKL LPFLGNLVEDNQSIAQKNGQTVTLSADGKIPENTTILANESYLYRAFNDV

```

913

	310	320	330	340	350	360
	370	380	390	400	410	420
m585.pep	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
a585	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
	370	380	390	400	410	420
	430	440	450	460	469	
m585.pep	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
a585	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1809>:

g586.seq..

```

1 atggcagccc atctcgaaga acaacaagag ttagacaact ttaaatattt
51 ttggaaaacc acgggcaaat ggctgtttgc cctgctgatt ttggcggcac
101 tccgctactt gggatacacg gtttaccaa accgtgcggc ttcccaaat
151 caggaagcgg cggcgggtgct ggcaaacatc gtggaaaagg cgcaaaacaa
201 agccccgcaa agcgaaatca atgccgaact gtccaaactc caacaaagct
251 acccccattc catttccgcc gcccaagcca cgctgatggc ggcggaacc
301 gaatttgacg cgcagcggtta cgatgttgcc gaaggtcatt tgaaatgggt
351 gttgtccaac caaaaagaca gcctgattca ggcgttgccg gcgcagcgctc
401 tggcgcttgt gttgttgcaa caaaaaaat acgatgccgc gcttgccgca
451 ctcgacacgc cggttgaggc ggacttcgcc cccctgctga tggaaactaa
501 agcgcatggt tatgccgcac aggaaaaaag ccaggaagcc ttaaaaaact
551 acggacaggc ttggaaaaa atgcctcaag attctgtcgg tcggaattg
601 ctcaaatga aactcgattc gctgaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1810; ORF 586.ng>:

g586.pep..

```

1 MAAHLEEQQE LDNFKYFWKT TGKWLFALLI LAALGYLGYT VYONRAASON
51 QEAAAVLANI VEKAQNKAPQ SEINAELSKL QQSYPHSISA AQATLMAAAT
101 EFDQRYDVA EGHLKWVLSN QKDSLIQALA AQLRGVLLQ QKKYDAALAA
151 LDTFVEADFA PLLMETKGDV YAAQKSQEA LKNYQALEK MPQDSVGREL
201 LQMKLDSLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1811>:

m586.seq

```

1 ATGCGAGCCC ATCTCGAAGA ACAACAAGAG TTAGACAAC TTAATATTT
51 TTGGAAAACC ACGGGCAAAT GGCTGTTTGC CTTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTACCAAA ACCGTAAAGT TTCCCAAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAAACATC GTAGAAAGG CGCAAGCAA
201 AGCCCCGCAA AGCGAAATCA ATGCGGAATT GACCAAACTC CAACAAAGCT
251 ACCCGCATTC CATTTCCGCC GCCCAAGCCA CACTGATGGC GGCGGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAATGGGT
351 GTTGTCCAAC CAAAAGACA GCCTGATTCA AGCGTTGGCG GCGCAGCGTC
401 TGGCGTGTGT GTTGTGCAA CAAAAAAAT ACCGATGCCG GCTTGCCGCG
451 CTCGATACGC CGGTTGAAGC GGACTTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGAAAAG CCAGGAAGCC TTAAAAACT
551 ACGGACAGGC TTTAGAAAA ATGCCTCAAG ATTCTGTCGG TCGCGAATTG
601 GTTCAATGA AACTTGATTC GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1812; ORF 586>:

m586.pep

```

1 MAAHLEEQQE LDNFKYFWKT TGKWLFALLI LAALGYLGYT VYQNRKVSQN
51 QEAAAVLANI VEKAQSKAPQ SEINAELTKL QQSYPHSISA AQATLMAAAT
101 EFDQRYDVA EGHLKWVLSN QKDSLIQALA AQLRGVLLQ QKKYDAALAA
151 LDTFVEADFA PLLMETKGDV YAAQKSQEA LKNYQALEK MPQDSVGREL
201 VQMKLDSLK*

```

m586 / g586 97.1% identity in 209 aa overlap

	10	20	30	40	50	60
m586.pep	MAAHLEEQQELDNFKYFWKTITGKWL FALLI LAALGYLGYTVYQNRKVSQNEAAVLANI					

914

```

g586      MAAHLEEQQE LDNFKYFWKT TGKWLFAVLI LAALGYLGYT VYQNRAASQNQEAAAVLANI
           10      20      30      40      50      60

           70      80      90      100     110     120
m586.pep  VEKAQSKAPQSEINAELTKLQSYPHSISAQAATLMAAAATEFDAQRYDVAEGHLKWVLSN
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      VEKAQNKAPQSEINAELSKLQSYPHSISAQAATLMAAAATEFDAQRYDVAEGHLKWVLSN
           70      80      90      100     110     120

           130     140     150     160     170     180
m586.pep  QKDSLIIQALAAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGSQEA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      QKDSLIIQALAAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQKSQEA
           130     140     150     160     170     180

           190     200     210
m586.pep  LKNYGQALEKMPQDSVGRELVMKLDLSLKX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      LKNYGQALEKMPQDSVGRELLQMKLDLSLKX
           190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1813>:

```

a586.seq
1  ATGGCAGCCC ATTTGGAAGA ACAACAAGAG TTGGACAAC TTAATATTT
51 TTGGA AAAACC ACGGGCAAAT GGCTGTTGCG CGTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTTACCAA ACCGTGCGGC TCCCCAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAAACATC GTGGAAAAGG CGCAAACAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT GGCCAAGCTC CAACAAAGCT
251 ACCCCCATTC CATTTCGCCG GCCCAAGCCA CGCTGATGGC GGCAGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAATGGGT
351 ATTGTC AAC CAAAAAGACA GCCTGATCCA GGCCTTGGCG SCGCAGCGTC
401 TGGGCGTTGT GTTGTGCAA CAAAAAAT ACGATGCCGC SCTTGCCGCA
451 CTCGACACGC CGGTTGAAGC GGACTTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGAAAAG CCAGGAAGCC TTA AAAA ACT
551 ACGGACAGGC TTAGAAAAA ATGCCTCAAG ATTCTGTCGG TCGCGAATTG
601 GTTCAAATGA AACTTGATTG GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1814; ORF 586.a>:

```

a586.pep
1  MAAHLEEQQE LDNFKYFWKT TGKWLFAVLI LAALGYLGYT VYQNRAASQN
51  QEAAAVLANI VEKAQNKAPQ SEINAELAKL QSYPHSISA QAATLMAAAT
101 EFDAQRYDVA EGHKLVLSN QKDSLIIQALA AQLGVVLLQ QKKYDAALAA
151 LDTPVEADFA PLLMETKGDV YAAQGSQEA LKNYGQALEK MPQDSVGREL
201 VQMKLDLSLK*

m586/a586  97.6% identity in 209 aa overlap

           10      20      30      40      50      60
m586.pep  MAAHLEEQQE LDNFKYFWKT TGKWLFAVLI LAALGYLGYT VYQNRAASQNQEAAAVLANI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      MAAHLEEQQE LDNFKYFWKT TGKWLFAVLI LAALGYLGYT VYQNRAASQNQEAAAVLANI
           10      20      30      40      50      60

           70      80      90      100     110     120
m586.pep  VEKAQSKAPQSEINAELTKLQSYPHSISAQAATLMAAAATEFDAQRYDVAEGHLKWVLSN
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      VEKAQNKAPQSEINAELAKLQSYPHSISAQAATLMAAAATEFDAQRYDVAEGHLKWVLSN
           70      80      90      100     110     120

           130     140     150     160     170     180
m586.pep  QKDSLIIQALAAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGSQEA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      QKDSLIIQALAAQRLGVVLLQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGSQEA
           130     140     150     160     170     180

```

915

```

                190      200      210
m586.pep      LKNYGQALEKMPQDSVGRELVMKLDLKLX
                |||||
a586          LKNYGQALEKMPQDSVGRELVMKLDLKLX
                190      200      210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1815>:

```

g587.seq..
1  atgaaacgta tctttttgcc cgccttgccc gccatcctgc ctttatccgc
51  ttatgccgac ctgcccttga cgattgaaga cataatgacc gacaagggaa
101 aatggaaact ggaaacttcc cttacctatc tgaatagcga aaacagccgc
151 gccgcacttg ccgcaccggt ttacattcaa accggcgcaa cctcgtttat
201 ccccatctcg accgaaattc aagaaaacgg cagcaatacc gatatgctcg
251 ccggcacgct cggtttgccg tacggactga ccggcaatac cgacatttac
301 ggcagcggca gctatctgtg gcacgaagaa cgaaaactcg acggcaacgg
351 caaaacccgc aacaaacgga tgtccgacat atccgccggc atcagccaca
401 ccttccttaa agacggcaaa aaccccgccc taatcagctt tcttgaaagc
451 acggtttacg aaaaatcgcg caacaaagcc tcgttaatca aaaaaagggg
501 gctttgcccc tttataact taaggataaa ttatgaatat taa

```

This corresponds to the amino acid sequence <SEQ ID 1816; ORF 587.ng>:

```

g587.pep..
1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSNSNR
51  AALAAPVYIQ TGATSFIPIP TEIQENGSTNT DMLAGTLGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNKTR NKRMSDISAG ISHTFLKDGK NPALISFLES
151 TVYEKSRNKA SLIKRGLCP FYNLRINYEY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1817>:

```

m587.seq..
1  ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
51  TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101 AATGGAAGCTT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACCTTG CCGCACCGGT TTACATTCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATCTCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TCGGCACGCT CGGTTTGCGC TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACAG
351 CAAAACCCGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551 CCGCCGCCTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601 TACAAATCGG GCAACTACCT GCTGCTCAAC CCCAACATCT CATTGCTGTC
651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701 CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751 GCCCATTTTC GCGCAGGTTT CGGTTTCACC AAAACACCGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCGAA CTGAAATTTG
851 GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1818; ORF 587>:

```

m587.pep..
1  MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSNNR
51  AELAAPVYIQ TGATSFIPIP TEIQENGSTNT DMLVGTGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTSLDGIR
201 YKSGNYLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m587 / g587 95.0% identity in 161 aa overlap

10 20 30 40 50 60

```
a587.seq
1  ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51  TTATGCCGAC TGCCTTGA CAATATGACC GACAAGGGCA
101 ATAGTAAACT GGAACTTCC CTTACTACC TGAACGACA AAACAACCGC
151 GCCGAACCTG CCGCACCGGT TTACATCCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTTCC ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCAGCTC CGGTTTGCGT TACGGACTGA CCGGAAATAC GCACATTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACGG
351 CAAAACCCGA AACAACGGA TGTCGACGCT ATCCTTCGGC ATCAGCCACA
401 CTTCTCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTTAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAGCC TCGTCGGGAA AATCTCGGCT
501 CATCGGCGCC ACCACCTACA AAGCATCGA CCCCCTCGTC CTCTCATTGA
551 CCGCTGCTTA CCGTATCAAC GGCAGCAAAA CCCTTTCAGT CAACACCAAA
601 TACAAAGCAG GCAATTACTG GATGCTGAAT CCCAATATAT CCTTCGCGCC
651 CAACGACAGA ATCAGCTCA CGGCGGCAT CCAATGGCTG GCGAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTCC GCGCAGGTTT CGGTTTCACC AAAACCAGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCGGAA CTGAAATTTG
851 GCGTACAGTA TACGTTTAA
```

```
a587.pep
  1  MKRIFLFPALP  AILPLSAYAD  LPLTIEDIMT  DKGKWKLETS  LTYLNSENNK
51  AELAAPVYIQ  TGATSFIPIP  TEIQENGST  DMLVGTGLGR  YLGTGNTDIY
101 GSGSYLWHEE  RKLDGNGKTR  NKRMDSVSLG  ISHTFLKDDK  NPALISFLES
151 TVYEKSRNKA  SSGKSWLIGA  TTYKAIDPVV  LSLTAAYRIN  GSKTLSNNTK
201 YKAGNYWMLN  PNISFAANDR  ILSGTGGIQWL  GKQPDRLDGK  KESARNTSTY
251 AHFGAGFVGT  KTTALNASAR  FNVSGOSSSE  LKFGVOHTF*
```

	10	20	30	40	50	60
m587.pep	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
	:					
a587	MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m587.pep	TGATSFIPITPEIQENGSNITDMLVGTGLRLYGLTGNTDIYSGGSYLWHEERKLDGNSKTR					
a587	TGATSFIPITPEIQENGSNITDMLVGTGLRLYGLTGNTDIYSGGSYLWHEERKLDGNGKTR					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m587.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a587	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m587.pep	LSLTAAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a587	LSLTAAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m587.pep	RESSRNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVCHTFX					
a587	KESARNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVCHTFX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1821>:

```

g588.seq
1  atgcttaaac atctcgcat cctactgccc gccatgatgt tcgccctccc
51  cgcccagacc gccgtcctaa gccctatca ggaaaccggc tgcacctacg
101 aaggcgggat cggaaaagac gggcttcctt caggcaaagg catatggcgt
151 tgccgggatg ggcgcgctta taccggttca ttcaaaaacg gcaaattcga
201 cgggcaaggc gtttataccg ttgccgccgg ccgcgaagta tttctcgagc
251 cgttcaattc cgacagtacc aaattccgca atatggcatt gtcgggcacg
301 ttcaaaacaa gcttggcaca cggcagggtt gccgcctcgc aaaacggcga
351 aaccctcttt tattatgaaa tgcaaacacg gcatgattaa

```

This corresponds to the amino acid sequence <SEQ ID 1822; ORF 588.ng>:

```

g588.pep..
1  MLKHLAFLLP AMMFALPAQT AVLSPYQETG CTYEGGIGKD GLPSGKGIWR
51  CRDGRGYTGS FKNGKFDGQG VYTVAAGREV FLEPFNSDST KFRNMALSGT
101 FKQGLAHGRF AASQNGETLF YYEMRTRHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1823>:

```

m588.seq..
1  ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51  CACTTCGGCC GCCGTCTGA CTTCCTATCA AGAACCAGGC TGCACCTACG
101 ACGGCAATGT CGGCAAAGAC GGTAACCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTCT TTTAAAAACG GCAAATTCGA
201 CGGGCAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATCCGCA ACATGGTACT CTCGGGCACG
301 TTCAAAAAG GCTTGGCACA CCGCAGATTT ACCGTCTCGC AAAACGGCGA
351 AACCCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAAC
401 TGCCCCAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1824; ORF 588>:

```

m588.pep..
1  MLKHLAFLLP AMMFALPSTA AVLTSYQEPG CTYDGNVGKD GKPAGKGTWR
51  QDGRNYTGS FKNGKFDGQG VYTVAANREI FIEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENGMK EVKLPKNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m588 / g588 82.5% identity in 120 aa overlap

10 20 30 40 50 60

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```

m588.pep    MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVGKDGKPKAGKGTWRCQDGRNYTGS
g588        MLKHLAFLLPAMMFALPAQTAVLSPYQETGCTYEGGIGKDGLP SGKGIWRCRDGRGYTGS
              10      20      30      40      50      60

              70      80      90      100     110     120
m588.pep    FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
g588        FKNGKFDGQGVYTVAAAGREVFLEPFNSDSTKFRNMALSGTFKQGLAHGRFAASQNGETLF
              70      80      90      100     110     120

              130     139
m588.pep    IMKCENGMKEVKLPKNKX
g588        YYEMRTRHDX
              130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1825>:

```

a588.seq
1   ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51  CGCCGCGTCC GCCGTTCTGA CTTCTATCA AGAACCCGGC TGCACCTACG
101 AAGGCGATGT CGGCAAAGAC GGTAAACCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTCTG TTTAAAAATG GCAAATTCGA
201 CGGACAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATCCGCA ACATGGTACT CTCGGGCACA
301 TTCAAAAAAG GCTTGGCACA CGGCAGATTT ACCGTCTCGC AAAACGGCGA
351 AACCCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAA GAAGTGAAGC
401 TGCCCCAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1826; ORF 588.a>:

```

a588.pep
1   MLKHLAFLLP AMMFALPAAS AVLTSYQEPG CTYEGDVGKD GKPAGKGTWR
51  CQDGRNYTGS FKNGKFDGQG VYTVAAANREI FIEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENGMK EVKLPKNK*

m588/a588    96.4% identity in 138 aa overlap

              10      20      30      40      50      60
m588.pep    MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVGKDGKPKAGKGTWRCQDGRNYTGS
a588        MLKHLAFLLPAMMFALPAASAVLTSYQEPGCTYEGDVGKDGKPKAGKGTWRCQDGRNYTGS
              10      20      30      40      50      60

              70      80      90      100     110     120
m588.pep    FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
a588        FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
              70      80      90      100     110     120

              130     139
m588.pep    IMKCENGMKEVKLPKNKX
a588        IMKCENGMKEVKLPKNKX
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1827>:

```

g589.seq..
1   atgcaacaaa aaatccgttt ccaaatcgag gcgatgacct gtcaggcatg
51  tgcttcgcgc attgaaaaag tgttgaaaca aaaagatttt gtcgaatcgg
101 cgggagtga ctttgccagt gaggaagcgc aggttacgtt tgacggcagc
151 aaaacctcgg ttgccgacat tgccaaaatc attgagaaaa ccggttacgg
201 cgcgaaaggaa aaaacggaag atacattgcc gcaacctgaa gcagaacacc
251 atatcggtcg gcggttggtg cttttgctga ccatcaatat cccgttcctt

```

```

301 atcggatgtag tagggatgat gctaaaaggg ctgaattgga caccgcacga
351 ttggatgatt ccgcctgtat ggcatgttgt actggcaagc atagtgaac
401 ttggctggc aatcccgttt tacaaaagcg cgtgggcaag cattaagggc
451 gggctggcga atatggacgt actcgttacc atcggcacgg tgcgattta
501 cctgtattcc gtttatatgc tgtttttcag ttcgcatcgg gcgcacggta
551 tggcgcatgt gtattttgaa gcgggctgga tggatgatcgg ttttgtgtcg
601 ctgggtaagt ttttgaaca ccgcaccaaa aaatccagcc tgaacagctt
651 gggcttactg ctaaaactca cggcgaccca agtcaacgtg caacgcaacg
701 gcgaatggaa acaactgccc atcgaccaag tgcaaatcgg cgaccttatc
751 cgcaccaacc acggcgaaacg catcgtctgc gacggcatta tcgaaagcgg
801 cagcgggttg gcggacgaaa gccaccttac cggcgaaatcc aatcccgaag
851 agaaaaaggg gggcgcaaaa gtgttggcgg gcgcgctgat gaccgaaggc
901 agcgtggtgt accgcgccgc gcagctcggc agccaaaccc tgctcggcga
951 catgatgaac gcgctctctg aagcacaagg cagtaaagca ccgattgcgc
1001 gcgtggccga taaagcggcg gcggtatttg tgccaactgt cgtgggcac
1051 gcgcttctga cttttatcgt tgcctggctg attaagggcg attggacggg
1101 cgcactgatg caccgcgttg ccgttttggg gattgcctgc ccgtgcgcgc
1151 tcggctctggc gacccttgcg gcgattatgg tcggcatggg caaagcgggtg
1201 aaacacggca tttggtttaa agacgcggcg gcaatggagg aagcagccca
1251 cgtcgatgcc gtcgtattgg acaaaaccgg tacgctgacc gaaggcaggc
1301 cgcaggttgc cgcgctttat tacgttcccc acagcggcct tgacgaagac
1351 gctttgtacc gcatcgccgc cgcgctcgag caaaacgcgg cccaccgcgt
1401 gcgccgcggc atcgtctccg ccgcacaagc gcgcggttgg gagattcccg
1451 ctgcacaaaa tgcgcaaacg gttgtcggag caggcattac cgcogaagtg
1501 gaagcgtggg gtttggtgaa atcaggcaaa gccgaatttg ccgaactgac
1551 cttgcogaag ttttcagacg gcgtttggga aatcgccagt gcggttaccg
1601 tatctgtaaa cggcaaacgg atcggcgcat tcgcactctc cgacgcgttg
1651 aaagccgata ccgccgaagc catagggcgt ctgaaaaaac acaatatcga
1701 tgtctatatt atgagcggcg ataaccaaag tacggtcgaa tacgtcgcca
1751 aacaactggg catcgcacac gccttcggta atatgagtcg gtgcgacaaa
1801 gccgccgaag tgcagaaact caaagccgcg ggcaaaaccg tggcgatggg
1851 gggcgacggc atcaacgacg cgcgcgcgct tgccgcgcgc aacgtcagct
1901 tcgccatgaa aggcggtgcg gacgttgccg aacacaccgc ctccgccacy
1951 ctgatgcagc attcgggtcaa tcagctcgcc gatgccctgc tgatatcgca
2001 ggcaacggtt gaaaaacatca agcaaaacct atttttcgce ttcttctaca
2051 atatatggg cattccgctc gccgcgctcg gctttttaa tcccgtcata
2101 gcaggcggcg caatggcggc aagctcgggt tcggtatttg gcaatgccct
2151 gcgcctgaaa tgggtaaaaa tcgattga

```

This corresponds to the amino acid sequence <SEQ ID 1828; ORF 589.ng>:

g589.pep..

```

1  MQQKIRFQIE AMTCQACASR IEKVLNKKDF VESAGVNFAS EEAQVTFDGS
51  KTSVADIAKI IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLLTINIPFL
101 IGMVGMMLKG LNWTRHDWMI PPVWQFVLAS IVQLWLAI PF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSSHA AHGMAHVYFE AGVMVIGFVS
201 LGKFLEHRTK KSSLNSLGLL LKLTPTQVNV QRNGEWKQLP IDQVQIGDLI
251 RTNHGERIAA DGIIESGSGW ADESHLTGES NPEEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPTVVGI
351 ALLTFIVAWL IKGDWTV ALM HAVAVLV VIAC PCALGLATPA AIMVGMGKAV
401 KHGIWEKDAA AMEEAAHVDA VVLDKTGTLT EGRPOVAAYV YVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPAAQNAQT VVGAGITAEV
501 EGVGLVKSGK AEFAELTLPK FSDGVWEIAS AVTVSVNGKP IGAFALSDAL
551 KADTAEAIGR LKKHNIDVYI MSGDNQSTVE YVAKQLGIAH AFGNMSPCDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGA DVAEHTASAT
651 LMQHSVNQLA DALLISQATL ENIKQNLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLGNALRLK WVKID*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1829>:

m589.seq..

```

1  ATGCAACAAA AAATCCGTTT CCAAATCGAA GGCATGACCT GCCAGGCCTG
51  CGCTTCGCGC ATTGAAAAAG TGTGAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTTCCGCCAGC GAAGAGGCGC AGGTAGTGTG TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GCGCTGTGG CTGCTGTTCA CCATCAACGT CCCGTTTCCTT

```


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```

301 ATCGGCATGG CGGGGATGAT GATCGGCAGA CACGATTGGA TGATTCCGCC
351 GTTGTGGCAG TTCGCATTGG CAAGCGTGGT GCAGCTTTGG CTGGCAATCC
401 CGTTTTACAA AAGCGCGTGG GCGAGCATTG AGGGCGGACT GGCGAATATG
451 GACGTGCTGG TTACCATCGG CACGGTCTCG ATTTACCTGT ATTCCGCTCA
501 TATGCTGTTT TTCAGCCCGC ACGCGGCGTA CGGTATGGCG CATGTGTATT
551 TTGAAGTGGG CGTGATGGTG ATCGGTTTTG TGTCACCTGG TAAATTTTGG
601 GAACACCGTA CCAAAAAATC CAGCCTCAAC AGCTTGGGCT TGCTGCTCAA
651 ACTTACACCA ACCCAAGTCA ACGTGCAACG CAACGGCGAA TGGAAACAGC
701 TTCCCATCGA CCAAGTGCAA ATCGGCGACC TTATCCGCGC CAACCACGGC
751 GAACGCATTG CCGCAGACGG CATCATTGAA AGCGGCAGCG GTTGGGCGGA
801 CGAGAGCCAT CTTACGCGCG AATCCAATCC TGAAGAAAAA AAGCGGGGCG
851 GCAAAGTGTG GCGGGGCGCG TTAATGACCG AAGGCAGTGT GGTGTACCGC
901 GCCACGCAGC TCGGCAGCCA AACCAGCTC GCGGACATGA TGAACGCGCT
951 CTTGAAGCA CAAGGCAGTA AAGCACCGAT TCGCGCGCTA GCCGATAAAG
1001 CGGCTGCGGT ATTCTGTCCT GCCGTCTGG GCATTGCGTT GTTGACTTTT
1051 ATTTGTACTT GGCTGATTAA GGGCGATTGG ACGGTTCGCG TGATGCACGC
1101 CGTCGCGGTT TTGGTGATTG CCTGCCCGTG CCGCTGGGT CTGGCAACCC
1151 CTGCGCGGAT TATGGTCGGT ATGGGCAAAG CGGTTAAACA CGGTATTTGG
1201 TTTAAAGACG CGGCAGCAAT GGAGGAAGCC GCCACGTCG ATGCCGTCG
1251 GTTGACAAA ACCGGTACGC TGACCGAAGG CAGCCCGCAG GTTGCCGCCG
1301 TTTATTGCGT TCCGACAGC GGCTTTGACG AAGACGCTTT GTACCGCATC
1351 GCGCGCGCG TCGAACAAAA CGCGGCCCAT CGCTCGCCC GTGCCATCGT
1401 CTCGCGCGCC CAAGCGCGCG GTTTGGACAT TCCCGCCGCA CAAAACGCAC
1451 AAACCGTTGT CGGCGCAGG ATTACGCGG AAGTGAAGG CGTGGGTTTG
1501 GTGAAAGCAG GCAAAGCCGA ATTGGCCGAA CTGGCCTTGC CGAAGTTTTT
1551 AGACGGCGTT TGGGATATTG CAAGCATTGT TCGGCTCTCA GTCCATAACA
1601 AACCCTACGG CGCATTTCGA CTTGCCGACG CGTTGAAAGC CGATACCGCC
1651 GAAGCCATAG GCCGTCTGAA AAAACACAAT ATCGATGTCT ATATTATGAG
1701 CGGCGACAAC CAAGGCACGG TCGAATACGT CGCCAAACAA CTGGGCATCG
1751 CACACGCCTT CGGCAACATG AGTCCGCGCG ATAAAGCTGC CGAAGTGCAA
1801 AAACCTCAAAG CCGCCGGCAA AACCGTGGCG ATGGTCGCGC ACGGCATCAA
1851 CGACGCGCCC GCGCTTGCCG CCGCTAACGT CAGCTTCGCC ATGAAAGGCG
1901 GAGCGGACGT TCGCGAACAT ACCGCATCCG CCACGCTGAT GCAGCATTCG
1951 GTCAACCAAC TCGCCGATGC TCTGCTGGTG TCGCAAGCCA CTTTAAAAAA
2001 CATCAAGCAA AACCTGTTTT TCGCCTTCTT CTACAATATT TTGGGCATTG
2051 CTCTCGCCGC GCTTGGCTTT TTAATCCCG TCATCGCTGG CGCGGCAATG
2101 GCGGCAAGCT CGGTTTCCGT GTTGAGCAAT GCCTTGCGCC TGAACGGGT
2151 AAAAAATCGAT TAG

```

This corresponds to the amino acid sequence <SEQ ID 1830; ORF 589>:

m589.pep..

```

1  MQQKIRFQIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
51  KTSVADIARI IEKTGYGAKE KTEDTLQPE AEHHIGWRLW LLFTINVPFL
101 IGMAGMMIGR HDWMIPPLWQ FALASVQLW LAIPFYKSAW ASIKGGLANM
151 DVLVTIGTVS IYLYSVYMLF FSPHAAYGMA HVEFEVGMV IGFVSLGKFL
201 EHRTKSSSLN SLGLLLKLTP TQVNVQRNGE WKQLPIDQVQ IGDILIRANHG
251 ERIAADGIEE SSGWADESH LTGESNPEEK KAGGKVLAGA LMTEGSVVYR
301 ATQLGSQTQL GDMMNALSEA QGSKAPIARV ADKAAAVFVP AVVGIALLTG
351 IVTWLIKGDW TVALMHAVAV LVIACPCALG LATPAAIMVG MGKAVKHGIW
401 FKDAAMEEA AHVDAVLDK TGTLTGSPQ VAAVYCVFDS GFDEDALYRI
451 AAAVEQNAAH PLARAIVSAA QARGLDIPAA QNAQTUVGAG ITAEVEGVGL
501 VKAGKAFAE LALPKFLDGV WDIASIVAVS VDNKPIGAF A LADALKADTA
551 EAIGRLKKHN IDVYIMSGDN QGTVEYVAKQ LGIAHAFGNM SPRDKAAEVQ
601 KLKAAGKTVA MVGDGINDAP ALAAANVSFA MKGGADVAEH TASATLMQHS
651 VNQLADALLV SQATLKNIKQ NLFFAFFYNI LGIPLAALGF LNPVIAGAAM
701 AASSSVLSN ALRLKRVKID *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m589 / g589 94.2% identity in 725 aa overlap

```

          10      20      30      40      50      60
m589.pep  MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIARI
          |||||:|||||||||||||||||||||||||||:| |||||

```

g589	MQQKIRFQIEAMTCQACASRIEVLNKKDFVESAGVNFASEEAQVTFDGSKTSVADIAKI	10	20	30	40	50	60
m589.pep	IEKTGYGAKEKTEDTLQPPEAEHHIGWRLWLLFTINVPFLIGMAGMMIG-----RHDWMI	70	80	90	100	110	
g589	IEKTGYGAKEKTEDTLQPPEAEHHIGWRLWLLLTINIPFLIGMVGMMLKGLNWTRHDWMI	70	80	90	100	110	120
m589.pep	PPLWQFALASVVQLWLAIPFYKSASAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSFPHA	120	130	140	150	160	170
g589	PPVWQFVLASIVQLWLAIPFYKSASAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSSSHA	130	140	150	160	170	180
m589.pep	AYGMAHVYFEVGVMVIGFVSLGKFLEHRTKKSSLSLGLLLKLTPTQVNVQRNGEWKQLP	180	190	200	210	220	230
g589	AHGMAHVYFEAGVMVIGFVSLGKFLEHRTKKSSLSLGLLLKLTPTQVNVQRNGEWKQLP	190	200	210	220	230	240
m589.pep	IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPPEKKAGGKVLGALMTEG	240	250	260	270	280	290
g589	IDQVQIGDLIRTNHGERIAADGIIESGSGWADESHLTGESNPPEKKAGGKVLGALMTEG	250	260	270	280	290	300
m589.pep	SVVYRATQLGSQTQLGDMNALSEAQGSKAPIARVADKAAAVFVPVAVGIALLTFFIVTWL	300	310	320	330	340	350
g589	SVVYRAAQLGSQTLLGDMNALSEAQGSKAPIARVADKAAAVFVPTVVGIALLTFFIVAWL	310	320	330	340	350	360

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	360	370	380	390	400	410
m589.pep	IKGDWTVALMHAVAVLVIACPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
g589	IKGDWTVALMHAVAVLVIACPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
	370	380	390	400	410	420
	420	430	440	450	460	470
m589.pep	VVLDKTGTLTEGSPQVAAVYCVDPDSGFDEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
g589	VVLDKTGTLTEGRPQVAAVYYVPDSGFDEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
	430	440	450	460	470	480
	480	490	500	510	520	530
m589.pep	DIPAAQNAQTVVGAGITAEEVGVGLVKAGKAEFAELALPKFLDGVWDIASIVAVSVDNKP					
g589	EIPAAQNAQTVVGAGITAEEVGVGLVKSAGKAEFAELTLPKFSDGVWEIASAVTVSVNGKP					
	490	500	510	520	530	540
	540	550	560	570	580	590
m589.pep	IGAFALADALKADTAEAI GRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
g589	IGAFALSDALKADTAEAI GRLKKHNIDVYIMSGDNQSTVEYVAKQLGIAHAFGNMSPCDK					
	550	560	570	580	590	600
	600	610	620	630	640	650
m589.pep	AAEVQKLKAAGKTVAMVGDGINAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
g589	AAEVQKLKAAGKTVAMVGDGINAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
	610	620	630	640	650	660
	660	670	680	690	700	710
m589.pep	DALLVSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLGNALRLK					
g589	DALLISQATLENIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLGNALRLK					
	670	680	690	700	710	720
	720					
m589.pep	RVKIDX					
g589	WVKIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1831>:

```

a589.seq
1  ATGCAACAAA AAGTCCGTTT CCAAAATCGAA GGCATGACCT GCCAGGCATG
51  TGCTTCGCGC ATTGAAAAAG TGTGAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTTGCCAGC GAAGAGGCTC AGGTAGTGT TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GAGGTTGTGG CTTTGTCTGG CCATCAATAT CCCGTTCTCT
301 ATCGGTATGG TAGGGATGAT GCTAAAAGGG CTGAATTGGA CACGGCATGA
351 TTGGATGTTG TCGCCCTTGT TGCAGTTTGC ATTGGCGAGT GTGGTGCAGC
401 TTTGGCTGGC GGTGCCATT TACAAAAGCG CGTGGGCGAG CATTAAAGGC
451 GGGCTGGCGA ATATGGACGT ACTCGTTACC ATCGGCACGG TCTCGATTTA
501 CCTGTATTCC GTCTATATGC TGTTTTTCAG CCCGCACGCG GCGTACGGTA
551 TGGCGCATGT GTATTTTGAA GTAGGCATAA TGGTGATTGG TTTTGTGTCA
601 CTGGGTAAAT TTTTGGAACA CCGCACCAAA AAATCCAGCC TGAACAGCTT
651 GGGCTTGCTG CTCAAATCA CGCAACCCA AGTCAACGTG CAACGCGATG
701 ACGAATGGCG GCAGCTACCC ATCGACCAAG TGCAAATCGG GCACCTAATC
751 CGCGCCAATC ACGCGCAACG CATTGCCGCC GACGGCATCA TAGAAAGCGG
801 CAGCGGCTGG GCGGACGAAA GCCATCTTAC CGCGGAATCC AATCCCGAAG
851 AGAAAAAGGC AGGCGGCAAA GTATTGGCGG GCGCGCTGAT GACTGAAGGC
901 ACGGTGGTGT ACCGCGCCGC GCAGCTCGGC AGCCAAACCC TGCTCGGCGA
951 CATGATGAAC GCGCTCTCCG AAGCGCAAGG CAGTAAACCA CCGATTGCGC
1001 GTGTGGCGGA CAAGGCGGCG GCGGTATTCTG TGCTGCGGT GTGGGATC
1051 GCACTTTTGA CTTTATATCG TACTTGGCTG ATTAAGGCGG ATTGGACGCT
1101 CGCATTGATG CACGCCGTCG CCGTTTGGT GATTGCTGCG CCGTGTGCAC

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```
1151 TCGGTTTGGC AACCCCTGCT GCGATTATGG TCGGTATGGG CAAAGCGGTT
1201 AAACACGGTA TTTGGTTTAA AGACGCGGCA GCAATGGAAG AAGCCGCCCA
1251 CGTTGATGCC GTCGTGCTGG ACAAACCGG CACGCTGACC GAAGGCAAGC
1301 CGCAGGTTGC CGCCGTTTAT TGTGTTCCCG ACAGCGGCTT TGACGAAGAC
1351 GCTTTGTACC GCATCGCCGC CGCCGTCGAA CAAAACGCCG CCCATCCGCT
1401 CGCCCGTGCC ATCGTCTCCG CCGCCAGGC GCGCGGTTTG GAGATTCCCA
1451 CCGCACAAAA TGCCCAAACC ATTGTCGGCG CGGGCATTAC CGCCGAAGTA
1501 AAAGGCGCGG GTTTGGTAAA AGCAGGCAAA GCCGAATTG CCGAACTGAC
1551 CTTGCCGAAG TTTTCAGACG GCGTTTGGGA AATCGCCAGT GTGGTTGCCG
1601 TATCTGTAAA CGGCAACCT ATCGGCGCAT TCGCACTCGC CGACGCGTTG
1651 AAAGCCGATA CCGCCGAAGC CATAGGCCGT CTGAAAAAAC ACAATATCGA
1701 TGTCTATATT ATGAGCGGCG ATAACCAAGG CACGCTCGAG TACGTCGCCA
1751 AACAACTGGG CATCGCACAC GCCTTCGGTA ATATGAGTCC GCGCGACAAA
1801 GCCGCCGAAG TGCAGAACT CAAAGCCGCC GCGAAAACCG TGGCGATGGT
1851 CGCGGACGGC ATCAACGACG CGCCCGCGCT CGCCGCCGCC AACGTCAGCT
1901 TCGCCATGAA AGGCGGTGCA GACGTTGCCG AACACACCGC ATCCGCCACA
1951 CTGATGCAGC ATTCGGTCAA CCAGCTCGCC GATGCGCTAT CGGTATCGCG
2001 AGCGACGTTG AAAAACATCA AGCAAAACCT GTTTTTCGCC TTCTTCTACA
2051 ATATTTTGGG CATTCCCTC GCGCGCTCG GCTTTTAAA CCCCCTCATC
2101 GCAGGCGCGG CAATGGCGGC AAGCTCGGTT TCCGTGTTGA GCAACGCCTT
2151 GCGCCTGAAA CGGGTAAAAA TCGATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1832; ORF 589.a>:

```
a589.pep
1  MQQKVRFQIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
51  KTSVADI AKI IEKTGYGAKE KTEDTLQPE AEHHIGWRLW LLLAINIPFL
101 IGMVGMMLKG LNWTRHDWML SPLLOFALAS VVQLWLAVPF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSPHA AYGMHVYFE VGIMVIGFVS
201 LGKFLERHTK KSSLNSLGLL LKLTPTQVNV QRDGEWRQLP IDQVQIGDLI
251 RANHGERIAA DGIIESGSGW ADESHLTGES NPEEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPAVVGI
351 ALLTFIATWL IKGDWTLALM HAVAVLVIA PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGKPQVAAY CVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPTAQNAQT IVGAGITAEV
501 KGAGLVKAGK AEFaelTLpk FSDGVWEIAS VVAVSVNGKP IGAFALADAL
551 KADTAEAIGR LKKHNIDVYI MSGDNQGTVE YVAKQLGIAH AFGNMSPRDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGGG DVAHTASAT
651 LMQHSVNQLA DALSVSRATL KNIKQLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLSNALRLK RVKID*

m589/a589 94.9% identity in 725 aa overlap

          10      20      30      40      50      60
m589.pep  MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADI AKI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      MQQKVRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADI AKI
          10      20      30      40      50      60

          70      80      90      100     110
m589.pep  IEKTGYGAKEKTEDTLQPEAEHHIGWRLWLLFTINVPFLIGMAGMMIG-----RHDWMI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      IEKTGYGAKEKTEDTLQPEAEHHIGWRLWLLLAINIPFLIGMVGMMLKGLNWTRHDWML
          70      80      90      100     110     120

          120     130     140     150     160     170
m589.pep  PPLWQFALASVVQLWLAIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      SPLLOFALASVVQLWLAVPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
          130     140     150     160     170     180

          180     190     200     210     220     230
m589.pep  AYGMHVYFEVGMVIGFVSLGKFLERHTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      AYGMHVYFEVGIMVIGFVSLGKFLERHTKKSSLNSLGLLLKLTPTQVNVQRDGEWRQLP
          190     200     210     220     230     240
```

924

m589.pep	240	250	260	270	280	290
	IDQVQIGDLIRANHGERIAADGII	ESGSGWADESHLTGESNPEEK	KAGGKVL	LAGALMTEG		
a589	IDQVQIGDLIRANHGERIAADGII	ESGSGWADESHLTGESNPEEK	KAGGKVL	LAGALMTEG		
	250	260	270	280	290	300
m589.pep	300	310	320	330	340	350
	SVVYRATQLGSQTQLGDMMNAL	SEAQGSKAPIARVADKAAAV	FVPAVVGIALLT	FIIVTWL		
a589	SVVYRATQLGSQTQLGDMMNAL	SEAQGSKAPIARVADKAAAV	FVPAVVGIALLT	FIIVTWL		
	310	320	330	340	350	360
m589.pep	360	370	380	390	400	410
	IKGDWTVALMHAVAVLVIA	CPALGLATPAAIMVGMGKAV	KHGIWFKDAAAMEE	AAHVDA		
a589	IKGDWTVALMHAVAVLVIA	CPALGLATPAAIMVGMGKAV	KHGIWFKDAAAMEE	AAHVDA		
	370	380	390	400	410	420
m589.pep	420	430	440	450	460	470
	VVLDKTGTLTGEGSPQVA	AVYCVPSGDFEDALYRIA	AAVEQNAAHPLARA	IVSAAQARGL		
a589	VVLDKTGTLTGEGSPQVA	AVYCVPSGDFEDALYRIA	AAVEQNAAHPLARA	IVSAAQARGL		
	430	440	450	460	470	480
m589.pep	480	490	500	510	520	530
	DIPAAQNAQTVVAGITA	EVGVLVKAGKAFAEL	LPKFLDGVWDIA	IVAVSVDNKP		
a589	EIPTAQNQITVAGITA	EVGVLVKAGKAFAEL	LPKFLDGVWDIA	IVAVSVDNKP		
	490	500	510	520	530	540
m589.pep	540	550	560	570	580	590
	IGAFALADALKADTAE	AIGRLKKNIDVYIMSGDN	QGTVEYVAKQLG	IAHAFGNMSPRDK		
a589	IGAFALADALKADTAE	AIGRLKKNIDVYIMSGDN	QGTVEYVAKQLG	IAHAFGNMSPRDK		
	550	560	570	580	590	600
m589.pep	600	610	620	630	640	650
	AAEVQKLKAAGKT	VAMVGDGINDAPALAA	ANVSFAMKGGADVA	EHTASATLMQHSVN	QLA	
a589	AAEVQKLKAAGKT	VAMVGDGINDAPALAA	ANVSFAMKGGADVA	EHTASATLMQHSVN	QLA	
	610	620	630	640	650	660
m589.pep	660	670	680	690	700	710
	DALLVSQATLKNIKQ	NLFFAFFYNILGIPLA	ALGFLNPVIAGA	AMAASSVSVLSNAL	RRLK	
a589	DALLVSQATLKNIKQ	NLFFAFFYNILGIPLA	ALGFLNPVIAGA	AMAASSVSVLSNAL	RRLK	
	670	680	690	700	710	720
m589.pep	720					
	RVKIDX					
a589	RVKIDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1833>:

g590.seq..

```

1  atgaaaaaac ctttgatttc agttgcggca gtattgctcg gcggttgcctt
51  ggggtacacct tattatttgg gtgtcaaaagc agaagaaagt ctgacgcagc
101 agcaaaaaat attgcagaaa acgggctttt tgaccgtcga atcgaccag
151 tatgatcgag gctggtttac ctctacggaa acgacggtea tccgtctgaa
201 acccgagttg ctgcataatg cgcagaaata cctgccggat aacttgaaaa
251 tagtgttgga acagccgggt acgctggtta accatatcac gcacggccct
301 ttcgccggcg gattcggcac gcaggcgcac attgaaaccg agttcaaata
351 cgcgcctgaa acggaaaaag ttttggaaac cttttttggg aaacaagttc
401 cggtttccct tgccaatacc gtttatttca acggcagcgg taaaatggaa
451 gtcagtgttc cgcctttcga ttatgaagaa ctgtcgggca tcaggctgca

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925

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501 ctgggaagggc ctgacggggg aaacgggttta tcaaaaaggt ttcaaaagct
551 accgcaacag ctatgatgcg cccttggtca aaatcaagct ggcagacaaa
601 ggcgatgccc cggttgaaaa agcgcatttc gattcggaaa cttcagacgg
651 catcaatccg cttgctttgg gcagcagcaa tctgactttg gaaaaatttt
701 cgctcgaaag gaaagagggg gtcgattaca acgtcaaat gaacgaactg
751 gtcaaccccg ttaccgattt gcagatcggc gcgtttatca atcccaacgg
801 cagcatcgca ccttccaaaa tcgaagtcgg caagctggct ttttcaacca
851 agaccggggg atcgggcgcg tttatcgaca gcgaaggcg gttccgtttc
901 gatacgttgg tgtacggcga tgaataatc ggcgcgctgg acatccatat
951 cgctgcccga cacctcgatg cttctgcctt aacggtattg aaacgcaagt
1001 ttgcacaaat ttctgccaaa aaaatgactg aggaacaaat ccgcaatgat
1051 ttgattggcg cagtcacagg cgatgcttcc ggattattta cccatgaccc
1101 ggtactaaat atcaaaattt tccgtttcac cctgcctcag ggaaaaattg
1151 atgtggggcg aaaaatcatg tttaaaggca tgaagaagga agatttgaac
1201 caattgggac tgatgttaaa gaaaaccgag gcaaacatca gaatgagtat
1251 tctcaaaaa atgttggaag atttggcggt aagtcaggct ggaaatattt
1301 tcagtgtaaa tgccgaagat gaggcggaag ccagagcaag cattgccgat
1351 attaatgaaa cattgcgctt gatggtggac agtacggtcc aaagtatggc
1401 aagggaaaaa tatcttactt tagacggtaa tcagattgat acggtcattt
1451 cccttaaaaa caacgccctg aagttaaacg ggaacgct gcaaatgaa
1501 cccgatcctg attttgacga gggagatag gtttccggcc agccgcatta
1551 a

```

This corresponds to the amino acid sequence <SEQ ID 1834; ORF 590.ng>:

g590.pep..

```

1 MKKPLISVAA VLLGVALGTP YYLGVKAEES LTQQQKILQK TGFLTVESHQ
51 YDRGWFTSTE TTVIRLKP EL LHNAQKYL PD NLKIVLEQPV TLVNHITHGP
101 FAGFGTQAH IETEFKYAP E TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFYDEE LSGIRLHWEG LTGETVYQKG FKSyrNSYDA PLFKIKLADK
201 GDAAFEKAHF DSETSDGINP LALGSSNLT L EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FIDSEGRFRF
301 DTLVYGD EKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTEQIRND
351 LIAAVKGDAS GLFTHDPVLN IKIFRFTLPQ GKIDVGGKIM FKGMKKEDLN
401 QLGLMLKKTE ANIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEARASIA D
451 INETLRLMVD STVQSMAREK YLTLDGNQID TVISLKNAL KLNGKTLQNE
501 PDPDFDEGDM VSGQPH*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1835>:

m590.seq (partial) ..

```

1 ..TGGTTTACCT CTATGGAAC GACGGTCATC CGTCTGAAAC CCGAGTTGCT
51 GAATAATGCC CGAAATACC TGCCGGATAA CCTGAAACA GTGTGGAAC
101 AGCCGGTTAC GCTGGTTAAC CATATCACGC ACGGCCCTTT CGCCGGCGGA
151 TTCGCACGCG AGGCGTACAT TGAAACCGAG TTCAAATACG CGCCTGAAAC
201 GGAAAAAGTT CTGGAACGCT TTTTGGGAAA ACAAGTCCCG GCTTCCCTTG
251 CCAATACCGT TTATTTTAA GGCAGCGGTA AAATGGAAGT CAGTGTTCCT
301 GCCTTCGATT ATGAAGAGCT GTCGGGCATc AG . CTGCACT GGGAAKGCCT
351 GACGGGAGAA ACGGTTTATC AAAAAGGTTT CAAAAGCTAC CGGAACGGCT
401 ATGATGCCCC CTTGTTTAAA ATCAAGCTGG CAGACAAAGG CGATGCCGCG
451 TTTGAAAAAG TGCATTTCGA TTCGGAAACT TCAGACGGCA TCAATCCGCT
501 TGCTTTGGGC AGCAGCAATC TGACCTTGGA AAAATTCTCC CTAGAATGGA
551 AAGAGGGTGT CGATTACAAC GTCAAGTTAA ACGAACTGGT CAATCTTGTT
601 ACCGATTTCG AGATTGGCGC GTTTATCAAT CCCAACGGCA GCATCGCACC
651 TTCCAAATC GAAGTCGGCA AACTGGCTTT TTCAACCAAG ACCGGGGAAT
701 CAGGCGCGTT TATCAACAGT GAAGGGCAGT TCCGTTTCGA TACACTGGTG
751 TACGGCGATG AAAAATACGG CCCGCTGGAC ATCCATATCG CTGCCGAACA
801 CCTCGATGCT TCTGCCTTAA CCGTATTGAA ACGCAAGTTT GCACAAATTT
851 CCGCCAAAAA AATGACCGAG GAACAAATCC GCAATGATTG GATTGCCGCC
901 GTCAAAGGAG AGGCTTCCGG ACTGTTCCAC AACAAATCCC TATTGGACAT
951 TAAAACCTTC CGATTACGCG TGCCATCGGG AAAAATCGAT GTGGGCGGAA
1001 AAATCATCTT TAAACACATG AAGAAGGAAG ATTTGAATCA ATTGGGTTTG
1051 ATGCTGGAAG AAAACGAAGC CGACATCAGA ATGACTATT CCAAAAAAT
1101 GCTGGAAGAC TTGGCGGTCA GTCAGCAGG CAATATTTTC AGCGTCAATG
1151 CCGAAGATGA GCGGAAGGC AGGGCAAGTC TTGACGACAT CAACGAGACC
1201 TTGCCCTTGA TGGTGGACAG TACGTTTAC AGTATGGCAA GGAAAAATA
1251 TCTGACTTTG AACGGCGACC AGATTGATAC TGCCATTTC TGA AAAACA
1301 ATCAGTTGAA ATTGAACGGT AAAACGTTGC AAAACGAACC GGAGCCGGAT
1351 TTTGATGAAG GCGGTATGCT TTCAGAGCCG CAGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1836; ORF 590>:

1	WFTSMETTVI	RLKPELLNNA	RKYPDLNLKT	VLEQPVTLVN	HITHGPFAGG
51	FGTQAYITEV	FKYAPETKEV	LERFPFGKPV	ASLANTVYFN	GSGKHEVSVF
101	AFDYHEELSGI	KLHWEXPLTK	TVYQKGQFSP	RNGYDAPLKF	IKLADKGDA
151	FEKVHFDSET	SDGINPLALG	SSNLTLLEKFS	LEWKEGVVDY	VKLNLVLNLV
201	TDLQIGAFIN	PNGSIAPFSKI	EVGKLAFSTK	TGESGAFINS	EQGFRTDLTV
251	YGDEKYGPLD	THIAAEHLDA	SALTVLKRKF	AQISAKMTE	EQRINDLIAA
301	VKGASGLFTP	NNPVLDIRTF	IKFTLPSGKD	VGKGIKPKDM	KEKDLNLQGL
351	MLKKTEADIR	MSIPQKMLED	LAVSQAGNIF	SVNAEAEAG	RASLDDINET
401	LRLMVDSTVP	SMAREKYLTL	NGDQIDTAIS	LKNNQLKLNG	KTQLNEPEPD
451	FDEGGMVSEQ	QQ*			

m590 / g590 93.1% identity in 462 aa overlap

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1837>:

```
a590.seq
1  ATGAAAAAAC CTTTGATTTC GGTTCGCGCA GCATTGCTCG GCGTTGCTTT
51  GGGCAGCCCT TATTATTTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA GCGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTACGGAA ACGACGGTCA TCCGCTTGAA
201 ACCCGAGTTG CTGCATAATG CGCAGAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTGGGA ACAGCCGGTT ACGCTGGTAA ACCATATCAC GCACGGTCCT
301 TTTGCCGGCG GATTGCGCAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
401 CGGTTTCCCT TGCCAATACC GTTATTTTA ACGGCAGCGG TAAATGGAA
451 GTCAGTGTTT CCGCCTTCGA TTATGAAGAG CTGTGCGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GCGGATGCCG CGTTTGAAAA AGTGCATTTC GATTGCGAAA CTTCAGACGG
651 CATCAACCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTTT
701 CCTTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACCAACTG
751 GTCAATCTTG TTACCGATTG GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAGCTGGCT TTTTCAACCA
851 AGACCGGGGA ATCGGGCGCG TTTATCGATA GCGAAGGCGA GTTCCGTTTT
901 GGCACGCTGG TTTACGGCGA TGAAAAATAC GGCCCTCTGG ACATCCATAT
951 CGGTGCCGAA CACCTCGATG CTCTGCTT AACCCTATTG AAACGCAAGT
1001 TTGCACGAAT TTCTGCCAAA AAAATGACTG AAGAACAAAT CCGCAATGAT
1051 TTGATTGCGG CAGTCAAAGG CGAGGCTTCC GGATTATTTA CCCATAACCC
1101 AGTATTGGAC ATTAAACTTT TCCGATTACG GCTGCCATCG GGAAAAATCG
1151 ATGTGGGCGG AAAAATCATG TTAAAGACA TGAAGAAGGA AGATTGTAAC
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT
1251 TCCCCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGCCTCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAACGTT GCAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A
```

This corresponds to the amino acid sequence <SEQ ID 1838; ORF 590.a>:

```
a590.pep
1  MKKPLISVAA ALLGVALGTP YYLGVAEES LTQQQKILQE AGFLTVESHQ
51  YERGWFTSTE TTVIRLKP EL LHNAQKYL PD NLKTVLEQ PV TLVNHITHGP
101 FAGGFQTQAY IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
201 GDAAFEKVHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA PSTKTGESGA FIDSEGQFRF
301 GTLVYGDKEY GPLDIHIAAE HLDASALTVL KRKFARISAK KMTEEQIRND
351 LIAAVKGEAS GLFTHNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
401 QLGLMLKKEE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDE
451 INETLRLMVD STVQSMAREK YLTNGDQID TAISLKNNQL KLNGKTLQNE
501 PEPDFDEGGM VSEPQQ*
```

m590/a590 97.8% identity in 462 aa overlap

```

                                10      20      30
m590.pep                                WFTSMETTVIRLKPPELLNNARKYLPDNLKT
a590      VKAEESLTQQQKILQEAGFLTVESHQYERGWFTSTETTVIRLKPPELLHNAQKYL PDNLKT
           30      40      50      60      70      80

           40      50      60      70      80      90
m590.pep      VLEQPVTLVNHITHGPFAGGFQTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
a590      VLEQPVTLVNHITHGPFAGGFQTQAYIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN
           90     100     110     120     130     140

           100     110     120     130     140     150
m590.pep      GSGKMEVSVPAFDYEEELSGIXLHWEXLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
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928

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|||||
a590      GSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
          150      160      170      180      190      200

          160      170      180      190      200      210
m590.pep  FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGV DYNVKNELVNLVTDLQIGAFIN
          |||||
a590      FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGV DYNVKNELVNLVTDLQIGAFIN
          210      220      230      240      250      260

          220      230      240      250      260      270
m590.pep  PNGSIAPSKIEVGKLAFFSTKTGESGAFINSEGGQFRFDTLVYGDEKYGPLDIHIAAEHLDA
          |||||
a590      PNGSIAPSKIEVGKLAFFSTKTGESGAFIDSEGGQFRFGTLVYGDEKYGPLDIHIAAEHLDA
          270      280      290      300      310      320

          280      290      300      310      320      330
m590.pep  SALTVLKRKFAQISAKKMTTEEQIRNDLIAAVKGEASGLFTNPNVLDIKTFRFTLPSPGKID
          |||||
a590      SALTVLKRKFARISAKKMTTEEQIRNDLIAAVKGEASGLFTNPNVLDIKTFRFTLPSPGKID
          330      340      350      360      370      380

          340      350      360      370      380      390
m590.pep  VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG
          |||||
a590      VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG
          390      400      410      420      430      440

          400      410      420      430      440      450
m590.pep  RASLDDINETLRLMVDSTVQSMAREKYLTNGDQIDTAISLKNQKLKNGKTLQNEPEPD
          |||||
a590      RASLDDINETLRLMVDSTVQSMAREKYLTNGDQIDTAISLKNQKLKNGKTLQNEPEPD
          450      460      470      480      490      500

          460
m590.pep  FDEGGMVSEPPQX
          |||||
a590      FDEGGMVSEPPQX
          510

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1839>:

m590-1.seq

```

1  ATGAAAAAAC CTTTGATTTC GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA ACGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTATGGAA ACGACGGTCA TCCGTCTGAA
201 ACCCGAGTTG CTGAATAATG CCCGAAAATA CCTGCCGAT AACCTGAAAA
251 CAGTGTGGA ACAGCCGGTT ACGCTGGTTA ACCATATCAC GCACGGCCCT
301 TTCGCCGCG GATTCGGCAC GCAGGCGTAC ATTGAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
401 CGGCTTCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAATGGAA
451 GTCACTGTT CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GGCATGCGG GTTGTGAAAA AGTGCATTTC GATTCGGAAT CTCAGACGG
651 CATCAATCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTCT
701 CCCTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAACG
751 TGCATCTTG TTACCGATTT GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAACTGGCT TTTTCAACCA
851 AGACCGGGGA ATCAGGCGCG TTTATCAACA GTGAAGGGCA GTTCCGTTT
901 GATACACTGG GTACGGCGA TGAAAAATAC GGCCCGCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AACGCAAST
1001 TTGCACAAAT TTCCGCCAAA AAAATGACCG AGGAACAAAT CCGCAATGAT
1051 TTGATTGCCG CCGTCAAAGG AGAGGCTTCC GGACTGTCCA CCAACAATCC
1101 CGTATTGGAC ATTAATACTT TCCGATTAC GCTGCCATCG GAAAAATCG
1151 ATGTGGGCGG AAAAATCATG TTTAAAGACA TGAAGAAGGA AGATTTGAAT
1201 CAATTGGGTT TGATGCTGAA GAAACCGAA GCCGACATCA GAATGAGTAT

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1251 TCCCCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
 1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
 1351 ATCAACGAGA CCTTGCCTCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
 1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
 1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAAAGTT GCAAAACGAA
 1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
 1551 A

This corresponds to the amino acid sequence <SEQ ID 1840; ORF 590-1>:

m590-1.pep

1 MKKPLISVAA ALLGVALGTP YYLGVKAES LTQQQKILQE TGFLTVESHO
 51 YERGWFSTME TTVIRLKP EL LNNARKYLPD NLKTVLEQPV TLVNHITHGP
 101 FAGGFGCTQAY IETEFKYAPE TEKVLERFFG KQVPASLANT VYFNGSGKME
 151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
 201 GDAAFEKVHF DSETSDGINP LALGSSNLTLEKFSLEWKEG VDYNVKLNEL
 251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FINSEGQFRF
 301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KRRFAQISAK KMTTEEQIRND
 351 LIAAVKGEAS GLFTNNPVL D IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
 401 QLGMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASIDD
 451 INETLRLMVD STVQSMAREK YLTNGDQID TAISLKNQL KLNGKTLQNE
 501 PEPDFDEGGM VSEPPQ*

m590-1/g590 93.6% identity in 516 aa overlap

	10	20	30	40	50	60
m590-1.pep	MKKPLISVAAALLGVALGTPYYLGVKAESLTQQQKILQETGFLTVESHQYERGWFSTME					
g590	MKKPLISVAAALLGVALGTPYYLGVKAESLTQQQKILQETGFLTVESHQYDRGWFSTTE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m590-1.pep	TTVIRLKPPELLNNARKYLPDNLKTVLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPE					
g590	TTVIRLKPPELLHNAQKYLDPNLKIVLEQPVTLVNHITHGPFAGGFGTQAHIETEFKYAPE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m590-1.pep	TEKVLERFFGKQVPASLANTVYFNGSGKMEVSVPAFDYEE LSGIRLHWEGLTGETVYQKG					
g590	TEKVLERFFGKQVPASLANTVYFNGSGKMEVSVPAFDYEE LSGIRLHWEGLTGETVYQKG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m590-1.pep	FKSYRNGYDAPLFKIKLADKGDAAFEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEG					
g590	FKSYRNSYDAPLFKIKLADKGDAAFEKAHFDSETSDGINPLALGSSNLTLEKFSLEWKEG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m590-1.pep	VDYNVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLA FSTKTGESGA FINSEGQFRF					
g590	VDYNVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLA FSTKTGESGA FIDSEGRFRF					
	250	260	270	280	290	300
	310	320	330	340	350	360
m590-1.pep	DTLVYGDEKYGPLDIHIAAEHLASALTVLKRRFAQISAKKMTTEEQIRNDLIAAVKGEAS					
g590	DTLVYGDEKYGPLDIHIAAEHLASALTVLKRRFAQISAKKMTTEEQIRNDLIAAVKGDAS					
	310	320	330	340	350	360
	370	380	390	400	410	420
m590-1.pep	GLFTNNPVL DIKTFRFTLPSGKIDVGGKINFKDMKKEDLNQLGLMLKKTEADIRMSIPQK					
g590	GLFTHDPVLN I KIFRFTLPQSGKIDVGGKINFKGMKKEDLNQLGLMLKKTEANIRMSIPQK					
	370	380	390	400	410	420
	430	440	450	460	470	480
m590-1.pep	MLEDLAVSQAGNIFSVNAEDEAEGRASLDDINETLRLMVDSTVQSMAREKYLTNGDQID					
g590	MLEDLAVSQAGNIFSVNAEDEAEARASLDDINETLRLMVDSTVQSMAREKYLTLDGNDQID					
	430	440	450	460	470	480
	490	500	510			
m590-1.pep	TAISLKNQLKLNGKTLQNEPEPDFDEGGNVS-EPQQX					

[illegible]

g591.seq

1	TTGCAAAACC	TTCTAGCTTT	TATCTTCGCC	ATCCTGATTT	TGGTCAGCCT
51	GCACGAATTC	GGACACTACA	TCTCGCCAG	GTGTGCGGC	GTCAGGTTG
101	TGCGTTTTC	CGTCGCCTC	GGCAACCGT	TTTTCCCGC	AAGCGCGGC
151	GACACCGAAT	GGTGCTCGC	CCCGATTCCG	TTGGCCGGT	ACGTCAAAAT
201	GGTCGATACG	CGCGAAGGCG	AAGTATCAGA	AGCCGATTTA	CCCTACGCTT
251	TTGACAAAAC	ACACCCCGCC	AAGCGCATCG	CCATCGCTCG	CGCCGGTCCG
301	CTGGCAACAC	TCGCActggc	ggTTTTGCTG	TACGGATCTGa	gctTtctctt
351	cggcgtaacc	GAATGCGGC	CCtatgtcgg	cacagctqaA	cccgacacc

931

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401 ttgccgCCCC CACCGGCTTC caaagcggcg acaaAATACa atccgtcaac
451 ggcgtTtccg tCCAAGACTG GAGCAGCGCG CAAACCGAAA TCGTcctcAA
501 CCTCGAAGCC Ggcaaagtcg ccgtcggcgT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATcgAT GCCGCAGGCA CGCCGGAAGC CGGTAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGc cteaTGGCAG
751 GAATGggcaa acctgACcg cCAAAGCCG ggcAAAAAAA Tcaccctgac
801 ctacgAaCGC GUcggacaaa cccaTaccgc CGACATCCG CccgATactg
851 TCGAAcagcc cgACCACACC CTGATCgggc gcgTCGGCCT CCGtccgcaG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCCCTCA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCTGTTCAGC
1051 CATATTTCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAAATTTT AGCGTTGGT AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGGCACCTC
1201 GTGTTTATA CTGTCGAATG GATACGCGGC AAACCTTTGG GCGAACGTGT
1251 CCAAAACATC GGTTTGCGCT TCGGGCTCGC CCTGATGATG CTGATGATGG
1301 CGGCGCCTT CTCAACGAC GTTACCGGC TGATCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1842; ORF 591.ng>:

g591.pep..

```

1 LQTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF SKPFFTRKRG
51 DTEWCLAPIP LGGYVKMVDI REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTVAARTGF QSGDKIQSVN
151 GVSVDWSSA QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTYER AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGLVNL L PVPVLDGGHL
401 VFYTVIEWIRG KPLGERVQNI GLRFLGLALMM LMMAAFFND VTRLIG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1843>:

m591.seq

```

1 TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51 GCACGAGTTC GGACACTACA TCGTTGCCAG ATTGTGCGGC GTCAAAGTCG
101 TACGCTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GTTCGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCA
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTAACC GAACTGCGCC CCTACGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCC CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGCGCT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAA TCACCTGAA
801 TACGAACGC GCGGACAAA CCCATACCGC CGACATCCG CCGGATACTG
851 TCGAACAGTC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCCCTCA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCCGTGAGC
1051 CATATTTCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAAATTTT AGCACTGGT AGCATCAGCC
1151 TCGGCGTGCT GAACCTACTG CCCGTCCCTG TTTTGGACGG CGGGCACCTC
1201 GTGTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CCAAAACATC GGTTTGCGCT TCGGGCTCGC CCTCATGATG CTGATGATGG
1301 CCGTCGCTT CTCAACGAC GTTACCGGC TGCTCGGTTA G

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This corresponds to the amino acid sequence <SEQ ID 1844; ORF 591>:

m591.pep..

932

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1  LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKRK
51 DTEWCLAPIP LGGYVKMVD T REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV E PDTIAARAGF QSGDKIQSVN
151 GTPVADWGS A QTEIVLNLEA GXVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTROSP GKKITLNYER AGQHTADIR PDTVEQSDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFGALMM LMMVAFFND VTRL LG*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m591 / g591 97.3% identity in 446 aa overlap

	10	20	30	40	50	60
m591.pep	LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKRGDTEWCLAPIP					
g591	LQTLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKRGDTEWCLAPIP					
	10	20	30	40	50	60
m591.pep	LGGYVKMVD TREGEVSEADL PYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT					
g591	LGGYVKMVD TREGEVSEADL PYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT					
	70	80	90	100	110	120
m591.pep	LGGYVKMVD TREGEVSEADL PYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT					
g591	LGGYVKMVD TREGEVSEADL PYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT					
	70	80	90	100	110	120
m591.pep	ELRPYVGTV E PDTIAARAGF QSGDKIQSVNGT PVADWGS AQTEIVLNLEAGKVAVGVQTA					
g591	ELRPYVGTV E PDTVAARTG FQSGDKIQSVNGV SVQDWSS AQTEIVLNLEAGKVAVGVQTA					
	130	140	150	160	170	180
m591.pep	ELRPYVGTV E PDTIAARAGF QSGDKIQSVNGT PVADWGS AQTEIVLNLEAGKVAVGVQTA					
g591	ELRPYVGTV E PDTVAARTG FQSGDKIQSVNGV SVQDWSS AQTEIVLNLEAGKVAVGVQTA					
	130	140	150	160	170	180
m591.pep	SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGRDLTA					
g591	SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGRDLTA					
	190	200	210	220	230	240
m591.pep	SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGRDLTA					
g591	SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGRDLTA					
	190	200	210	220	230	240
m591.pep	ADGKPIASWQEWANLTROSPGKKITLNYERAGQHTADIRPDTVEQSDHTLIGRVGLRPQ					
g591	ADGKPIASWQEWANLTROSPGKKITLTYERAGQHTADIRPDTVEQPDHTLIGRVGLRPQ					
	250	260	270	280	290	300
m591.pep	ADGKPIASWQEWANLTROSPGKKITLNYERAGQHTADIRPDTVEQSDHTLIGRVGLRPQ					
g591	ADGKPIASWQEWANLTROSPGKKITLTYERAGQHTADIRPDTVEQPDHTLIGRVGLRPQ					
	250	260	270	280	290	300
m591.pep	PDRAWDAQIRRSYRPSVVRAF GMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
g591	PDRAWDAQIRRSYRPSVVRAF GMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
	310	320	330	340	350	360
m591.pep	PDRAWDAQIRRSYRPSVVRAF GMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
g591	PDRAWDAQIRRSYRPSVVRAF GMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
	310	320	330	340	350	360
m591.pep	IAGQSAELGLQSYLEFLALVSISLGVNLLPVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
g591	IAGQSAELGLQSYLEFLALVSISLGVNLLPVPVLDGGHLVFYTVIEWIRGKPLGERVQNI					
	370	380	390	400	410	420
m591.pep	IAGQSAELGLQSYLEFLALVSISLGVNLLPVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
g591	IAGQSAELGLQSYLEFLALVSISLGVNLLPVPVLDGGHLVFYTVIEWIRGKPLGERVQNI					
	370	380	390	400	410	420
m591.pep	GLRFGALMMLMMAVAFFNDVTRL LGX					
g591	GLRFGALMMLMMAAFAFFNDVTRL IGX					
	430	440				
m591.pep	GLRFGALMMLMMAVAFFNDVTRL LGX					
g591	GLRFGALMMLMMAAFAFFNDVTRL IGX					
	430	440				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1845>:

a591.seq

933

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1   TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG ATTGTGCGGC GTCAAGGTTG
101 TGCGTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCGG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTCGACACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCG
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCCTTACC GAACTGCGCC CCTATGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCC CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAC
451 GGCACACCCG TTGCAGATTG GGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGAGGCA CGCGGAAGC CGGTAAATC
601 GCAAAAACC AAGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TCGCGCGCGC GTGAAAAAG GCAGCCCGC CGAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGCA AACCCATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCUCG GGCAAAAAA TCACCCTGAC
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGCC CGACCACACC CTGATCGGCG CCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAA AACCCTTTCC CACTCGTGGA
1001 CAACCCTCAA ATTTTTCGGC AACTAATCA GCGGCAACGC CTCGTCAGC
1051 CATATTTCCG GTCGCTGAC CATGCCGAT ATTGCCGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGAATTTT GGCACTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCG TTTTGACGG CGGCCACCTC
1201 GTGTTTATA CTGCCGAATG GATACGCGC AAACCTTTGG GCGAACCGCT
1251 CCAAACATC GGTTCGCGT TCGGGCTTGC CCTCATGATG CTGATGATCG
1301 CCGTCGCCTT CTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1846; ORF 591.a>:

```

a591.pep
1   LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GXPFFTRKRG
51  DTEWCLAPIP LGGYVKMVD T REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV PDI AARAGF QSGDKIQSVN
151 GTPVADWGS A QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTyer AGQHTADIR PDVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVR FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFGALMM LMAVAFFND VTRLLG*

```

m591/a591 99.6% identity in 446 aa overlap

	10	20	30	40	50	60
m591.pep	LHTLLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GXPFFTRKRG	DTEWCLAPIP
a591	LHTLLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GXPFFTRKRG	DTEWCLAPIP
	10	20	30	40	50	60
m591.pep	LGGYVKMVD	TREGEVSEADL	PYAFDKQHPA	KRIAIVAAGP	LTNLALAVLL	YGLSFSFGVT
a591	LGGYVKMVD	TREGEVSEADL	PYAFDKQHPA	KRIAIVAAGP	LTNLALAVLL	YGLSFSFGVT
	70	80	90	100	110	120
m591.pep	ELRPYVGTV	PDIAARAGF	QSGDKIQSVN	GTVPVADWGS	QAQTEIVLNLEA	GKVAVGVQTA
a591	ELRPYVGTV	PDIAARAGF	QSGDKIQSVN	GTVPVADWGS	QAQTEIVLNLEA	GKVAVGVQTA
	130	140	150	160	170	180
m591.pep	SGAQTVRTID	AAGTPEAGKI	AKNQGYIGLM	PFKITTVAGG	VEKGSPEAKA	GLKPGDRLTA
a591	SGAQTVRTID	AAGTPEAGKI	AKNQGYIGLM	PFKITTVAGG	VEKGSPEAKA	GLKPGDRLTA
	190	200	210	220	230	240
m591.pep	SGAQTVRTID	AAGTPEAGKI	AKNQGYIGLM	PFKITTVAGG	VEKGSPEAKA	GLKPGDRLTA
a591	SGAQTVRTID	AAGTPEAGKI	AKNQGYIGLM	PFKITTVAGG	VEKGSPEAKA	GLKPGDRLTA

934

	250	260	270	280	290	300
m591 . pep	ADGKPIASWQEWANLTRQSPGKKITLNYERAGQTHADIRPDTVEQSDHTLIGRVGLRPQ					
a591	ADGKPIASWQEWANLTRQSPGKKITLTYERAGQTHADIRPDTVEQPDHTLIGRVGLRPQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m591 . pep	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
a591	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
	310	320	330	340	350	360
	370	380	390	400	410	420
m591 . pep	IAGQSAELGLQSYLEFLALVVISLGVNLPLVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
a591	IAGQSAELGLQSYLEFLALVVISLGVNLPLVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
	370	380	390	400	410	420
	430	440				
m591 . pep	GLRFGLALMMLMMAVAFFNOVTRLLGX					
a591	GLRFGLALMMLMMAVAFFNOVTRLLGX					
	430	44C				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1847>:

g592.seq..

```

1  atgattccgg acgtgttcgg tcagatTTTT tcgggcgcgt tcaaattcga
51  cgccgcagca ggcggcttac tcggcggctc gatttcgcaa acgatgatga
101 tgggcatcaa acgcggcctg tattccaaag aggcgggtat gggttccgcg
151 ccgaaccccg ccgcccgcgc cgaagtgaag caccctgttt cgcaaggtat
201 gattcaaatg ctgggcgtgt ttgtcgatac catcatcggt tgttcttgca
251 ccgccttcac catcttgatt taccaacagc cttatggcga tttagcggtt
301 gcggcgctga cgcaggcggc gattgtcagc caagtggggc aatggggcgc
351 ggggtttcct gccgtcatcc tgtttatggt tgccctttcc accgttatcg
401 gcaactatgc ctatgccgag tccaacgtcc aattcatcaa aagccattgg
451 ctgattaccg ccgttttcgg tatgctgggt ttggcggtgg tctatttcgg
501 cgcggttgcc aatgtgcctt tggctcggga tatggcggtt atggcgatgg
551 gcatcatggc gtggatcaac ctgcgtcgca tcctgctgct ctgccatttg
601 gcgttttatg tgctgcgcga ttacacgcgc aagctgaaaa tgggcaagaa
651 ccccgagttc aaactttccg aacatccggg cctgaaacgc cgcatacaat
701 ccgatgtttg gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1848; ORF 592.ng>:

g592.pep ..

```

1  MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGSA
51  PNAAAAAEVK HPVSQGMIM LGVFVDIIIV CSCTAFIILI YQPYGDLGG
101 AALTQAAIVS QVGQWAGFL AVILFMFAPS TVIGNYAYAE SNVQFIKSHW
151 LITAVFRMLV LANVYFGAVA NVPLVNDMAD MAMGIMAWIN LVAILLLSPL
201 AFMLLRDYTA KLKMGKDPEF KLSEHGLKR RIKSDVW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1849>:

m592.seq ..

```

1  ATGATTCCGG ACGTGTTCGG TCAGATTTTT TCGGGCGCGT TCAAATTCGA
51  CGCGGCAGCA GCGGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
101 TGGGCATCAA ACGCGGCTG TATTCCAACG AGGCGGGTAT GGGTTCGCG
151 CCGAACCCCG CCGCGCCCGC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
201 GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTCTTGCA
251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTACGCGCA TTTGAGCGGT
301 CGCGGCTGTA CGCAGGCGGC GATTGTCAGC CAAGTGGGCG AATGGGCGC
351 GGGCTTCCTC GCGTCATCC TGTATTGTT TGCTTTTCC ACCGTTATCG
401 GCAACTATGC CTATGCCGAG TCCAAGTCC AATTTCATCA AAGCCATTGG
451 CTGATTACCG CCGTTTTCGG TATGCTGGTT TTGGCGTGG TCTATTTCGG
501 CGCGGTTGCC AATGTGCCCT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
551 GCATTATGGC GTGGATCAAC CTTGTGCCA TCCTGCTGCT CTCGCCCTTG

```

935

601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCCAGGTTT AACTTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1850; ORF 592>:

m592.pep ..
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRG LYSNEAGMGSA
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDTIIV CSCTAFIILI YQQPYGDL SG
 101 AALTQAAIVS QVGQWGAGFL AVILEMFAPF TVIGNYAYAR SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592 / g592 100.0% identity in 237 aa overlap

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAAGLLGGLISQTMMGIKRG LYSNEAGMGSAFNAAAAAEVK					
g592	MIPDVFGQIFSGAFKFDAAAAGLLGGLISQTMMGIKRG LYSNEAGMGSAFNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMQIMLGVFVDTIIVCSCTAFIILIYQQPYGDL SGAALTQAAIVSQVGQWGAGFL					
g592	HPVSQGMQIMLGVFVDTIIVCSCTAFIILIYQQPYGDL SGAALTQAAIVSQVGQWGAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILEMFAPFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
g592	AVILEMFAPFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHPGLKRRRIKSDVW*					
g592	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHPGLKRRRIKSDVW*					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1851>:

a592.seq
 1 ATGATTCGCG ACGTGTTCCG TCAGATTTTT TCGGGCGCGT TCAAATTCGA
 51 CGCGGCAGCA GCGGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
 101 TGGGCATCAA ACGCGCCTG TATTCCAACG AGGCGGGTAT GGGTTCGCGC
 151 CCGAACGCCG CCGCCGCCGC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
 201 GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTCTTGCA
 251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT
 301 CCGGCGCTGA CGCAGGCGGC GATTGTGAGC CAAGTGGGGC AATGGGGCGC
 351 GGGCTTCCTC GCCGTCATCC TGTATTATGT TGCCTTTTCC ACCGTTATCG
 401 GCAACTATGC CTATGCCGAG TCCACGCTCC AATTCATCAA AAGCCATTGG
 451 CTGATTACCG CCGTTTTCGG TATGCTGGTT TTGGCGTGGG TCTATTTCCG
 501 CGCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
 551 GCATTATGGC GTGGATCAAC CTTGTGCGCA TCCTGCTGCT CTCGCCCTTG
 601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCCAGGTTT AACTTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1852; ORF 592.a>:

a592.pep
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRG LYSNEAGMGSA
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDTIIV CSCTAFIILI YQQPYGDL SG
 101 AALTQAAIVS QVGQWGAGFL AVILEMFAPF TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592/a592 100.0% identity in 237 aa overlap

936

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMIMGIRGLYSNEAGMGSAPNAAAAAEVK					
a592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMIMGIRGLYSNEAGMGSAPNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMIOQLGVFVDTIIVCSCTAFIILIYQQPYGDLGAALTQAAIVSQVGQWGAGFL					
a592	HPVSQGMIOQLGVFVDTIIVCSCTAFIILIYQQPYGDLGAALTQAAIVSQVGQWGAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
a592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLMGKDEPKLSEHPGLKRRIKSDVWX					
a592	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLMGKDEPKLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1853>:

g593.seq..

```

1  atgcttgaac tgaacggact ctgcaaatgc ttcggcggca aaacggctcg
51  cgacaacatc tgcctgactg tcgggcgcgg caaaatactc gccgtactgg
101 ggcggtcggg ctgcggcaaa tccaccctgc tgaatatgat tgcgggcac
151 gtccggccgg acggcggcga aattcggctg aacggggaaa acattacctg
201 tatccgcccc gaaaaacgcc gtatctcgct gatgtttcaa gattacgcgc
251 tgtttcccca tatgagtgcg ctggaaaata cggcattcgg tttgaaaatg
301 caaaaaatgc cgaaagccga agccgaacgc ctgccttgt cggcacttgc
351 cgaagtcggg ctggaaaacg aggcgcaccg caagcctgaa aaactttccg
401 gaggcgagaa gcaacggttg gcaactggcg gcgctttggt tgtccgcctt
451 tccctgctgt tgcctgatga atcgttttcc agtttggaac cgcatttgcg
501 tcaccggctg cgccgtatga ccgccgaacg catccgcaag ggcggcatcc
551 ctgccgtttt ggtaacgcat tcgccgaag aggcctgcac ggcggcggac
601 gaaatcgccg tcatgcacga ggggaaaatc cttcaatgcg gacgcccga
651 aaccttgatt caaacgcctg ccggcgtgca ggtcgcccg cgtatggggc
701 tgcccaatc cgacgatgac cgccatattc cgcaaatgc cgtgtgcttg
751 gacaatcatg gaacggaatg ccgtctgctg tccctcgctc gcctgcccga
801 ctgctcccg ctttcgccc tccatcccga acacggcgag ctgaccttaa
851 acctgactgt cggacaacat acggacggta tttccgaaa cggtacggtc
901 cgcacccgcg tcgatgaagg gcgtatcgct cgtttccgat ga

```

This corresponds to the amino acid sequence <SEQ ID 1854; ORF 593.ng>:

g593.pep..

```

1  MLELNLCKC FGGKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIRL NGENITCMPP EKRRISLMFQ DYALFPHMSA LENTAFGLKM
101 QKMPKAEAEER LALSALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLI QTPAGVQVAR LMGLPNTDDD RHIPQNAVCL
251 DNHGTECRLL SLVRLPDSL RLSAVHPEHGE LTLNLTVGQH TDGISGNQTV
301 RIRVDEGRIV RFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1855>:

m593.seq

```

1  ATGCTTGAAC TGAACGGACT CTGCAAAACGC TTCGGCAATA AAACCGTCGC
51  CGACAACATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTGG
101 GGCGGTCGGG CTGCGGAAAA TCCACCCTGC TGAATATAAT TGCGGGGATT
151 GTCCGGCCGG ACGGCGGGGA AATATGGCTG AACGGAGAAA ACATTACCCG

```

937

```

201 TATGCCGCCC GAAAAACGCC GTATCTCGCT GATGTTTCAA GATTACGCGC
251 TGTTTCCCCA TATGAGTGCG CTGGAAAATG CGGCATTTCG TTTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAACGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAAAACG AGGCGCACCG CAAGCCTGAA AACTTTCCG
401 GAGGCGAGAA GCAACGGCTG GCGTTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTGGACGA ATCGTTTTC AGTTTGGACA CGCATTTCG
501 CGGCACGCTG CGCCGTATGA CTGCCGAACG TATCCGAAAC GGCGGCATCC
551 CTGCCGTTTT GGTAAACGCAT TCGCCCGAAG AAGCCTGTAC GACGGCAGAC
601 GAAATCGCCG TGATGCATAA AGGGAGGATT CTACAATACG GTACGCCCGA
651 AACATTGGTC AAAACACCAT CCTGCGTGCA GGTGCGCCGA CTGATGGGTT
701 TGCCAATAC CGACGATAAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTGCCCGA
801 ATCGTTCAGC CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCGGCACGCC GGGCGGGTAT CGGCAAGGA TACGGTACGC
901 ATCCATATCG AAGAACGGGA AATCGTCCGC TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1856; ORF 593>:

```

m593.pep  ..
1  MLELNLCKR FGNKTVADNI CLTVGRGKIL AVLGRSGCGK STILLNIIAGI
51  VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAFLGLKM
101 QKMPKAEAEER LAMAALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRGTL RRMTAERIRN GGIPAVLVTH SPEEACTTAD
201 EIAVMHKGRI LQYGPETLV KTPSCVQVAR LMGLPNTDDN RHIPQHVRP
251 DQDGMCECVL SRTCLPESFS LSVLHPEHGI LWLNLDMRHA GAVSGKDTV
301 IHIEEREIVR FR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m593 / g593 83.4% identity in 313 aa overlap

```

          10      20      30      40      50      60
m593.pep  MLELNLCKRFGNKTVDNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGGEIWL
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g593       MLELNLCKCFGGKTVADNICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGGEIRL
          10      20      30      40      50      60

          70      80      90     100     110     120
m593.pep  NGENITRMPPEKRRISLMFQDYALFPHMSALENAFLGLKMOKMPKAEAEERLAMAALAEVG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g593       NGENITCMPPEKRRISLMFQDYALFPHMSALENTAFGLKMOKMPKAEAEERLALSALAEVG
          70      80      90     100     110     120

          130     140     150     160     170     180
m593.pep  LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRGTLRRMTAERIRN
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g593       LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRDRLRMTAERIRK
          130     140     150     160     170     180

          190     200     210     220     230     240
m593.pep  GGIPAVLVTHSPEEACTTADEIAVMHKGRI LQYGPETLVKTPSCVQVARLMGLPNTDDN
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g593       GGIPAVLVTHSPEEACTTADEIAVMHEGKILQCGTPETLIQTPAGVQVARLMGLPNTDDD
          190     200     210     220     230     240

```

938

	250	260	270	280	290	299
m593.pep	RHIPQHAVRFDQDGMCECRVLSRTCLPESFSLSVLHPEHGILWLNLDLMD-RHAGAVSGKDTV					
	: : : : : : : : : : : : : : : : : :					
g593	RHIPQNAVCLDNHGTCECRLLSLVRLPDSLRLSAVHPEHGELTNLTVGQHTDGISGNGTV					
	250	260	270	280	290	300
	300	310				
m593.pep	RIHIEEREIVRFRX					
	: : : : : :					
g593	RIRVDEGRIVRFRX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1857>:

```
a593.seq
1  ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGCGGCA AAACGGTTGC
51  CGACGATATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTGG
101 GCGCGTCGGG CTGCGGCAAA TCCACCCTGC TGAATATGAT TCGGGGCATC
151 GTCCGGCCGG ACGGCGGGGA AATATGGCTG AATGGGAAA ACATTACCCG
201 TATGCCGCCG GAAAAACGCC GTATTTTCGT GATGTTTCAA GATTACGCGC
251 TGTTCCTCCA TATGAGTGCA CTGGAATATG CGGCATTCCG TTTGAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAAAGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAACACG AGGCGCACCG CAAGCCTGAN AAACCTTCCG
401 GAGGCGAAAA GCAACGGTTG GCACTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTGGACGA ATCGTTTTC AGTTTGGACA CGCATTGCG
501 CGACCGGCTG CGCGCATGA CTGCCGAACG TATCCGCAAG GCGGCGATCC
551 CTGCCGTTTT GGTAAACGAT TCGCCCGAAG AGGCCTGCAC GCGGCGAGAC
601 GAAATCGCCG TCATGCACGA GGGGAAAATC CTTCAATGCG GTACGCCCGA
651 AACCTTGGTT CAAACGCCTG CCGGCGTGCA GGTGCGCCAT CTGATGGGGC
701 TGCCCAATAC CGACGATGAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTTGCCCGA
801 ATCGTTCAGC CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCCGCACGCC GGTGAAATAT CGGGAAACGA TACGGTACGC
901 ATCCATATCG AAGACAGGGA AATCGTCCGC TTCCGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1858; ORF 593.a>:

```
a593.pep
1  MLELNLCKR FGGKTVADDI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAALVVRP
101 QMPKAEAES LAMAALAEVG LENEHRKPX KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLV QTPAGVQVAH LMGLPNTDDD RHIPQHAVRF
251 DQDGMCECVL SRTCLPESFS LSVLHPEHGI LWLNLDMPHA GEISGNDTVR
301 IHIEDREIVR FR*
```

m593/a593 92.9% identity in 312 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGNKTVDNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRDPGGEIWL					
	: : : : : : : : : : : : : : : : : :					
a593	MLELNLCKRFGGKTVADDICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRDPGGEIWL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPPEKRRISLMFQDYALFPHMSALENAALVVRPQMPKAEAEERLAMAALAEVG					
	: : : : : : : : : : : : : : : : : :					
a593	NGENITRMPPEKRRISLMFQDYALFPHMSALENAALVVRPQMPKAEAEERLAMAALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEAHRKPXKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRDRLRRMTAERIRN					
	: : : : : : : : : : : : : : : : : :					
a593	LENEAHRKPXKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRDRLRRMTAERIRK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACTTADEIAVMHKGRILQYGTPTLVKTPSCVQVARLMGLPNTDDN					

939

```

|||||:|||||:|:| | |||||:|:| | |||||:|||||:
a593  GGIPAVLVTHSPEEACTAADEIAVMHEGKILQCGTPETLVQTPAGVQVAHLMGLPNTDDO
      190      200      210      220      230      240

      250      260      270      280      290      300
m593.pep RHIPQHAVRFDDQGMESRVLSRTCLPESFSLSVLHPEHGILWLNLDMRHAGAVSGKDTVR
|||||:|||||:|:| | |||||:|:| | |||||:|:| |
a593  RHIPQHAVRFDDQGMESRVLSRTCLPESFSLSVLHPEHGILWLNLDMPHAGEISGNDTVR
      250      260      270      280      290      300

      310
m593.pep IHIEEREIVRFRX
|||||:|||||:|:| |
a593  IHIEDREIVRFRX
      310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1859>:

g594.seq..

```

1  atgggtgcag ataccgatgg cgacaaggat gttcggctta atcgaacggg
51  tctcgTTTTT agcatactcc ggctgctgtt ccgcatcgga attgggatcg
101 gtaagttcgc cgttcaggcc ttccaggtct ttaagctgct gatctgtacg
151 gttgagcacc caaatcggtt tgccttgcca ctccggcggtc agcagctgac
201 ccgcttcgat ttactgaca tccacctcga cggcagcacc ggaggccttg
251 gctttttccg aagggaAAAA actggccaca aacggcggtg ccacacccaa
301 tgctgccact ccgccgcgc cgcaggtcgc aagtgtcagg aaacggcggc
351 ggccgttggt gatttcttga ttatccatta ttacgtcgtc ctaatatattt
401 gggaatgccg agccattaaa cattgcaatt ttaccagtt tgcagtgata
451 ctcaaagcat tatttaaaat aaggtaa

```

This corresponds to the amino acid sequence <SEQ ID 1860; ORF 594.ng>:

g594.pep

```

1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHFNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFREK TGHKRRCHTQ
101 CCHSARAAGR KCQETAAVV DFLIIHYSVV LIFWECRAIK HCNFTQFAVI
151 LKALFKIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1861>:

m594.seq

```

1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAGCTGAC
201 CCGCTTCGAT TTACTGACA TCCACCTCGA CGGCAGCACC GCGCGCCTTG
251 GCTTTTTCG AAGGGAaaaa ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCCGCGC CGCAGGTGCG GAGTGTcAGG AAACGGCGGC
351 GGCCGTGTTT GATTCTTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 GGGAATACCG AGCCATTAAA CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTAAAAAT AAGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1862; ORF 594>:

m594.pep

```

1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHFNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAVV DFLIIHYSVV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m594 / g594 98.1% identity in 158 aa overlap

940

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
g594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
g594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
g594	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1863>:

```
a594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTCGTC AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAACTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GGCGGCCTTG
251 GCTTTTCCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGTGCCACT CCGCCGCGC CGCAGGTCGC GAGTGTGAGC AAACGGCGGC
351 GGCCGTTGTT GATTCTTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 GGGAAATACG AGCCATTAAA CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTAAAAAT AAGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1864; ORF 594.a>:

```
a594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIIHYSV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*
```

m594/a594 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
a594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
a594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
a594	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1865>:

```
g595.seq..
1  atgagaaaat tcaatttgac cgcattgtcc gtgatgcttg ccttgggttt
51  gaccgcgtgc cagccgccgg aggcggagaa agccgcgccg gccgcgtccg
101 gtgagaccac atccgccaac gaaggcggtt cggtcggtat cgccgtcaac
```

```
151 gacaatgcct gcgaaccgat gaatctgacc gtgccgagcg gacaggttgt
201 gttcaatatt aaaaaacaaca gcggccgcaa gctcgaatgg gaaatcctga
251 agggcgtgat ggtggtggac gaacgcgaaa atatcgcccc cgggctttcc
301 gacaaaatga accgtaacct gctgccgggc gaatacgaaa tgacctgcgg
351 ccttttgacc aatccgcgcg gcaagctggt ggtagccgac agcggcttta
401 aagacaccgc caacgaagcg gatttgga aaactgcccc accgctcgcc
451 gactataaag cctacgttca aggcgaggtt aaagagctgg cggcgaaaac
501 caaaaccttt accgaagccg tcaaaagcagg cgacattgaa aaggcgaaat
551 ccctgtttgc cgccaccgc gtccattacg aacgcacga accgattgcc
601 gagcttttca gcgaactcga ccccgtcac gatgcgtgtg aagacgactt
651 caaagacggg gcgaaagatg ccgggtttac cggttccac cgtatcgaa
701 acgccctttg ggtggaaaaa gacgtatccg gcgtgaagga aaccgcggcc
751 aaactgatga ccgatgtcga agccctgcaa aaagaaatcg acgcattggc
801 gttccctccg ggcaaagtgg tcggcggcgc gtccgaactg attgaagaag
851 cggcgggcag taaaatcagc ggcaagaag accgttacag ccacaccgat
901 ttgagcgact tccaagctaa tgcggacgga tctaaaaaaa tcgtcgattt
951 gttccgtccg ttgattgagg ccaaaaacaa agccttggtg gaaaaaacgg
1001 ataccaactt caaacaggtc aacgaaatc tggcgaata ccgcaccaa
```

942

1051 gacgggttttg aaacctacga caagctgagc gaagccgacc gcaaagcatt
 1101 acaggctcct attaacgcgc ttgccgaaga ccttgcccaa cttegcgga
 1151 tactcggctt gaaataa

This corresponds to the amino acid sequence <SEQ ID 1866; ORF 595.ng>:

g595.pep ..
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIQAVN
 51 DNACEPMNLT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
 101 DKMNRNLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLPQPLA
 151 DYKAYVQGEV KELAATKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
 201 ELFSELDPIV DATEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEAAGSKIS GEEDRYSHTD
 301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDNFKQV NEILAKYRTK
 351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRIGILGLK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1867>:

m595.seq
 1 ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CTTAGGTTT
 51 GACCGCGTGC CAGCCGCCGG AGCGGAGAAA AGCTGCGCCG GCAGCGTCCG
 101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCACTAT CGCCGTCAAC
 151 GACAATGCCT GCGAACCGAT GGAACGTACC GTGCCGAGCG GACAGGTTGT
 201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
 251 AAGCGGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTCC
 301 GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGAATTGCGG
 351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
 401 AAGACACCGC CAACGAAGCG GATTGGGAAA AACTGTCCCA ACCGCTCGCC
 451 GACTATAAAG CCTACGTTCA AGCGGAGGTT AAAGAGCTGG TGGCGAAAC
 501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
 551 CCCTGTTTGC CGACACCGCG GTCCATTACG AACGCATCGA ACCGATTGCC
 601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
 651 CAAAGACGGC GCGAAAGATG CCGGATTAC CGGCTTTCAC CGTATCGAAT
 701 ACGCCCTTTG GGTGGAAGAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
 751 AAACCTGATG CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
 801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAACTG ATTGAAGAAG
 851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
 901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATTT
 951 GTTCCGTCG CTGATCGAGG CCAAAAACAA AGCCTTGTG GAAAAAACCG
 1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAATA CCGGACTAAA
 1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
 1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTGCGCGCA
 1151 TACTCGGCTT GAAATAA

This corresponds to the amino acid sequence <SEQ ID 1868; ORF 595>:

m595.pep
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIAVN
 51 DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
 101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
 151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
 201 ELFSELDPIV DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
 301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDNFKQV NEILAKYRTK
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRIGILGLK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m595 / g595 95.4% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLALS	VMLALGLTAC	QPPEAEKAAP	AASGEAQTAN	EGGSVSIAVN	DNACEPMELT
g595	MRKFNLALS	VMLALGLTAC	QPPEAEKAAP	AASGETQSAN	EGGSVGIQAVN	DNACEPMNLT
	10	20	30	40	50	60
	70	80	90	100	110	120

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m595.pep	VPSGQVVFN	IKNNSGRKLEWEI	ILKGMVVDERENI	APGLSDKMTVTLLPGEYEMTCGLLT
g595	VPSGQVVFN	IKNNSGRKLEWEI	ILKGMVVDERENI	APGLSDKMNRNLLPGEYEMTCGLLT
	70	80	90	100 110 120
m595.pep	130	140	150	160 170 180
	NPRGKLVVTD	SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE		
g595	NPRGKLVVAD	SGFKDTANEADLEKLQPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE		
	130	140	150	160 170 180
m595.pep	190	200	210	220 230 240
	KAKSLFADTRVHYERIEPIAE	LFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK		
g595	KAKSLFAATRVHYERIEPIAE	LFSELDPVIDACEDDFKDGAKDAGFTGFHRIEHALWVEK		
	190	200	210	220 230 240
m595.pep	250	260	270	280 290 300
	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD			
g595	DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEAAGSKISGEEDRYSHTD			
	250	260	270	280 290 300
m595.pep	310	320	330	340 350 360
	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG			
g595	LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLS			
	310	320	330	340 350 360
m595.pep	370	380	389	
	EADRKALQASINALAEDLAQLRGI	GLKX		
g595	EADRKALQAPINALAEDLAQLRGI	GLKX		
	370	380		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1869>:

a595.seq

1	ATGAGAAAAT	TCAATTTGAC	CGCATTGTCC	GTGATGCTTG	CCTTAGGTTT
51	GACCGCGTGC	CAGCCGCGCG	AGGCGGAGAA	AGCTGCGCCG	GCAGCGTCCG
101	GTGAGGCGCA	AACCGCCAAC	GAGGCGGTT	CGGTCAGTAT	CGCCGTCAAC
151	GACAAATGCC	GCGAACCGAT	GGAACGTACC	GTGCCGAGCG	GACAGGTTGT
201	GTTCAATATT	AAAAACAACA	GCGGCCGCAA	GCTCGAATGG	GAAATCCTGA
251	AAGCGGTGAT	GGTGGTGGAC	GAGCGCGAAA	ACATCGCCCC	CGGACTTTCC
301	GATAAAATGA	CCGTCACCCCT	GTGCGCGGC	GAATACGAAA	TGACTTGCGG
351	TCCTTTGACC	AATCCGCGCG	GCAAGCTGGT	GGTAACCGAC	AGCGGCTTTA
401	AAGACACCGC	CAACGAAGCG	GATTGGGAAA	AACTGTCCCA	ACCGCTCGCC
451	GACTATAAAG	CCTATGTTCA	AGGCGAAGTC	AAAGAGCTGG	TGGCGAAAAC
501	CAAAACCTTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	AAGGCGAAAT
551	CCCTGTTTGC	CGACACCCGC	GTCCATTACG	AACGCATCGA	ACCGATTGCC
601	GAGCTTTTCA	GCGAACTCGA	CCCCGTCATC	GATGCGCGTG	AAGACGACTT
651	CAAAGACGGC	GCGAAAGATG	CCGGATTAC	CGGCTTCCAC	CGTATCGAAT
701	ACGCCCTTTG	GGTGGAAAAA	GACGTGTCCG	GCGTGAAGGA	AATTGCAGCG
751	AAACTGATGA	CCGATGTCGA	AGCCCTGCAA	AAAGAAATCG	ACGCATTGGC
801	GTTTCCTCCG	GGCAAGGTGG	TCGGCGGCGC	GTCCGAACCTG	ATTGAAGAAG
851	TGGCGGGCAG	TAAATCAGC	GGCGAAGAAG	ACCGGTACAG	CCACACCGAT
901	TTGAGCGACT	TCCAAGCCAA	TGTGGACGGA	TCGAAAAAAA	TCGTCGATTT
951	GTTCGTCGCG	TTGATCGAGA	CCAAAAACAA	AGCCTTGTGTG	GAAAAAACCG
1001	ATACCAACTT	CAACAGGTC	AACGAAATTC	TGGCGAAATA	CCGGACTAAA
1051	GACGGTTTTG	AAACCTACGA	CAAGCTGGGC	GAAGCCGACC	GCAAAGCGTT
1101	ACAGGCCTCT	ATTAACGCGC	TTGCCGAAGA	CCTTGCCCAA	CTTCGCGGCA
1151	TACTCGGCTT	GAAATAA			

This corresponds to the amino acid sequence <SEQ ID 1870; ORF 595.a>:

a595.pep

1	MRKENLTALS	VMLALGLTAC	QPPEAEKAAP	AASGEAQTN	EGGSVSIAVN
51	DNACEPMELT	VPSGQVVFNI	KNNSGRKLEW	EILKGMVVVD	ERENIAPGLS

944

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101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

```

m595/a595 99.7% identity in 388 aa overlap

m595.pep	10	20	30	40	50	60
	MRKFNL	TALSVMLALGLT	ACQPPEAEKAAPAASGEAQTANEGGSVSIAVNDNACEPMELT			
a595	10	20	30	40	50	60
	MRKFNL	TALSVMLALGLT	ACQPPEAEKAAPAASGEAQTANEGGSVSIAVNDNACEPMELT			
m595.pep	70	80	90	100	110	120
	VPSGQVVFNIKNN	SGRKLWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT				
a595	70	80	90	100	110	120
	VPSGQVVFNIKNN	SGRKLWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT				
m595.pep	130	140	150	160	170	180
	NPRGKLVVTD	SGFKDTANEA	DLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE			
a595	130	140	150	160	170	180
	NPRGKLVVTD	SGFKDTANEA	DLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE			
m595.pep	190	200	210	220	230	240
	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
a595	190	200	210	220	230	240
	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
m595.pep	250	260	270	280	290	300
	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD					
a595	250	260	270	280	290	300
	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD					
m595.pep	310	320	330	340	350	360
	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFEYDKLG					
a595	310	320	330	340	350	360
	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDGFEYDKLG					
m595.pep	370	380	389			
	EADRKALQAS	INALAEDLAQLRGILGLKX				
a595	370	380				
	EADRKALQAS	INALAEDLAQLRGILGLKX				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1871>:

g596.seq. (partial).

```

1  ..atgctgctct tggacgagcc gaccaaccac ttggatgcggy aatcggtgga
51  atggctggag caattcctcg tgcgcttccc cggcacagt gtcgcggtaa
101 cgcacgaccg ctacttcctc gacaacgccg ccgaatggat ttggaactc
151 gaccgcggac acggcattcc gtggaaggc aattactcgt cttggctgga
201 gcagaaagaa aaacgcttgg aaaacgaggc gaaatccgaa gccgcgcgcg
251 tgaaggcgat gaagcaggaa ttggaatggg tgcgcaaaa tgccaaaggc
301 gcgcaagcca agcccaaagc gcgtttggcg cgttttgaag aaatgagcaa
351 ctacgaatac caaaaacgca acgaaactca ggaatcttt atccctgttg
401 ccgagcggtt gggtaacgaa gtgattgaat ttgtgaatgt ttccaaatcg

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945

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451   ttccggcgata aagtgtctga- tgacgggtttg agcttcaaa- tgccggcgagg
501   cgcgattgtc ggcacatctc gcccgaacgg cgcgggtaaa tcgacgctgt
551   tcaaaatgat tgcgggcaaa gagcagcccg attcgggcga agtgaaaatc
601   gggcaaacgg tgaaaatgag cttgattgac caaagcccg- aaggtttgca
651   aaacgacaaa accgtgttcg acaacattgc cgaaggtcgc gatattttgc
701   aggtcggaca gtttgaaatc cccgcccgc- aatatttggg acgcttcaac
751   tttaaaggca gcgaccaaag caaaatcgca aggcagcttt ccggcgcgca
801   acgcggccgt ctgcacttgg caaaaacctt gttgggcggc ggcaatgtgt
851   tgctgtctga cgaaccgtcc aacgatctcg acgtggaac cctgcgcgcg
901   ttggaagacg cattgttga- atttgccgc- agcgtgatgg tgatttcgca
951   cgaccgttgg tttctcgacc gcatagccac gcatacttg gcgtgtgaag
1001  qcgactccaa atgggtgttc ttcgacggca actatcaaga atacgaagcc
1051  gacaagaaac gccgactcgg caaagaaggc gcgaaaccga aacgcatcaa
1101  atacaaaccg gtaacgcgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 1872; ORF 596.ng>:

g596.pep (partial).

```

1   ..MLLLDEPTNH LDAESVEWLE QFLVRFPQTV VAVTHDRYFL DNAAEWILEL
51  DRGHGIPWK NYSSWLEQKE KRLNEAKSE AARVKAMRQE LEWVRQNAKG
101 RQAKPKARLA RFEEMSNEY QKRNETQEIF IPVAERLNE VIEFVNVSKS
151 FGDKVLIDGL SFKVPAGAIV GIIGPNGAGK STLFKMIAGK EQPDSGEVKI
201 GQTVKMSLID QSREGLQNDK TVFDNIAEGR DILQVGQFEI PARQYLGFRN
251 FKSDQSKIA RQLSGGERGR LHLAKTLGG GNVLLDDEPS NDLDVETLRA
301 LEDALLEFAG SVMVISHDRW FLDRIATHIL ACEGDSKWVF FQGNVQYEYA
351 DKRRRLGKEG AKPKRIKYKP VTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1873>:

m596.seq..

```

1   ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCG
51  GCCGCAGAAA ACCATCATT AAGATATTTT CCTTCTTTT TTCCCCGGCG
101 CGAAAAATCGG CCTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGA TAAGGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGCATC AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGCGAGGAA GTGGAAAGCG GTTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAAGA AGTGTATGCC GAGTACGCCA ATCTGTATGC
351 GGATTTTGAC GCGTTGGCAG AAGAGCAGGG CCGCTTGGA GCGATTATIG
401 CGGCAGGTTT GTCCACGGGC GCGGTGCGG AACACGAATT GGAAATCGCC
451 GCCGACGCGC TGCGCCTGCC GGAATGGGAT GCCAAATCG ATAATTTGTC
501 CGGCGGTGAA AACGCGCGCG TTGCCTTTGT CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGA TGCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCCGGCA CAGTCGTTGC
651 GGTAACGCAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGCCATGGT ATTCCGTGGA AAGGCAATTA CTCGTCTTGG
751 CTGGAGCAGA AAGAAAAACG CTTGGAAAAC GAGGCAAAAT CCGAAGCCGC
801 GCGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGGCCGCCA AGCCAAGTCC AAAGCGCGTT TGGCTCGTTT TGAAGAAATG
901 AGCAACTACG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTTATTCC
951 CGTTGCCGAG CGTTTGGGTA ACGAAGTAT TGAATTTGTA AATGTTTCCA
1001 AATCGTTGCG CGATAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
1051 GCGGGCGCGA TTGTCGGCAT CATCGGCCCG AACGGCGCGG GTAAATCTAC
1101 GCTGTTCAAA ATGATTTCGG GCAAAGAGCA GCCTGATTCC GCGGAGGTGA
1151 AAATCGGACA AACCGTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAG GCCGCGACAT
1251 TTTGCAGGTT GGTGAGTTTG AAATCCCGC CCGCAATAT TTGGGGCGTT
1301 TCAACTTCAA AGGCAGCGAC CAAAGCAAAA TTGCAGGTCA ATTGTCTGGC
1351 GGCGAAGCGG GTCGTCTGCA CTTGGCAAAA ACCTTGTTGA GCGGCGGCAA
1401 TGTATTGCTG CTGGATGAAC CGTCTAACGA CCTTGACGTG GAAACCCTGC
1451 GCGCGTTGGA AGACGCATTG TTGGAATTTG CCGGCAGCGT GATGGTGATT
1501 TCGCAGGACC GTTGGTTCCT CGACCGCATC GCCACGCATA TCTTGGCGTG
1551 TGAAGGCGAC TCTAAATGGG TGTTCTTCGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGT TTGGGCGAAG AAGGCGCGAA ACCGAAACGC
1651 ATCAAAATACA AACCGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1874; ORF 596>:

m596.pep..

946

```

1  MSQQYVYSML RVSKVVPQK TIIKDISLSF FPGAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEPD LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADF ALAEEQGRLE AIIAAGSSTG GGAEHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAAE WILELDRGHG IPWKGNYSW
251 LEQKEKRLN EAKSEAAVRK AMKQELEWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNEVIEFV NVSKSFGDKV LIDDLSEFKVP
351 AGAIVGIIGP NGAGKSTLFK MISGKEQPDG GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKIAGQLSG
451 GERGRHLAK TLLSGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGNV QEYADKKRR LGEEGAKPKR
551 IKYKPVTR*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m596 g596 98.4% identity in 373 aa overlap

```

          160      170      180      190      200      210
m596.pep  LPWDADAKIDNLSGGEKRRVALCKLLLSKPDMLLDPEPTNHLDAESVLEWLEQFLVRFPGTV
          |||||
g596      MLLLDPEPTNHLDAESVLEWLEQFLVRFPGTV
                  10      20      30

          220      230      240      250      260      270
m596.pep  VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLNEAKSEAAVRKAMKQE
          |||||
g596      VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLNEAKSEAAVRKAMKQE
                  40      50      60      70      80      90

          280      290      300      310      320      330
m596.pep  LEWVRQNAKGRQAKSKARLARFEEMSNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKS
          |||||
g596      LEWVRQNAKGRQAKPKARLARFEEMSNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKS
                  100     110     120     130     140     150

          340      350      360      370      380      390
m596.pep  FGDKVLIDDLSEFKVPAGAIVGIIGPNGAGKSTLFKMISGKEQPDGSEVKIGQTVKMSLID
          |||||
g596      FGDKVLIDGLSEFKVPAGAIVGIIGPNGAGKSTLFKMIAGKEQPDGSEVKIGQTVKMSLID
                  160     170     180     190     200     210

          400      410      420      430      440      450
m596.pep  QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGFRNFKGSDQSKIAGQLSGGERGR
          |||||
g596      QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGFRNFKGSDQSKIARQLSGGERGR
                  220     230     240     250     260     270

```

947

	460	470	480	490	500	510
m596.pep	LHLAKTLLSGGNVLLLDDEPSNDLDVETLRALEDALLEFAGSVMVISHDRWFLDRIATHIL					
	:					
g596	LHLAKTLLSGGNVLLLDDEPSNDLDVETLRALEDALLEFAGSVMVISHDRWFLDRIATHIL					
	280	290	300	310	320	330
	520	530	540	550	559	
m596.pep	ACEGDSKWVFFDGNVQEYADKKRRLGEEGAKPKRIKYKPVTRX					
	:					
g596	ACEGDSKWVFFDGNVQEYADKKRRLGEEGAKPKRIKYKPVTRX					
	340	350	360	370		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1875>:

```

a596.seq
1  ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTGTGCGC
51  GCCGCAGAAA ACCATCATT AAGATATTTT CCTTTCTTTC TTCCCCGGCG
101 CGAAAATCGG TTTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGG TAAAGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGTATT AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGTGAGGAA GTGGAAAGCG GTTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAGGA AGTGTATGCC GAGTACGCCA ATCCCGATGC
351 GGATTTTGAC GCCTTGGCGG AAGAGCAGGG GCGTTTGGA GCGATTATTG
401 CGGCGGGTTC GTCCACGGGC GCGGTGCGG AACACGAATT GGAAATCGCT
451 GCGCAGCGCG TCGCCTGCC GGAATGGGAT GCCAAAATCG ATAATTTGTC
501 CGGCGGTGAA AAACGCCGCG TCGCTTTGTG CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGGG TCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCCGTA CAGTCGTTGC
651 CGTAACACAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGGCAGCGT ATTCCGTGGA AAGGAAATTA CTCGTCTTGG
751 TTGGAGCAGA AAGAAAAACG TTTGAAAAAC GAGGCGAAT CCGAAGCCGC
801 GCGCGTGAAA GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGGCGGTCA AGCCAAGTCC AAAGCGCGTT TGGCGCGTT TGAAGAAATG
901 AGCAACTATG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTCATTCC
951 CGTCGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTTGTG AATGTTTCCA
1001 AATCGTTCCG CGACAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCCT
1051 GCGGCGCGCA TTGTCGGCAT CATCGGTCCG AACGGCGCGG GTAAATCGAC
1101 ACTGTTTAAA ATGATTGCGG GCAAAGAGCA GCCCGATTCC GSTGAAGTGA
1151 AAATCGGGCA AACCGTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAA ACCTTGTGAG GTCGCGATAT
1251 TTTACAGGTC GGGCAGTTTG AAATCCCCG CCGCCAATAT TTGGGACGCT
1301 TCAATTTCAA AGGCAGCGAC CAAAGCAAAA TCACGGGGCA GCTTTCCGGC
1351 GGCGAACGCG GACGTTTGCA CTTGGCAAAA ACCTTGTGAG GCGGTGGCAA
1401 TGTGTTGCTG CTGGACGAAC CGTCCAACGA CCTCGACGTG GAAACCTGCG
1451 GCGCGTTGGA AGACGCATTG CTGGAATTG CCGGCAGCGT GATGGTGATT
1501 TCGCAGGACC GCTGGTTCCT CGACCGTATT GCTACGCATA TCTTGGCTTG
1551 CGAAGGCGAC TCCAATGGG TGTCTTTGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGA CTCGGCGAAG AAGGCACGAA ACCGAAACGC
1651 ATCAAATACA AACCGGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1876; ORF 596.a>:

```

a596.pep
1  MSQQYVYSML RVSKVVPQK TIIKDISLSF FPGAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEP LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADF ALAEEQGRLE AIIAAGSSTG GGAHEHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAEF WIEELDRGHG IPWKGNYSWS
251 LEQKEKRLN EAKSEAARVK AMQKELEWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNIEVIEF NVSKSFGDKV LDDLSFKVP
351 AGAIVGIIGP NGAGKSTLFK MIAGKEQPDS GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSQ QSKITGQLSG
451 GERGRLHLAK TLLGGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGNV QEYADKKRRR LGEEGTPKPKR
551 IKYKPVTR*

```

m596/a596 99.3% identity in 558 aa overlap

948

	10	20	30	40	50	60
m596.pep	MSQQYVYSMLRVSKVVPQKTI	IKDISLSFFPGAKIGLLGLNGAGKSTVLR	IMAGVDKEF			
a596	MSQQYVYSMLRVSKVVPQKTI	IKDISLSFFPGAKIGLLGLNGAGKSTVLR	IMAGVDKEF			
	10	20	30	40	50	60
	70	80	90	100	110	120
m596.pep	EGEAVPMGGIKIGYLPQEP	ELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADFD				
a596	EGEAVPMGGIKIGYLPQEP	ELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADFD				
	70	80	90	100	110	120
	130	140	150	160	170	180
m596.pep	ALAEEOGRLEAIIAAGSSTGGGA	EHLEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL				
a596	ALAEEOGRLEAIIAAGSSTGGGA	EHLEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL				
	130	140	150	160	170	180
	190	200	210	220	230	240
m596.pep	LSKPDMLLDDEPTNHLDAESV	EWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILEDRGHG				
a596	LSKPDMLLDDEPTNHLDAESV	EWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILEDRGHG				
	190	200	210	220	230	240
	250	260	270	280	290	300
m596.pep	IPWKGNYSWLEQKEKRL	ENAKSEAARVKAMKQELEWVRQNAKGRQAKSKARLARFEEM				
a596	IPWKGNYSWLEQKEKRL	ENAKSEAARVKAMKQELEWVRQNAKGRQAKSKARLARFEEM				
	250	260	270	280	290	300
	310	320	330	340	350	360
m596.pep	SNYEYQKRNETQEIFIPV	AERLGNIEVFVNVSKSFGDKVLIDDLSEFKVPAGAIVGIIGP				
a596	SNYEYQKRNETQEIFIPV	AERLGNIEVFVNVSKSFGDKVLIDDLSEFKVPAGAIVGIIGP				
	310	320	330	340	350	360
	370	380	390	400	410	420
m596.pep	NGAGKSTLFKMI	SGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV				
a596	NGAGKSTLFKMI	SGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV				
	370	380	390	400	410	420
	430	440	450	460	470	480
m596.pep	GQFEIPARQYLGRFN	FKGSDQSKIAGQLSGGERGRHLAKTLLSGGNVLLDEPSNDLDV				
a596	GQFEIPARQYLGRFN	FKGSDQSKIAGQLSGGERGRHLAKTLLSGGNVLLDEPSNDLDV				
	430	440	450	460	470	480
	490	500	510	520	530	540
m596.pep	ETLRALEDALLEFAGS	VMVISHDRWFLDRIATHILACEGDSKWVFFDGNVQYEYADKKRR				
a596	ETLRALEDALLEFAGS	VMVISHDRWFLDRIATHILACEGDSKWVFFDGNVQYEYADKKRR				
	490	500	510	520	530	540
	550	559				
m596.pep	LGEEGAKPKRIKYPVTRX					
a596	LGEEGTKPKRIKYPVTRX					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1877>

g597.seq

1 ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51 CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACCGCAA CAGCGCGAGG CTTGGGACAA ATTCCAAAAA

949

```

151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAATCGCCG CTACGAAAGC
201 GCAGATTTCG CGTTTCGTAT CGGGGAACTA TAAAAACAGC CGGCCGAATG
251 CGGTTGCCCT GTTCCTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCTCC AATCGGGAAG TTGTCAAGGA
351 TTTGGAAGAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTTGAAG AAAATTCAGG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TCGCGCGGAA CAGACGGAAA GCCCGAGACA
501 GAATGCCAAA ATCTCCAAAG ATGCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACAGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGgagaa aaaaaaagcc
601 gaacaccgCA TTcaggAtgc: ggAagcaaaA agaAATTGG CTGAaagCaa
651 actGgcggca gccgAAAAAG CCAGAAAAGA AGCGGCGCAG CAGAAGGCTG
701 AAGCGCGACG TCGCGAAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGgTT TCAGCCGCAT
801 GCAGGGACGT TTGAAAAAAC CGGTTGACGG TGTGCCGACC GGGCTTTTTCG
851 GGCAGAACCG GAGCGGcggc GATGTTTGA AAGGCGTgTT CTATTCCACT
901 CGCGCTGCAAG CGGTTGAAAG CATTGCGCcg gGAACggtaa GCTATGCGGA
951 cgaGTTGGAC GGCTACGGCA AAGTGGTCTG GATCGATCAC GGCGAGAATC
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTTCGCCCG CAAGGGTTAT
1051 AAGGTCGCGG CAGGAAGCAA AATCGGCAG AGCGGTCGCG TGCCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCGAGGTGAG GTGTTGAACC
1151 CTTCCGGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1878; ORF 597>:

m597.pep

```

1  MLLHVSNSLK QLQEEIRIQE RIRQERIROA RGNLASVNRK QREAWDKFQK
51  LNTELNRKLT EVAATKAQIS RFVSGNYKNS RPNVALFLK NAEFGQKNRF
101 LRYTRVYNAS NREVVKDLEK QQKALAVQEQ KINNELARLK KIQANVQSLL
151 KKQGVTDAAE QTESRRQNAK ISKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEAKLAA AEKARKEAAG QKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVIDH GENYISIIYAG LSEISAGKGY
351 TVAAGSKIGT SGSLPDGEEG LYLOIRYRGQ VLNPSGWIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1879>:

m597.seq

```

1  ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51  CCGCCCAAGAG CGTATCCGTC AGGCGCGCGG CAACCTTGCT TCCGTCAACC
101 GCAAAACAGCG CGAGGCTTGG GACAAGTTCC AAAAATCAA TACCGAGCTG
151 AACCGTTTGA AAACGGAAGT CGCCGCTACG AAAGCGCAGA TTTCCCGTTT
201 CGTATCGGGG AACTATAAAA ACAGCCAGCC GAATCGCGTT GCCCTGTTC
251 TGAATAACGC CGAACCggGT CAGAAAAACC GCTTTTTCG TTATACGCGT
301 TATGTAACG CCTCCAATCG GGAAGTTGTC AAGGATTGGA AAAAAAGCA
351 GAAGGCTTTC GCGGTACAAG AGCAGAAAAT CAACAATGAG CTTGCCCGTT
401 TGAAGAAAAA TCAGGCAAAAC GTGCAATCTC TGCTGAAAAA CAGGGTGTA
451 ACCGATGCGG CGGAACAGAC GGAAGCCGCG AGACAGAATG CCAAAATCGC
501 CAAAGATGCC CGAAAACTGC TGAACAGAAA AGGGAACGAG CAGCAGCTGA
551 ACAAGCTCTT GAGCAATTG GAGAAGAAAA AGGCCGAACA CCGCATTCAG
601 GATGCGGAAG CAAAAAGAAA ATTGGCTGAA GCCAGACTGG CGGCAGCCGA
651 AAAAGCCAGA AAAGAGCGG CGCAGCAGAA GGCTGAAGCA CGAGTGCAGG
701 AAATGTCCAA CCGTACCGCC GAAGACAGGA ACATCCAAGC GCCTTCGGTT
751 ATGGGTATCG GCAGTGCCGA CGGTTTCAGC CGCATGCAAG GACGTTTGAA
801 AAAACCGGTT GACGGTGTGC CGACCGGACT TTTCCGGCAG AACCGGAGCG
851 GCGGCGATAT TTGAAAGGC GTGTCTATT CCACTGCACC GGCACCGGTT
901 GAAAGCATTG CGCCGGGAAC GGTAAGCTAT GCGGACGAGT TGGACGGCTA
951 CGGCAAAATG GTCGTGGTGC ATCAGGGCGA GAACTACATC AGCATCTATG
1001 CCGGTTTGAG CGAAATTTCC GTCGGCAAGG GTTATATGGT CGCGGCAGGA
1051 AGCAAAATCG GCTCGAGCG GTGCTGCGG GACGGGGAAG AGCGGCTTTA
1101 CCTGCAAAAT CGTTATCAAG GTCAGGTATT GAACCTTCG AGCTGGATAC
1151 GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1880; ORF 597>:

m597.pep

```

1  MLLHVSNSLK QLQEEIRIQE RIRQARGNLA SVNRRQREAW DKFQKLNTEL
51  NRLKTEVAAT KAQISRFVSG NYKNSOPNAV ALFLKNAEPG QKNRFLRYTR
101 YVNASNREVV KDLEKQKAL AVQEQKINNE LARLKKIQAN VQSLLKKQGV
151 TDAAEQTESR RQNAKIAKDA RKLLEQKGNE QQLNKLNSL EKKKAEHRIQ
201 DAEAKKKLAE ARLAAAEKAR KEAAQQAEEA RRAEMSNLTA EDRNIQAPSV
251 MGIGSADGFS RMQGRKKPV DGVPTGLFGQ NRSGGDIWKG VFYSTAPATV
301 ESIAPGTVSY ADELDTGKGV VVDHGENYI SIYAGLSEIS VGKGYMVAAG
351 SKIGSSGSLP DGEEGLYLQI RYQGVNLNPS SWIR*

```

950

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 597 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. gonorrhoeae*:

```
m597/g597    96.1% identity in 389 aa overlap

      10      20      30      40      50      60
g597.pep    MLLHVSNSLKQLQEERIRQERIRQERIRQARGNLSVNRKQREAWDKFQKLNTELNRLKT
            |||||
m597        MLLHVSNSLKQLQEERIRQ-----ARGNLSVNRKQREAWDKFQKLNTELNRLKT
            10      20      30      40      50

      70      80      90     100     110     120
g597.pep    EVAATKAQISRFSVSGNYKNSRPNNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK
            |||||
m597        EVAATKAQISRFSVSGNYKNSQPNNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK
            60      70      80      90     100     110

      130     140     150     160     170     180
g597.pep    QOKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKISKDARKLLE
            |||||
m597        COKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE
            120     130     140     150     160     170

      190     200     210     220     230     240
g597.pep    QKGNFQQLNKLILSNLEKKKAHRIQDAEAKRKLAEAKLAAAEKARKEAAQOKAEARRAEM
            |||||
m597        QKGNFQQLNKLILSNLEKKKAHRIQDAEAKRKLAEAKLAAAEKARKEAAQOKAEARRAEM
            180     190     200     210     220     230

      250     260     270     280     290     300
g597.pep    SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKRPVDPVPTGLFGQNRSGGDVWKGVFYST
            |||||
m597        SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKRPVDPVPTGLFGQNRSGGDIWKGVFYST
            240     250     260     270     280     290

      310     320     330     340     350     360
g597.pep    APATVESIAPGTVSYADELQGYGVVVIDHGENYISIIYAGLSEISAGKGYTVAAGSKI GT
            |||||
m597        APATVESIAPGTVSYADELQGYGVVVDHGENYISIIYAGLSEISVKGKGYMVAAGSKIGS
            300     310     320     330     340     350

      370     380     390
g597.pep    SSSLPDGEEGLYLQIRYRGQVLPNSGWIRX
            |||||
m597        SSSLPDGEEGLYLQIRYRGQVLPNSGWIRX
            360     370     380
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1881>

```
a597.seq
1  ATGCTGCTTC ATGTCAGCAA TTCCCTCAAG CAGCTTCAGG AAGAGCGTAT
51  CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACCGCAAA CAGCGCGAGG CTTGGGACAA GTTCCAAAAA
151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCGC CTACGAAAGC
201 GCAGATTTC CGTTTCGTAT CGGGGAAC TA AAAACAGC CAGCCGAATG
251 CGGTGCCCT GTTCCTGAAA AACGCCGAAC CGGTCAGAA AAACCGCTT
301 TTGCGTTATA CGCGTTATGT AAACGCCCTC AATCGGGAAG TTGTCAGGA
351 TTTGGAAAAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTTGAAG AAAATTCAGG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TCGGCGCGAA CAGACGGAAA GCCGCAGACA
501 GAATGCCAAA ATGCCCAAAG ATGCCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTGGAGAA GAAAAAGGCC
601 GAACACCGCA TTCAGGATGC GGAAGCAAAA AGAAAATTGG CTGAAGCCAG
651 ACTGGCGGCA CGCGAAAAAG CCAGAAAAAG AGCGGCGCAG CAGAAGGCTG
701 AAGCAGCAGC TCGGGAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGTTATGGG TATCGGCAGT GCCGACGGT TCAGCCGCAT
801 GCAGGACGT TTGAAAAAAC CGGTGACGG TGTGCCGACC GGACTTTTCG
851 GGCAGACCG GAGCGCGGC GATGTTTGA AAGGCGTGT CTATTCCACT
901 GCACCGCAA CGGTTGAAAG CATTCGCCG GGAACGGTAA GCTATGCGGA
```

951

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951 CGAGTTGGAC GGCTACGGCA AAGTGGTCGT GGTGATCAC GCGGAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTTCCGTCGG CAAGGGTTAT
1051 ATGTCGCGG CAGGAAGCAA AATCGGCTCG AGCGGGTCGC TGCCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCAAGGTCAG GTATTGAACC
1151 CTTGAGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1882; ORF 597.a>:

```

a597.pep
1  MLLHVSNSLK QLQEERIRQE RIRQERIRQA RGNLASVNRK QREAWDKFQK
51  LNTELNLRLKT EVAATKAQIS RFVSGNYKNS QPNAVALFLK NAEFGQKNRF
101 LRYTRYVNAS NREVVKDLEK QQKALAVQEQ KINNELARLK KIQANVQSL
151 KKQGVTDAAE QTESRRQNAK IAKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEARLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVDH GENYISIIYAG LSEISVGKGY
351 MVAAGSKIGS SGSLPDGEEG LYLQIRYQGQ VLPSSWIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 597 shows 98.5% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. meningitidis*

m597/a597 98.5% identity in 389 aa overlap

	10	20	30	40	50	60
a597.pep	MLLHVSNSLKQLQEERIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNLRLKT					
m597	MLLHVSNSLKQLQEERIRQERIRQ-----ARGNLASVNRKQREAWDKFQKLNTELNLRLKT					
	10	20	30	40	50	
	70	80	90	100	110	120
a597.pep	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
	60	70	80	90	100	110
	130	140	150	160	170	180
a597.pep	QQKALAVQEQKINNELARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
m597	QQKALAVQEQKINNELARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
	120	130	140	150	160	170
	190	200	210	220	230	240
a597.pep	QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
m597	QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
	180	190	200	210	220	230
	250	260	270	280	290	300
a597.pep	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKKPVDGVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKKPVDGVPTGLFGQNRSGGDIWKGVFYST					
	240	250	260	270	280	290
	310	320	330	340	350	360
a597.pep	APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGKGYMVAAGSKIGS					
m597	APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGKGYMVAAGSKIGS					
	300	310	320	330	340	350
	370	380	390			
a597.pep	SGSLPDGEEGLYLQIRYQGQVLPSSWIRX					
m597	SGSLPDGEEGLYLQIRYQGQVLPSSWIRX					
	360	370	380			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1883>:

```
g601.seq
1  ATGTTCCCAA CCGGCAATTT GGTCGACGAA ATTGATGTGC CGAATATAGG
51  TCGTCTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ACGCCGCCGA CTTGGGCTAC ACGGCAAAG AGTTGCAGGA CGACATCAAC
151 AACGATGCCG CCGCGCTGGA AAAATTTGAA ACCATCCGCG CATATGGCGC
201 GCTGAAAATG GGTTCGATCA GCGACGTATC CGAAGCCGCC GCCCGCGCGC
251 GCACGCCGAA ACCCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGCGGCAAAA CCGTAAACGC CGCCGACATC GATTTCGCGG TACGCGCCCT
351 GAGCATGGGC AAATGACACC ACGCTATGAT GGGCATCGCC TCGGTCGCCA
401 TCGCCGCCGC CGTGCTCGGT ACGCTGGTCA ACCTTGCCGC AGGCGGCGGA
451 ACGCGTAAAG AAGTGCCTT CCGGCATCCG TCAGGTACGC TCGGTGTCGG
501 TGCTGCCGCG GAATGTCAGG ACGGACAATG GACGCCGCGc aaagcggta
551 tgaGCCGCAG CGCACgcgtg attatggaaa gttgGGTCg cgttcccgat
601 gattGTTTTT GA
```

This corresponds to the amino acid sequence <SEQ ID 1884; ORF 601.ng>:

```
g601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE TIRAYGALKM GLISDVSEAA ARARTPKPAF VAPAADYTAS
101 SGKTVNAADI DLPVRALSMG KLHHAMMGIA SVAIAAAVLG TLVNLAAAGG
151 TRKEVRFGHP SGTLRVGAAA ECQDQGWTA KAVMSRSARV IMESWVRVPD
201 DCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1885>:

```
m601.seq
1  ATGTTCCCAA CCGGCAATTT GGTCGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ATGCCGCCGA CTTGGGCTAC ACAGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CGGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCTCGCGCGC
251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAACGC CGCCGACATC GATTTCGCTG TACGCGCCCT
351 GAGCATGGGC AAATGACACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCCGCCGTA CCCGGTACGC TGGTCAACCT TGCCGCAGGC
451 GGCGGAACGC GTAAAGAAAGT GCGCTTCGGG CATCCTCCG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CGGTCATGAG CCGTAGCGCA CGCGTGATGA TGAAGGTTG GGTACGGGTG
601 CCTGAGGATT GTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1886; ORF 601>:

```
m601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151 GGTRKEVRFH HPSGTLRVGA AAECQDQQWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 601 shows 94.1% identity over a 205 aa overlap with a predicted ORF (ORF 601.ng) from *N. gonorrhoeae*:

m601/g601

	10	20	30	40	50	60
m601.pep	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
g601	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m601.pep	KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG					

953

```

|||||
g601      TIRAYGALKMGLISDVSEAAARATPKPAFVAPAADYTASSGKTVNAADIDLVRALSMG
              70      80      90      100     110     120

              130     140     150     160     170     180
m601.pep  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
|||||
g601      KLHHAMMGIA SVAI--AAAVLGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
              130     140     150     160     170

              190     200
m601.pep  ATKAVMSRSARVMMEGWVRVPEDCFX
|||
g601      AAKAVMSRSARVIMESWVRVPDDCFX
              180     190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1887>:

```

a601.seq
1  ATGTTCCCAA CCGGCAAITT GGTGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ATGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CAGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCCCGCGCGC
251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAATGC CGCCGACATC GATTTGCTGG TACGCGCCCT
351 GAGCATGGGC AAATTGCACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCCGCCGTG CCCGGTACGC TGGTCAACCT TGCCGCAGGC
451 GGCGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTTCCG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CGGTTATGAG CCGCAGCGCA CGCGTGATGA TGGAAGGTTG GGTCAAGGTC
601 CCGGAAGATT GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1888; ORF 601.a>:

```

a601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NCAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151 GTRKEVRFV HPSGTLRVGA AAECQDGQWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*

```

m601/a601 100.0% identity in 205 aa overlap

```

              10      20      30      40      50      60
m601.pep  MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
|||||
a601      MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
              10      20      30      40      50      60

              70      80      90      100     110     120
m601.pep  KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG
|||||
a601      KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG
              70      80      90      100     110     120

              130     140     150     160     170     180
m601.pep  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
|||||
a601      KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
              130     140     150     160     170     180

              190     200
m601.pep  ATKAVMSRSARVMMEGWVRVPEDCFX
|||||
a601      ATKAVMSRSARVMMEGWVRVPEDCFX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1889>:

```
g602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTC CCTTTCTGCT
51  CGGCGGGCAG ATAAACCGTC ATCGTCAGGC GAGCAACCGT GGATTGTGTT
101 CCTTCGGCGG TTTTCAGGGT AATCGGGAAG CGCAGGTCTT TAATGCCGAC
151 CTGATTGATC GGCAGGTTGC GCAAATCTCT GCTGGATTGC ACGTCTGCAA
201 TGGCGTTCAT GCGTTGTTT TCCTTAATAT TCAGATAATT ATTGAGATGT
251 GTGTATTGTA TGGCAGGcag atgccgtctg aAAAAacgct gtcggCCGCC
301 TGCCTGCAAA Tgcgagatta TATCACTTGC TTTtggcgcg TGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1890; ORF 602.ng>:

```
g602.pep
1  MLLHQCDKAR HMRPFLGGQ INRHRQASNR GLCSFGGFQG NREAQVFNAD
51  LIDRQVAQIS AGLHVCNGVH ALFVLNIQII IEMCVLYGRQ MPSEKTLCAA
101 CLQMRDYITC FWRLH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1891>:

```
m602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTC CCCTTCTGCT
51  CAGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAATGGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTCAT GAGTTGTTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC GCCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1892; ORF 602>:

```
m602.pep
1  MLLHQCDKTR HMRPILLSRQ VNRHGQTGNG GLDAFCSLQG NRKAQVFDTD
51  LIDRQIAQIS AGLHVCNSVH ELFFLNHIVI VEMCAWYGVSA AGEYTVNLQM
101 RDYITRF*QL H*
```

m602/g602 65.2% identity in 115 aa overlap

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPILLSRQVNRHGQTGNGGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
	: : : :: : : : : : : : : : :					
g602	MLLHQCDKARHMRPFLGGQINRHRQASNRGLCSFGGFQGNREAQVFNADLIDRQVAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNHIVIEMCAWYGVSA-GEYTVN--LQMRDYITRF*QLHX					
	: : : : : : : : : : :					
g602	AGLHVCNGVHALFVLNIQIIEMCVLYGRQMPSEKTLAAACLQMRDYITCFWRLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1893>:

```
a602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTA CCCTTCTGCT
51  CGGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAACTGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTCAT GAGTTGTTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC ACCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1894; ORF 602.a>:

```
a602.pep
1  MLLHQCDKAR HMRTLLLRQ VNRHGQTGNC GLDAFCSLQG NRKAQVFDTD
51  LIDRQIAQIS AGLHVCNSVH ELFFLNHIVI VEMCAWYGVSA TGEYTVNLQM
101 RDYITRF*QL H*
```

m602/a602 95.5% identity in 111 aa overlap

955

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLSRQVNRHGQTGNNGGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
a602	MLLHQCDKARHMRPLLSRQVNRHGQTGNNGGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSAEYTVNLQMRDYITRFQLHX					
a602	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSTGEYTVNLQMRDYITRFQLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1895>:

g603.seq

```

1  ATGGATTCCC GCCTGCGTGG GAATGACGCT AGGAAATACG GCATACGCTT
51  TGCCCAAAGA GGCCGTCTGA AACACACTCC GCCCAACGCC CATCCTTTT
101 CAGACGGCCC CGCACCAAAA AAACAACCAC AAATAACAAG GAGAAACATC
151 ATGTCCGACC AACTCATTCT TGTCCTGAAC TGCGTCAGTT CATCGCTCAA
201 AGGCGCCGTT ATCGACCGCA AAAGCGGCAG CGTCGTCCTA AGCTGCCTCG
251 GGGAAACGCTT GACTACGCCC GAAGCCGTCA TTACCTTCAA CAAAGACGGC
301 AACAAACGCC AAGTTCCTCT GAGCGGCCGC AACTGCCACG CCGCGCGCGT
351 GGGTATGCTG TTGAACGAAC TGGAAAAACA CGGACTGCAC GACCGCATCA
401 AAGCCATCGG CCGCCGCATC GCCCAGCGCG GCGAAAAATA TCACGAGTCC
451 GTCCTCATCG ACCAAGACGT CCTTGACGAA CTGAAAGCCT GCATCCCGTT
501 CGCCCGCGTG CACAACCCCG CCAACATCAG CGGCATCCTC GCCGCGCAGG
551 AACACTTTCC CGGCCTGCCC AACGTCGGCG TGATGGACAC CTCGTTCCAC
601 CAAACCATGC CGGAGCGGGC CTACACTTAT GCCGTGCCGC GCGAATTGCG
651 CAAAAAATAC GCCTTCCGCC GCTACGGTTT CCACGGTACC GGTATGCGTT
701 ACGTCGCCCC TGAAGCCGCA CGCATCTTGG GCAAACCTct ggaaGACATC
751 CGCATGATTA TTGCCCACTT AGGCAACGGC GCATCTATTA CCGCCGTCAA
801 AAACGGCAAA TCCGTCGATA CCGGTATGGG TTTACGCGCG ATCGAAGGTT
851 TGGTAATGGG TACAGTTTGC GCGACACCG ATCCGGGCGT ATACAGCTAT
901 CCGACTTTCC ACGCAGGGAT GGATGTTGCC CAAGTTGATG AAATGCTGAA
951 CGAAAAATCA GGTTCCTCCG GTATTTCCga actTCCCAAC GACTGCCGCA
1001 CCCTCGAAAT CGCCGCCGAC GAAGGCCGCG AAGCGCGCGC CCTCGCCCTc
1051 gaAGTCATGA CCTGCCGCTT CGCCAAATAC ATCGCTTCGA TGGCTGTGGC
1101 CTGCGGCAGT GTTGACGCAC TCGTGTTTCA CGCGGGTATC GCGGAAACT
1151 CGCGTAATAT CCGTGCCAAA ACCGTTTCTT ATCTTGATT CTGGGTCTG
1201 CATATCGACA CCAAAGCCAA TATGGAAAAA CGTACGGCA ATTCCGGCAT
1251 TATCAGCCCG ACCGATTCTT CTCCGGCTGT TTTGGTCGT CCGACCAATG
1301 AAGAACTGAT GATTGCCTGC GACACTGCCG AACTTGCCGG CATCTTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1896; ORF 603.ng>:

g603.pep

```

1  MDSRLRGND RYKIRFAQR GRLKHTPPNA HPFSDGPAPK KQPOTTRNI
51  MSDQLILVLN CVSSSLKGAV IDRKSGSVVL SCLGERLTTP EAVITFNKDG
101 NKRQVPLSGR NCHAGAVGML LNELEKHGLH DRIKAIGRRI AHGGEKYHES
151 VLIDQDVLDE LKACIPFAPL HNPANISGIL AAQEHFPLP NVGVMDTSFH
201 QTMPERAYTY AVPRELRKKY AFRRYGFHGT GMRYVAPEAA RILGKPLEDI
251 RMIIAHLNG ASITAVKNGK SVDTGMGFTP IEGLVMGTRC GDTDPGVYSY
301 PTFHAGMDVA QVDEMLNEKS GFPGISLPLN DCRTLEIAAD EGREGARLAL
351 EVMTCRLAKY IASMAVACGS VDALVFTGGI GENSRNIRAK TVSYLDLFLG
401 HDTKANMEK RYGNSGIISP TDSSPAVLVV PTNEELMIAC DTAEALGIL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1897>:

m603.seq

```

1  CTGTCTCTGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAACACCTT TGCGCCTGAT GTCTGC.CTT
101 TTTCAGACGA CCCACACTA AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT CCTCGTTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGCGCC GTTATCGACC GAmAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGCGCAACG cCtGACCACG CCCGAAGCCG TCATTACGTT CAACAAAGAC

```

m603.ppt

1	LSSRRRGRNN	DRKCGIRFAQ	RGRLKHLAPD	VXCFSDDP TL	KKQPQTTRRN
51	IMSDQLILVL	NCGSSSLKGA	VIDRXSGSVV	LSCLGERLTT	PEAVITFNKD
101	GNKRQVPLSG	RNCHAGAVPM	LLNELEKHGL	HDRIKAIGHR	IAHGGEKYSE
151	SVLIDQAVMD	ELNACIAPL	LHNPNANISGI	LAAQEHFPGI	PNVGVMDS TF
201	HQTMPERAYT	YAVPRELRKK	YAFRRYGFHG	TSMRYVAPEA	ARILGKPLED
251	IRMIIAHLGN	GASITAIKNG	KSVDTSMGFT	PIEGLVMGTR	CGDIDPGVYS
301	YLTSHAGMDV	AQVDEMLNKK	SGLLGISELS	NDCRTLEIAA	DEGHEGARLA
351	LEVMTYRLAK	YIASMAVCGC	GVDALVFTGG	IGENSRNIRA	KTVSYLDFLG
401	LHIDTKANME	KRYGNSGIIS	PTDSSPAVLV	VPTNEELMIA	CDTAEAGIL
451	*				

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 603 shows 91.6% identity over a 450 aa overlap with a predicted ORF (ORF 603.ng) from *N. gonorrhoeae*:

m603/g603

		10	20	30	40	50	60
m603 .pep		LSSRRRGRNND	RKCGIRFAQR	GLKHLAPDVC	XFSDDP	TLKKQPQT	TRRNIMSDQLILVL
		::	:			::	:
g603		MDSRLRG-ND	ARKYGIRFAQR	GLKHTPPNAH	PFSDGPA	PKKQPQT	TRRNIMSDQLILVL
			10	20	30	40	50
		70	80	90	100	110	120
m603 .pep		NCGSSSLKGA	VIDRXSGSV	LVLSCLGER	LTTPEAVIT	FNKDGNG	KRQVPLSGRNCHAGAVGM
g603		NCVSSSLKGA	VIDRXSGSV	LVLSCLGER	LTTPEAVIT	FNKDGNG	KRQVPLSGRNCHAGAVGM
	60	70	80	90	100	110	
		130	140	150	160	170	180
m603 .pep		LLNELEKHGL	HDRIKAIGH	RIAHGGBE	KYSESVLID	QAVMD	ELNACIPLAPLHPANISGI
g603		LLNELEKHGL	HDRIKAIGH	RRIAHGGBE	KYSESVLID	QDVLDEL	KACIPFAPLHPANISGI
	120	130	140	150	160	170	
		190	200	210	220	230	240
m603 .pep		LAAQEHFPGL	PNVGVMDT	SFHSHTMP	ERAYTYAV	PRELRK	KKYAFRRYGFHGTS

957

g603	LAAQEHFPGLPNVGVMDSF	HQTMPERAYTYAVPRELRK	KYAFRRYGFHGTGMRYVA	PEA		
	180	190	200	210	220	230
m603.pep	ARILGKPLEDIRMIIAHLG	NGASITAIKNGKSVDTSM	GFTPIEGLVMGTRCGDID	PGVYS		
g603	ARILGKPLEDIRMIIAHLG	NGASITAVKNGKSVDTGM	GFTPIEGLVMGTRCGDID	PGVYS		
	240	250	260	270	280	290
m603.pep	YLTSHAGMDVAQVDEMLN	KKSGLLGISLSNDCRTLE	IAADEGHEGARLALEVM	TYRLAK		
g603	YPTFHAGMDVAQVDEMLN	KKSGFPGISLPNDCRTLE	IAADEGREGARLALEVM	TCRLAK		
	300	310	320	330	340	350
m603.pep	YIASMAVCGGVDALVFTG	GIGENSRNIRAKTVSYLD	FLGLHIDTKANMEKRYGN	SGIIS		
g603	YIASMAVACGSVDALVFTG	GIGENSRNIRAKTVSYLD	FLGLHIDTKANMEKRYGN	SGIIS		
	360	370	380	390	400	410
m603.pep	PTDSSPAVLVVPTNEELMI	ACDTAELAGILX				
g603	PTDSSPAVLVVPTNEELMI	ACDTAELAGILX				
	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1899>:

```

a603.seq
1  CTGTCTCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCCAA AGAGGCCGTC TGAAACACAC TCCGCCCAAC GCCCATCCTT
101 TTTCAGACGA CCCACACC. AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT TCTTGTTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGTGCC GTTATCGACC GCAAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG CCTGACCACG CCCGAAGCCG TCATTACGTT CAGCAAAGAC
301 GGCAACAAAC GCCAAGTTCC CCTGAGCGGC CGGAAGTGCC ACGCCGGCGC
351 GGTGGGTATG CTGTTGAACG AACTGGAAAA ACACGAACTG CACGACCGCA
401 TTCAAGCCGT CGGCCACCGC ATCGCCACG GCGGCGAAAA ATACAGCGAG
451 TCTGTTTTGA TCGACCAGGC CGTAATGGAC GAACCTCAATG CCTGCATTCC
501 GCTTGCGCCG CTGCACAACC CCGCCAACAT CAGCGGCATC CTCGCCSCAC
551 AGGAACATTT CCCCGGTCTG CCCAATGTCG GCGTGATGGA TACTTCGTTT
601 CACCAAACCA TGCCGGAGCG TGCCTACACT TATGCCGTGC CGCGCGAGTT
651 GCGTAAAAAA TACGCTTTCC GCCGCTACGG TTTCCACGGC ACCAGTATGC
701 GTTACGTTGC CCCTGAAGCC GCATGCATCT TGGGCAAAAC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCCA CTIAGGCAAC GGCGCATCCA TTACCGCCAT
801 CAAAAACGGC AAATCCGTGC ATACCAGTAT GGGTTTCACG CCGATCGAAG
851 GTTTGGTAAT GGTACGCGC TCGCGCGATA TCGACCCGGG CGTATACAGC
901 TATCTGACTT CACACGCCGG TTTGGATGTT GCACAAGTTG ATGAAATGCT
951 GAATAAAAAA TCAGGCTTGC TCGGTATTTT CGAACTCTCC AACGACTGCC
1001 GCACCCTCGA AATCGCCGCC GACGAAGGCC ACGAAGGCGC GCGCCTCGCC
1051 CTCGAAGTTA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
1101 GGGCTGCGGC GCGGTTGACG CACTCGTGTT CACCGCGCGT ATCGGCGAAA
1151 ACTCGCGTAA TATCCGTGCC AAAACCGTTT CCTATCTTGA TTTCTTGGGT
1201 CTGCACATCG ACACCAAAGC CAATATGGAA AAACGCTACG GCAATTCGGG
1251 TATTATCAGC CCGACCGATT CTCTCCGGC TGTTTTGTT GTCCCGACCA
1301 ATGAAGAACT GATGATTGCC TCGGACACTG CCGAAGTTGT CGGCATCTTG
1351 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1900; ORF 603.a>:

```

a603.pep
1  LSSRRRGRNN DRKCGIRFAQ RGRLLKHTPPN AHPFSDDPTX KKQPQTTRRN
51  IMSDQLILVL NCGSSSLKGA VIDRKSGSVV LSCLGERLTT PEAVITFSKD
101 GNKRQVPLSG RNCHAGAVGM LLNELEKHEL HDRIQAVGHR IAHGGEKYSE
151 SVLIDQAVMD ELNACIPLAP LFNPNANISGI LAAQEHFPGLP NVGVMDSF

```

958

```

201  HQTMPERAYT YAVPRELRKK YAFRRYGFHG TSMRYVAPEA ACILGKPLED
251  IRMIIAHLGN GASITAIKNG KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS
301  YLTSHAGLDV AQVDEMLNKK SGLLGISELS NDCRTLEIAA DEGHEGARIA
351  LEVMTYRLAK YIASMAVGCG GVDALVFTGG IGNSRNIRA KTVSYLDFLG
401  LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELNIA CDTAELVGIL
451  *

```

m603/a603 96.7% identity in 450 aa overlap

```

          10      20      30      40      50      60
m603.pep  LSSRRRGRNDRKCGIRFAQRGLKHLAPDVCXFSDDPTLKKQPQTTRRNIMSDQLILVL
a603      LSSRRRGRNDRKCGIRFAQRGLKHTPPNAHPFSDPTXKKQPQTTRRNIMSDQLILVL
          10      20      30      40      50      60

          70      80      90      100     110     120
m603.pep  NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPAVITFNKDGNKQVPLSGRNCHAGAVGM
a603      NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPAVITFSKDGNKQVPLSGRNCHAGAVGM
          70      80      90      100     110     120

          130     140     150     160     170     180
m603.pep  LLNELEKHGLHDRIKAIGHRIAHHGGEKYESVLIQAVMDELNACIPLAPLHPANISGI
a603      LLNELEKHGLHDRIQAVGHRIAHHGGEKYESVLIQAVMDELNACIPLAPLHPANISGI
          130     140     150     160     170     180

          190     200     210     220     230     240
m603.pep  LAAQEHFPGLPNVGVMDSFHHQTMPERAYTYAVPRELRKKYAFRRYGFHGTSMRYVAPEA
a603      LAAQEHFPGLPNVGVMDSFHHQTMPERAYTYAVPRELRKKYAFRRYGFHGTSMRYVAPEA
          190     200     210     220     230     240

          250     260     270     280     290     300
m603.pep  ARILGKPLEDIRMIIAHLGNNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS
a603      ACILGKPLEDIRMIIAHLGNNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS
          250     260     270     280     290     300

          310     320     330     340     350     360
m603.pep  YLTSHAGMDVAQVDEMLNKKSGLLGISELSNDCRTLEIAADEGHEGARLALEVMTYRLAK
a603      YLTSHAGLDVAQVDEMLNKKSGLLGISELSNDCRTLEIAADEGHEGARLALEVMTYRLAK
          310     320     330     340     350     360

          370     380     390     400     410     420
m603.pep  YIASMAVGCGGVDALVFTGGIGNSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
a603      YIASMAVGCGGVDALVFTGGIGNSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
          370     380     390     400     410     420

          430     440     450
m603.pep  PTDSSPAVLVVPTNEELMIACDTAELAGILX
a603      PTDSSPAVLVVPTNEELMIACDTAELVGILX
          430     440     450

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1901>:

g604.seq

```

1  ATGCCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTGGA
51  CCAGCGTACC GAGCACGGCG GCGGCGATGG CGACCGAGGC GATGCCCATC
101 ATAGCGTGGT GCAGTTTGCC CATGCTCAGG GCGCGTACCG GCAAATCGAT
151 GTCGGCGGCG TTTACGGTTT TGCGCTGGA GCGGTGTAA TCGGCGGCGG
201 GCGCGACGAA GCGGGTTTC GCGTGCGCG GCGGGCGGC GGCTTCGGAT

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959

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251  ACGTCGCTGA TCAAACCCAT TTTCAGCGCG CCATATGCGC GGATGGTTTC
301  AAATTTTTC AGCGCGGCGG CATCGTTGTT GATGTCGTCC TGCAACTCTT
351  TGCCCGTGTA GCCCAAGTCG GCGGCGTTCA GGAAAACGGT CGGAATGCCC
401  GCGTTGATGA GCGTGGCTTT CAGACGACCT ATATTCGGCA CATCAATTTC
451  GTCGACCAAA TTGCCGGTTG GGAACATACT GCCTTcgcCG TCGGCTGGAT
501  CTAA

```

This corresponds to the amino acid sequence <SEQ ID 1902; ORF 604.ng>:

g604.pep

```

1  MPEAHFFTRS AACGKVDQRT EHGGDGDGRG DAHHSVVQFA HAQGAYRQID
51  VGGVYGFAAG GGVIGGGRDE GGFRRARAGG GFGYVADQTH FQRAICADGF
101 KFFQGGIVV DVVLQLFARV AQVGGVQENG RNARVDERGF QTTYIRHINF
151 VDQIAGWEHT AFAVGWI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1903>:

m604.seq

```

1  ATCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCTGCG GCAAGGTTGA
51  CCAGCGTACC GGGTACGGCG GCGGCGGTCG CAATGGCAAC AGAGGCGGTA
101 CCCATCATCG CGTGGTGCA GTTGCCCATG CTCAGGGCGC GTACCAGCAA
151 ATCGATGTCG GCGGCGTTCA CGGTTTGGCC ACTGGAGGCG GTGTAATCGG
201 CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG AGCGGCAGCT
251 TCGGATACGT CGCTGATCAG ACCCATTTTC AGCGCACCGT AAGCGCGGAT
301 TTTCTCGAAT TTTTCAAAG CCGCGGCATC GTTGTGTGATG TCGTCTTGCA
351 ACTCTTTGCC TGTGTAGCCC AAGTCGGCGG CATTCAAGAA AACGGTCGGA
401 ATGCCCGCGT TGATGAGCGT GGCTTTCAA CGGCCTATAT TCGGCACATC
451 AATTTCATCG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCGG
501 CTGGATC

```

This corresponds to the amino acid sequence <SEQ ID 1904; ORF 604>:

m604.pep

```

1  MPEAHFFTRS AACGKVDQRT GYGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
51  IDVGGVHGF A TGGGVIGGR DEGDFFRVRA SGSFGYVADQ THFQRTVSAD
101 FLEFFQSRGI VVDVVLQLFA CVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NFIDQIAGWE HTAFVGWI

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 604 shows 83.4% identity over a 169 aa overlap with a predicted ORF (ORF 604.ng)

from *N. gonorrhoeae*:

m604/g604

	10	20	30	40	50	60
m604.pep	MPEAHFFTRS AACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGF					
g604	MPEAHFFTRS AACGKVDQRTBHGGG--DGDGRDAHHSVVQFAHAQGAYRQIDVGGVYGFA					
	10	20	30	40	50	
	70	80	90	100	110	120
m604.pep	TGGGVIGGGRDEGDFFRVRASGSFGYVADQTHFQRTVSADFLEFFQSRGIVVDVVLQLFA					
g604	AGGGVIGGGRDEGGFRRARAGGFGYVADQTHFQRAICADGFKFFQGGIVVDVVLQLFA					
	60	70	80	90	100	110
	130	140	150	160	169	
m604.pep	CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVGWI					
g604	RVAQVGGVQENGRNARVDERGFQTTYIRHINFVDQIAGWEHTAFVGWIX					
	120	130	140	150	160	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1905>:

a604.seq

```

1  ATCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCTGCG GCAAGGTTGA
51  CCAGCGTACC GGGCACGGCG GCGGCGGTCG CAATGGCAAC AGAGGCGGTA
101 CCCATCATCG CGTGGTGCAA TTGCCCCATG CTCAGGGCGC GTACCAGCAA
151 ATCGATGTCG GCGGCATTCA CGGTTTGGCC ACTGGAGGCG GTGTAATCGG

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960

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201 CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG GCGGGCAGCT
251 TCGGATACGT CGCTGATCAG ACCCATTTTC AGCGCACCGT AAGCGCGGAT
301 TTTCTCGAAT TTTTCCAAAG CTGCGGCATC GTTGTGTGATG TCGTCTTGCA
351 ACTCTTTGCC CGTGTAGCCC AAGTCGGCGG CATTCAAGAA AACGGTCGGA
401 ATGCCCGCGT TGATGAGCGT GSCTTTCAAA CGGCCTATAT TCGGCACATC
451 AATTTCATCG ACCAAATTGC CAGTTGGGAA CATACTGCCT TCGCCGTCGG
501 CTGGATCAAG AAATTCGATT TGTACTTCGG CTGCCGGGAA CGTTACGCCG
551 TCGAGCTCAA AATCGCCTGT TTCCAAACT GCGCCGTTTT GCATCGGTAC
601 ATGGGCAATA ATGGTTTTCG CGATGTTTTT CTGCCAGATT TTGACTGTGC
651 AGATGCCGTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1906; ORF 604.a>:

```

a604.pep
1  MPEAHFFTRS AACGKVDQRT GHGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
51  IDVGGIHGFA TGGGVIGGGR DEGDFFRVRA GGSFGYVADQ THFQRTVSAD
101 FLEFFQSCGI VVDVVLQLEA RVAQVGIGQE NGRNARVDER GFQTAYIRHI
151 NFIDQIAGWE HTAFVGVWIK KFDLYFGCRE RYAVELKIAC FQNCVHLHRY
201 MGNGFADVF LPDFDCADAV *

```

m604/a604 97.0% identity in 169 aa overlap

	10	20	30	40	50	60
m604.pep	MPEAHFFTRS AACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGFA					
a604	MPEAHFFTRS AACGKVDQRTGHGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGIHGFA					
	10	20	30	40	50	60
m604.pep	TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFLFFQSRGIVVDVVLQLEA					
a604	TGGGVIGGGRDEGDFRRVRAGGSFGYVADQTHFQRTVSADFLFFQSCGIVVDVVLQLEA					
	70	80	90	100	110	120
m604.pep	TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFLFFQSRGIVVDVVLQLEA					
a604	TGGGVIGGGRDEGDFRRVRAGGSFGYVADQTHFQRTVSADFLFFQSCGIVVDVVLQLEA					
	70	80	90	100	110	120
m604.pep	CVAQVGIGQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVGVWIK					
a604	RVAQVGIGQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVGVWIKKFDLYFGCRE					
	130	140	150	160	169	
m604.pep	CVAQVGIGQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVGVWIK					
a604	RVAQVGIGQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVGVWIKKFDLYFGCRE					
	130	140	150	160	170	180
a604	RYAVELKIACFQNCVHLHRYMGNGFADVFLPDFDCADAVX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1907>:

```

g605.seq
1  ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTGGA
51  AATCGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTACCGGAC
151 TATATGCAGG CCGGCGACAG CAGCATTGAT TACGCCGCTa tGCCGGACAG
201 CATCATCAGC CCCGAAATCA AAGACGATgc cgtcaaagtc aaAGGCTATt
251 TCATCtaccC cgGCCAGCTT TTTTgcaata ttgccgcga agcCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGaa atCTTTACCG CGATTGAAAG
351 CTCCGCCTCC GGCTAcccgT CCGAACAAAG CATCAAAGGC TTGTTTGACG
401 ACTTCgACAC CACCAGCAGC CGGCTCGGCA GCACCGTTGC CGACAAAAAC
451 AAACGCCTTG CCGCCGTCCT TAAAGGCGTG GCGGAACTCG ATTTTCGGCAA
501 TTTTGAAGAC CACCGCATCG ACCTTTTCGG TGATGCCTAC GAATACCTGA
551 TTTCCAACTA CGCgcCAAC GCAGGCAAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TCTCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGGCAGGA
651 GAAAGTCAAC AAAATCTACG ACCCCGCTTG CGGCTCGGGC AGCCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAACACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAATATGTT
801 TCTGCACAAC GTCAATTACA ACAAAATCCA CATCGAATTG GGCACACGC
851 TGACCAACCC CAAACTCAAA GACAGCAAAC CCTTTGATGC CGTCGTCTCC
901 AATCCGCCCT ATTCCATCGA CTGGATAGGC AGCGACGACC CCACCTtgaT

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951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTCGCACCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCTA TCGTCTCATT CCCCGGCATT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATC CGCCAATATC TGGTGGAGGG CAACTATGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCTGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
1301 ACATTGCCGA AATCGTCAAA CTCTTCGCCG ACAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCCGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCGGTCAGC AGCTATGTG AAGCCGAAGA CACCCGCGAG GTCATCGACA
1451 TCAGACAGCT CAACGCCGAA ATCAGCGAAA CCgtcgCcaa AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAA CCTAG

```

This corresponds to the amino acid sequence <SEQ ID 1908; ORF 605.ng>:

g605.pep

```

1 MMTEMQORAQ LHRQIWKIAD EVRGAVDGDW FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNNTKLKE IFTAIESSAS GYPSEQGIKG LFDDFDTTSS RLGSTVADKN
151 KRLAAVLKGV AELDFGNFED HRIDLFGDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGOEKVN KIYDPACGSG SLLIQAKKQF DEHIEEGFF
251 GQENHHTTYN LARMNMFLHN VYNKFHIEL GDTLTNPKLK DSKPFDVAVS
301 NPPYSIDWIG SDDPTLINDD RFAPAGVLAP KSKADFAPIL HALNYLSGRG
351 RAALVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTCIAVNI
401 LVLKSKHKDNT DIQFIDASGF FKKETNNNVL TEEHIAEIVK LFADKADVPH
451 IAQNAAQQT V KDNNGYNLAVS SYVEAEDTRE VIDIRQLNAE ISETVAKIER
501 LRREIDEVIA EIET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1909>:

m605.seq

```

1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51 AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTCACCGAC
151 TATATGCAGG CAGGCGACAG CAGTATTGAT TACGCGGCTA TGCCGGACAG
201 CATCATCACC CCCGAAATCA AAGACGATGC CGTCAAAGTT AAAGGCTATT
251 TCATCTACCG CGGCCAGCTT TTTTGCAATA TTGCCCGCGA AGCCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTACCG CGATTGAAAG
351 CTCCGCCTCC GGCTATCCGT CCGAACAGGA CATCAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACTGTTCG CGACAAGAAC
451 AAACGCCTTG CCGCCGTCCT CAAAGCGGTG GCGGAACCTG ATTTCCGCAA
501 TTTTGAAAAC CACCACATCG ACCTTTTCGG CGATGCCTAC GAATACCTGA
551 TTTCCAACTA CGGTGCCAAC GCAGGCAAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGACAGGA
651 GAAAGTCAAC AAAATCTACG ACCAGCTTG CGGCTCGGCG AGTCTGCTCT
701 TGCAAGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAACATGTT
801 CCTGCACAAC GTCAATTACA ACCAATTCCA CATCGAATTG GGCGACACAC
851 TGACCAACCC AAAGCTCAAA GACAGCAAAC CCTTTGATGC CATCGTTTCC
901 AATCCGCCTT ATTCCATCAA CTGGATAGGC AGCGACGACC CCACCTTAAT
951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTTGCCCCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCGA TCGTCTCATT CCCCGGCATT TTCTATCGCG GCGGCGCAGA
1101 ACAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ATCGAAGAAC
1301 ACATTGCTGA AATCGTCAAA CTCTTCGCCG ATAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCTGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCGGTCAGC AGCTATGTG AAGCCGAAGA CACACGCGAA ATTATCGACA
1451 TCAAACAGCT CAACGCCGAA ATCGGCGAAA CCGTCGCCAA AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1910; ORF 605>:

m605.pep

```

1 MMTEMQORAQ LHRQIWKIAD EVRGAVDGDW FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ

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101 NEELNTKLKE IFTAIESSAS GYPSEQDIKG LFDDFDTTSS RLGSTVADKN
151 KRLA AVLKGV AELDFGNFEN HHIDLFGDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLQAKKQF DEHIEEGFF
251 GQEIHTTYN LARMNMFHVN VNYNQFHIEL GDTLTNPKLK DSKPFDAIVS
301 NPPYSINWIG SDDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG
351 RAAIVSFPGI FYRGAEQKI RQYLVEGNYV ETVIALAPNL FYGTGIAVNI
401 LVLSKHKDNT DIQFIDASGF FKKETNNNVL IEEHIAEIVK LFADKADVP
451 IAQNAAQOTV KONGYNLAVS SYVEAEDTRE IIDIKQLNAE IGETVAKIER
501 LRREIDEVIA EIEA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 605 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 605.ng) from *N. gonorrhoeae*:

m605/g605

m605.p	10	20	30	40	50	60
	MMTEMQRAQLHRQIWKIADEVRGAVDGFQYVLGTLFYRFISENFTDYMQAGDSSID					
g605	10	20	30	40	50	60
	MMTEMQRAQLHRQIWKIADEVRGAVDGFQYVLGTLFYRFISENFTDYMQAGDSSID					
m605.p	70	80	90	100	110	120
	YAAMPDSIITPEIKDDAVKVGKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
g605	70	80	90	100	110	120
	YAAMPDSIITPEIKDDAVKVGKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
m605.p	130	140	150	160	170	180
	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLA AVLKGV AELDFGNFENHHIDLFGDAY					
g605	130	140	150	160	170	180
	GYPSEQGIGLFLFDDFDTTSSRLGSTVADKNKRLA AVLKGV AELDFGNFEDHRIDLFGDAY					
m605.p	190	200	210	220	230	240
	EYLISNYAANAGKSGGEFFT PQSVSKLIAR LAVHGQEKVNKI YDPACGSGSLLQAKKQF					
g605	190	200	210	220	230	240
	EYLISNYAANAGKSGGEFFT PQSVSKLIAR LAVHGQEKVNKI YDPACGSGSLLQAKKQF					
m605.p	250	260	270	280	290	300
	DEHIEEGFFGQEIHTTYNLARMNMFHVN VNYNQFHIELGDTLTNPKLKDSKPFDAIVS					
g605	250	260	270	280	290	300
	DEHIEEGFFGQEIHTTYNLARMNMFHVN VNYNKFHIELGDTLTNPKLKDSKPFDAVVS					
m605.p	310	320	330	340	350	360
	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI					
g605	310	320	330	340	350	360
	NPPYSIDWIGSDDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI					
m605.p	370	380	390	400	410	420
	FYRGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF					
g605	370	380	390	400	410	420
	FYRGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF					
m605.p	430	440	450	460	470	480
	FKKETNNNVLIEEHIAEIVKLFADKADVP HIAQNAAQOTVKONGYNLAVSSYVEAEDTRE					
g605	FKKETNNNVLTEEHIAEIVKLFADKADVP HIAQNAAQOTVKONGYNLAVSSYVEAEDTRE					

```

      430      440      450      460      470      480
      490      500      510
m605.pép  IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX
          :||:|||||:|||||||:|||||:
g605      VIDIRQLNAEISETVAKIERLRREIDEVIAIETX
          490      500      510

```

a605.seq

This corresponds to the amino acid sequence <SEQ ID 1912; ORF 605.a>:

a605.pap

1	MMTEIQORAQ	LHRQIWKIAD	EVRGAVDGDW	FKQYVLGTLF	YRFISENFTD
51	YMQAGDSSID	YAAMPDSIIT	PEIKDQDAVKV	KGYFIYPQGL	FCNIAAEAHQ
101	NEELNLTKE	IFTAIESSAS	GYPSEQDIKG	LFDDFDTTSS	RLGSTVADKN
151	KRLAAVLKGV	ALDFGFSFED	HHIDLFGDAY	EYLISFNAYN	AGKSGGFEFT
201	PQSVSKLIAR	LAVHGOEKVN	KIYDPACGSG	SLLLOAKKQF	DEHIEEGGFF
251	GQEINHNTYN	LARMNMFLLN	VNYNKFHIEL	GDTLTNPCLK	DSKPFDAVVS
301	NPFPYSINWIG	SGDPTLINDH	RFAPAGVLAR	KSADFAFILL	HALNYLSRGV
351	RAAIVSFPGI	FYRGGAEQKI	RQYLVEGNYV	ETVIALAPNL	FYGTGIAVNI
401	LVLSKHKDNT	DIQNTDAGGF	EKKETNNNVL	TEEHIAEIVK	LFADKADVPH
451	IAQNAAQQTV	KDNGYNLAVS	SYVEPEDTRE	IIDIKQLNAE	ISETVAKIER
501	LBREIDEIVIA	EIEA*			

m605/a605 98.1% identity in 514 aa overlap

	10	20	30	40	50	60
m605.pep	MMTEMQQRALHRQIWKIADEVRGAVDGDGWFQKQYVLGTLFYRFISENFTDYMQAGDSSID					
	:					
a605	MMTEIQQRALHRQIWKIADEVRGAVDGDGWFQKQYVLGTLFYRFISENFTDYMQAGDSSID					
	10	20	30	40	50	60
	70	80	90	100	110	120
m605.pep	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHONEELNTKLKEIFTAIESSAS					

964

a605		YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS
	70 80 90 100 110 120	
m605.pep	130 140 150 160 170 180	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAEIDFGNFENHHIDLFGDAY
a605	130 140 150 160 170 180	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAEIDFGSFDHHLIDLFGDAY
m605.pep	190 200 210 220 230 240	EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGOEKVNKIYDPACGSGSLLLQAKKQF
a605	190 200 210 220 230 240	EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGOEKVNKIYDPACGSGSLLLQAKKQF
m605.pep	250 260 270 280 290 300	DEHIEEGFFGQEIINHNTYNLARMNMFHNNVYNQFHIELGDTLTNPCLKDSDKPFDAIVS
a605	250 260 270 280 290 300	DEHIEEGFFGQEIINHNTYNLARMNMFHNNVYNKFHIELGDTLTNPCLKDSDKPFDAVVS
m605.pep	310 320 330 340 350 360	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAPILHALNYLSGRGRAAIVSFPGI
a605	310 320 330 340 350 360	NPPYSINWIGSGDPTLINDDRFAPAGVLAPKSKADFAPILHALNYLSGRGRAAIVSFPGI
m605.pep	370 380 390 400 410 420	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIOFIDASGF
a605	370 380 390 400 410 420	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIOFIDAGGF
m605.pep	430 440 450 460 470 480	FKKETNNNVLEEIHAEIVKLFADKADVPHIAQNAAQCTVKDNGYNLAVSSYVEAEDTRE
a605	430 440 450 460 470 480	FKKETNNNVLTEEHAEIVKLFADKADVPHIAQNAAQCTVKDNGYNLAVSSYVEPEDTRE
m605.pep	490 500 510	IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX
a605	490 500 510	IIDIKQLNAEISSETVAKIERLRREIDEVIAEIEAX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1913>:

g606.seq

```

1  ATGTCCAAAT TTATCGCCAA ACAATCGGTC GGTGCGGAAG TCATCGACAC
51  GCCGcgCACC GAAGAAGAAG CCTGGCTTCT GAACACTGTC GAAGCCCAAg
101 cgcGGCAATG GAATCTGAAA ACGCCAGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCacc ggtttgctcg accaTatgaC GCGCGACgaa gtggaagcgc
251 tgTTGCGCA CGAAATGGCG CACGTGCGCA ACGGCGACAT GGTACGCTG
301 ACGCTGAtc AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTGCGCAT
351 TATTGCCAAC CTGATTGCC CAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTCTCT AGTCAGCATG GTATTCCAA TCCTGTTCGG CTCCTTGCC
451 AGCCTGATTG TCATGTGGTT CAGCCGCCAA CGCGAATACC GCGCCGAcgc
501 gggCGcgCA AAACCTGGTC GCGCACC3AA AATGATTTCC GCCTGCAAA
551 GGCTTAAAGG CAACCCGGTC GATTTGCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCA CTCCTGCTC AGCACCCACC CTTGCTGGA
651 CAACCGAATC GCCCGCCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1914; ORF606.ng>:

g606.pep

```

1  MSKFIKQSV  GAEVIDTPRT  EEEAWLLNTV  EAQARQWNLK  TPEVAIYHSP
51  EPNAFATGAS  RNSSLIAVST  GLLDHMTRE  VEAVLAHEMA  HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSL  LSTHPSLDNRI  ARLKSL*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1915>:

m606.seq

```

1  ATGTCCAAAT  TTATCGCCAA  ACAATCGGTC  GCGCGGAAG  TTATCGACAC
51  GCGCGCACCC  GAAGAAGAAG  CCTGGCTTTT  GAACACTGTC  GAAGCCCAAG
101 CGCGGCAATG  GAACCTGAAA  ACGCCCGAAG  TCGCCATCTA  CCACTCCCCC
151 GAACCCAATG  CCTTTGCCAC  GGGCGCATCG  AGAAACAGCT  CCCTGATCGC
201 CGTCAGCACCC  GGTGTGCTCG  ACCATATGAC  GCGTGACGAA  GTGGAAGCCG
251 TATTGGCGCA  CGAAATGGCA  CACGTCGGCA  ACGGCGATAT  GGTACGCTG
301 ACGCTGATTC  AAGGCGTGGT  CAATACCTTT  GTCGTGTTC  TGTCGCGCAT
351 TATTGCCAAC  CTGATTGCCC  GAAACAACGA  CGGCAGCCAG  TCCCAGGGAA
401 CTTATTTCTT  GGTGAGCATG  GTATTCCAAA  TCCTGTTCCG  CTTCTTGCC
451 AGCTTAATTG  TCATGTGGTT  CAGCCGACAA  CGCGAATACC  GCGCCGATGC
501 GGGCGCGGCA  AAACGTGGTC  GCGCGCCGAA  AATGATTTC  GCCCTGCAA
551 GGCTCAAAGG  CAACCCGGTC  GATTTGCCCG  AAGAAATGAA  CGCAATGGGC
601 ATCGCCGGAG  ATACGCGCGA  CTCCCTGCTC  AGCACCCACC  CTTGCTGGA
651 CAACCGTATC  GCCCGCCTCA  AATCGCTTTA  A
```

This corresponds to the amino acid sequence <SEQ ID 1916; ORF 606>:

m606.pep

```

1  MSKFIKQSV  GAEVIDTPRT  EEEAWLLNTV  EAQARQWNLK  TPEVAIYHSP
51  EPNAFATGAS  RNSSLIAVST  GLLDHMTRE  VEAVLAHEMA  HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSL  LSTHPSLDNRI  ARLKSL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 606 shows 100.0% identity over a 225 aa overlap with a predicted ORF (ORF 606.ng) from *N. gonorrhoeae*:

m606/g606

	10	20	30	40	50	60
m606.pep	MSKFIKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS					
g606	MSKFIKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS					
	10	20	30	40	50	60
m606.pep	RNSSLIAVSTGLLDHMTREVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
g606	RNSSLIAVSTGLLDHMTREVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
	70	80	90	100	110	120
m606.pep	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
g606	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
m606.pep	ALQRLKGNPVDLPEEMNAMGIAGDTRDSLSTHPSLDNRIARLKSLX					
g606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1917>:

a606.seq

966

```

1  ATGTCCAAAT TCATCGCCAA ACAATCGGTC GCGCGGAAG TTATCGACAC
51  GCGCGGCACC GAAGAAGAAG CCTGGCTTTT GAACACTETC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTTCGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GGTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCTT GGTGAGCATG GTATTCCAAA TCCTGTTCGG CTTCCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGACGC
501 GCGCGCGGCA AAACCTGGTC GCGCGCGGAA AATGATTTC GCCCTGCAAA
551 GGCTTAAAGG CAACCCGGTC GATTGCCCC AAGAAATGAA CGCAATGGGC
601 ATCGCCGAG ATACGCGCA CTCCCTGCTC AGCACCCACC CTTCGCTGGA
651 CAACCGAATC GCCCGCCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1918; ORF 606.a>:

```

a606.pep
1  MSKFIKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRE VEAFLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIAN LIARNNDGSQ SQGTFLVSM VFQILFGFLA
151 SLIVMWF SRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSL STHPSLDNRI ARLKSL*

```

m606/a606 100.0% identity in 226 aa overlap

m606.pep	10	20	30	40	50	60
	MSKFIKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPPEVAIYHSPEPNAFATGAS					
a606	MSKFIKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPPEVAIYHSPEPNAFATGAS					
	10	20	30	40	50	60
m606.pep	70	80	90	100	110	120
	RNSSLIAVSTGLLDHMTREVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIAN					
a606	RNSSLIAVSTGLLDHMTREVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIAN					
	70	80	90	100	110	120
m606.pep	130	140	150	160	170	180
	LIARNNDGSQSQGTFLVSMVFQILFGFLASLIVMWF SRQREYRADAGAAKLVGAPKMIS					
a606	LIARNNDGSQSQGTFLVSMVFQILFGFLASLIVMWF SRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
m606.pep	190	200	210	220		
	ALQRLKGNPVDLPPEEMNAMGIAGDTRDSLSTHPSLDNRIARLKSIX					
a606	ALQRLKGNPVDLPPEEMNAMGIAGDTRDSLSTHPSLDNRIARLKSIX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1919>:

```

g607.seq
1  ATGCTGCTCG accTcgacCG CTTTCTCTt tccGTCTTCC TGAAAGAAAT
51  CCGCTGCTG ACCGCCCTTG CCTGCCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CCGTTTCGTC GATACCGTGA TGGCGGGCGG TCGGGCAAG
151 GAAGATTGGC CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAACCC GgtgAAGCAG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTTC GGCTGATTTT GGGGATTTTC GGCATGATT TGTGTGGGC
351 GCGGATTACG CCGTTCGCA ACTGGCTGAC TTGAGCGAT TATGTGAAG
401 gcacAAtggc gcAGTATATG CTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCACTGCA CGCCTACGCT TCCAGCCTGA ACCGCCCGCG
501 CCTGATTATG TTGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGTGGCGCA

```

967

```

601 GGTTCGCGCG TGGCGACAAT GCGGGTGTTC TGGTTCAGCG CGCTGGCATT
651 GTGGATTTAT ATCGCCAAGG AAAAATTCTT CCGCCCGTTC GGAATGACAG
701 CGAAATTCGg caaACCGGat tGGgcGGTGT TCAAACAGAT TtGGAAAATC
751 gGcgcgCCCA TCGGGCTGTC TTATTTTTTG GAAGccaGcg cGTTTTCGTT
801 TATCGTGTTC TTGATTGCGC CTtccgCGA GGATTATGTG GCGGCGCAGC
851 AGGTCGGCAT CAGTTTGTCT GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCAG GGACGGTGGC CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951 TTCGCGGGCG CGTTATATTT CAGGAGTGTG GCTGGTGTCT GGCTGGGTGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTT GCCGCTGGCA
1051 AGCATGTACA ACGATGaTCC GGCAGTTTAA AGCATCGCCT CCACCGTCTT
1101 GCTGTTCCGC GGCTGTtcc aACCGGCAGA CTTCACCCAA TGTATCGCGT
1151 CCTATGCCCT GCGCGGTAC AAAGTCACCA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCTT TCTGGGGCTG CGGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CGTTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC AGCCGTGCGC TTGGTGTGGT GCTTGGAAAA ATACAGTATG
1351 GAGTTGGTCA AATCACACAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1920; ORF 607.ng>:

g607.pep

```

1 MLLDLDRFSF SVFLKEIRLL TALALPMLLA QVAQVGIGFV DTVMAGGAGK
51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT GEAGETGRQG
101 IWFLILGIF GMILMWAAT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRALHAYA SSLNRPRIM LVSFAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGVATMAVF WFSALALWIY IAKEKFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMIPQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWVLAVITVL SLVLFERSPLA
351 SMYNDPAVL SIASTVLLFA GLFQPADFTQ CIASVALRGY KVTKVPFMFIH
401 AAAFWCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAVA LVWCLEKYSM
451 ELVKSHKAV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1921>:

m607.seq

```

1 ATGCTGCTCG ACCTCAACCG CTTTTCCTTT CCCGTCTTCC TGAAAGAAGT
51 CCGCCTGCTG ACCACTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTTGTC GATACTGTGA TGGCGGGCGG TCGGGGCAAG
151 GAAGACTTGG CCGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAAACC GACGAAGTGG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTCG GGCTGTTTT GGGCGTGTTC GGCATGGTCT TGATGTGGGC
351 GGCGATTACG CCGTTCGCA ACTGGCTGAC CTTGAGCGAT TATGTGAAG
401 GCACGATGGC GCAGTATATG TTGTTACCA GCTTGGCGAT GCCGCGGCA
451 ATGGTACACC GCGCGCTGCA CGCCTACACT TCCAGCCTGA ACCGCCCAGC
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GCGGCTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTAT ATCGCCAAGG AAAATTCTT CCGCCCATTC GGAATGACGG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGGAAAATC
751 GGCGCACCCA TCGGGCTGTC TTATTTTTTG GAAGCCAGCG CGTTTTCGTT
801 TATCGTGTTC TTGATTGCGC CTTTCGCGCA GGATTATGTG GCGGCGCAGC
851 AGGTCGGCAT CAGTTTGTCT GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGGC CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951 TTCGCGGGCG CGTTATATTT CCGGCGGTGC ACTGGTGTTA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTT GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GCGGTTTAA AGCATCGCCG CCACCGTCTT
1101 ACTGTTGCGC GGCTTGTTCC AACCGGCAGA CTTCACCCAA TGTATCGCCT
1151 CCTACGCTTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCTT TTTGGGCTG CGGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CGTTTTCAAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1922; ORF 607>:

m607.pep

```

1 MLLDLNRFSS VFVLFKEVRL TALALPMLLA QVAQVGIGFV DTVMAGGAGK
51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG

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968

101 IWFGFLGVF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
 151 MVHRLHAYT SSLNRPRILM LVSFAAFVLN VPLNYIFVYG KPGMPALGGA
 201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVFKQIWKI
 251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQVVGISLS GILYMIPQSV
 301 GSAGTVRIGF SLGRREFSRA RYISGVSLVL GWMLAVITVL SLVLFPSPLV
 351 SMYNNDDPAVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMFIH
 401 AAAGWCGLL PGYLLAYRFN MGIYGFWTAL IASLTIAAIA LVWCLELCSR
 451 EMVRSHKAV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 607 shows 94.8% identity over a 459 aa overlap with a predicted ORF (ORF 607.ng) from *N. gonorrhoeae*:

m607/g607

	10	20	30	40	50	60
m607.pep	MLLDLNRFSFPVFLKEVRLTTLALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
g607	MLLDLDRFSFSVFLKEIRLLTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m607.pep	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGMVLWAAIT					
g607	SAFATVYITFMGIMAALNPMIAQLYGAGKTGEAGETGRQGIWFGFLGLIGFMIWAAIT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAHVHRLHAYTSSLNRPRILMLVSFAAFVLN					
g607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAHVHRLHAYASSLNRPRILMLVSFAAFVLN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m607.pep	VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD					
g607	VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD					
	190	200	210	220	230	240
	250	260	270	280	290	300
m607.pep	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQVVGISLSGILYMIPQSV					
g607	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQVVGISLSGILYMIPQSV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m607.pep	GSAGTVRIGFSLGRREFSRA RYISGVSLVLGWMLAVITVLSLVLFPSPLVSMYNNDDPAVL					
g607	GSAGTVRIGFSLGRREFSRA RYISGVSLVSGWMLAVITVLSLVLFPSPLASMYNNDDPAVL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m607.pep	SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPMFIHAAAFWCGLLPGYLLAYRFN					
g607	SIASTVLLFAGLFQPADFTQCIASYALRGYKVTKVPMFIHAAAFWCGLLPGYLLAYRFD					
	370	380	390	400	410	420
	430	440	450	460		
m607.pep	MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSKAVX					
g607	MGIYGFWTALIASLTIAAVALVWCLEKYSMEVRSKAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1923>:

```
a607.seq
1  ATGCTGCTCG ACCTCAACCG CTTTTCCTTT TCCGTCTTCC TGAAAGAAGT
51  CCGCTGCTG ACCGCTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTTGTC GATACCGTGA TGGCGGGCGG TGCGGGCAAG
151 GAAGACTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAAACC GACGAAAGTG GCGAAACGGG ACGGCAGGGG
301 ATTTGGTTTC GGCTGTTTTT GGGCGTGTTT GGCATGGTCT TGATGTGGGC
351 GGCATTACG CCGTTCGCA ACTGGCTGAC CTTGAGCGAT TATGTGAAG
401 GCACAATGGC GCAGTATATG CTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCACTGCA CGCTACGCC TCCAGCCTGA ACCGCCCGCG
501 CCGTATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 AATATATTTT CGTTTACGGC AAATTCGTA TGCCCGCTTT GGCGGGCGCA
601 GGCTGCGGAC TGGCGACGAT GGCAGTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTAT ATCGCCAAGG AAAATTTCTT CCGCCCATTC GGAATGACGG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGGAATATC
751 GCGGCACCCA TCGGGCTGTC TTATTTTGTG GAAGCCAGCG CGTTTTCGTT
801 TATCGTGTTC TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTGCGCAT CAGTTTGTG GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGCAGGTGCG CATCGGCTTT TCGCTTGGGC GGCAGCAATT
951 TTCGCGGGCG CGTTATATTT CCGGCGGTGC ACTGGTGTCA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGATAT TATTCCGTTT GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GCGGTTTTTA AGCATCGCCG CCACCGTCTT
1101 ACTGTTCCGC GGCTTGTTCC AACCGGCAGA CTTACCCCAA TGTATCGCCT
1151 CCTACGCCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCGCCTT TTTGGGCGTG CGGTCTGCTG CCGGGCTACC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGCCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCTGTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1924; ORF 607.a>:

```
a607.pep
1  MLLDLNRF SF SVFLKEVRLL TALALPMLLA QVAQVGIGFV DTVMAGGAGK
51  EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG
101 IWFGFLGVF GMVLMWAAIT PERNWLTLS D YVEGTMAQYM LFTSLAMPAA
151 MVHRLHAYA SSLNRPRIM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGLATMAVF WFSALALWIY IAKENFERPF GLTAKFGKPD WAVFQIWKI
251 GAPIGLSYFL EASAFSFI F LIAPFGEDYV AAQVVGISLS GILYMI PQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWMLAVITVL SLVLFSPPLV
351 SMYNNPDAVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMFIH
401 AAFAWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAIA LVWCLELC SR
451 EMVRSHKAV*
```

m607/a607 98.9% identity in 459 aa overlap

	10	20	30	40	50	60
m607.pep	MLLDLNRFSPVFLKEVRLLTTALPMLLAQVAQVGIGFVDTV MAGGAGKEDLAAVALGS					
a607	MLLDLNRFSPVFLKEVRLLTALPMLLAQVAQVGIGFVDTV MAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
m607.pep	70	80	90	100	110	120
a607	70	80	90	100	110	120
m607.pep	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGMVLMWAAIT					
a607	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGMVLMWAAIT					
	130	140	150	160	170	180
m607.pep	PERNWLTLSDYVEGTMAQYMLFTSLAMPAA MVHRLHAYTSSLNRPRIMLVSFAAFVLN					
a607	PERNWLTLSDYVEGTMAQYMLFTSLAMPAA MVHRLHAYTSSLNRPRIMLVSFAAFVLN					
	190	200	210	220	230	240

970

```

m607.pep  VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
a607      VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
           190      200      210      220      230      240

           250      260      270      280      290      300
m607.pep  WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV
a607      WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV
           250      260      270      280      290      300

           310      320      330      340      350      360
m607.pep  GSAGTVRIGFSLGRREFSRARYISGVSLVLGWMMLAVITVLSLVLFRSPLVSMYNNDAVL
a607      GSAGTVRIGFSLGRREFSRARYISGVSLVSGWMMLAVITVLSLVLFRSPLVSMYNNDAVL
           310      320      330      340      350      360

           370      380      390      400      410      420
m607.pep  SIAATVLLFAGLFQPADFTQCIASALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFN
a607      SIAATVLLFAGLFQPADFTQCIASALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFD
           370      380      390      400      410      420

           430      440      450      460
m607.pep  MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX
a607      MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX
           430      440      450      460

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1925>:

```

g608.seq
1  ATGTCCGCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTACCT CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAACTGGCG GGACGCATCA CAGAAGACGG TTTGCTCTCG
151 GCGGGAACG GCTTTGCAGA CACCGAAATT ACCTTCGCA ACAGCGCGAT
201 ACGGAAAATC CTCCAAGGCG GCGAACCCGG GGCTGGCGAC ATCAGGCTCG
251 AAGGCGACCT CATCTCGGC ATCGCGGTAC TGTCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGacgA ATTGGCACGG ATTTTCGCA CGCAGGCAGg
351 catcggcagc CGTGCCACCG ACATCGGACA CGGCATCaaa CAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCGGATTTT CCCGCGAACC CGAGTCcgCa
451 aacaccggca acgaagccct tgccgactgc ctCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACAGG CTCGAACGCG
551 ACATTGGAT AGACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1926; ORF 608.ng>:

```

g608.pep
1  MSALLPIINR LILQSPDSRS ELTSFAGKTL TLNIAGLKLA GRITEDGLLS
51  AGNGFADTEI TFRNSAIRKI LQGEPGAGD IRLEGDLILG IAVLSLLGSL
101 RSRASDELAR IFGTQAGIGS RATDIGHGIK QIGRNIAEQI GGFSREPESA
151 NTGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1927>:

```

m608.seq
1  ATGTCCGCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTGGCG CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAACG GCTTTGCAGA CACCGAAATT ACCTTCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGAG GCGAACCCGG GGCGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCTCGGC ATCGCGGTAC TGTCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCGG ACATCGGACA CGGCATCAAA CAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCGGATTTT CCCGCGAATC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT

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501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
 551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1928; ORF 608>:

m608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
 51 AGNGFADTEI TFRNSAVQKI LQGGEFGAGD IGLEGDILG IAVLSLLGSL
 101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GGFSRESESA
 151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 608 shows 95.2% identity over a 188 aa overlap with a predicted ORF (ORF 608.ng) from *N. gonorrhoeae*:

m608/g608

	10	20	30	40	50	60
m608.pep	MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	::					
g608	MSALLPIINRLILQSPDSRSELTSFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m608.pep	TFRNSAVQKILQGGEFGAGDIGLEGDILGIAVLSLLGSLRSRASDELARIFGTQADIGS					
	::					
g608	TFRNSAIRKILQGGEFGAGDIRLEGDILGIAVLSLLGSLRSRASDELARIFGTQAGIGS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m608.pep	RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR					
	:					
g608	RATDIGHGIKQIGRNIAEQIGGFSREPESANTGNEALADCLDEISRLRDGVERLNERLDR					
	130	140	150	160	170	180
	189					
m608.pep	LERDIWIDX					
g608	LERDIWIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1929>:

a608.seq

1 ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
 51 CAGCCGCTCG GAACTTGCCG CCTTCGCAGG CAAAACACTG ACCCTGAACA
 101 TTGCCGGGTT GAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
 151 GCGGGAACG GCTTTGCAGA CACCGAAATC ACCTCCGCA ACAGCGCGGT
 201 ACAGAAAATC CTCCAAGGCG GCGAACCCGG GCGGGCGGAC ATCGGGCTCG
 251 AAGGCGACCT CATCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
 301 CGTTCGCGC CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
 351 CATCGGCAGC CGTGCCGCCG ACATCGGACA CGGCATCAA CAAATCGGCA
 401 GGAACATCGC CGAACAAATC GGCAGATTTT CCCGCGAACC CGAGTCCGCA
 451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT
 501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
 551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1930; ORF 608.a>:

a608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
 51 AGNGFADTEI TFRNSAVQKI LQGGEFGAGD IGLEGDILG IAVLSLLGSL
 101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GRFSREPESA
 151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

m608/a608 98.9% identity in 188 aa overlap

10 20 30 40 50 60

```
g609.seq
1  ATG GTT TGG ATAGACTCGA AATCTCGCT CTCGACGACG AAACCTTTGA
5  TGC GTT TGT GGC AAT CAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACG AAT TTC GGT TTT CGTA GGC TTT TCG GTAACGATT TTTCATCGGG
151 GCG TTT GAGC AGCCGATAGA GTTGCGAGCT CGCCTCGCTT TCCACAATAT
201 CGATAACTTC CTGCATACCG ACTTCGCGAT CGGAAGTCAG GCTACGGTGA
251 ACG TCGCAAC GCTGATTATG CGCGCCATAT TGGGAATTT CTTTGAACA
301 CGGCGAAGC GAGGTTACGG GAATCATGAC CTTTCATACT TGGCGGTATG
351 CCCCGCTCTT TATTCAACC GTGAGGCTAG CATCATACG CAGGtaa
```

g609.pap

1	MVVDRLLEILA	LDDETLDAFV	GNQRSSDIAH	HIFHEFRVfV	GLFGNVFFfG
51	AFEQAVELAAH	RLRFHIIDNF	LDTDFG ¹ GSQ	ADGNVRTLIM	RAILGNFFGT
101	BAKRGRYNNH	LHTVAVCPVF	HETREADIII	Q*	

```
m609.seq
1  ATGGTTGTGG  ATAGACTCGA  AATTCTCGCT  CTCGACGACG  AAACCTTTGA
5  TGCCTTTGTC  GGC AATCAGC  GAAGTAGCGA  CATCGCGCAC  CATATCTTCC
101 ACGAATTTTCG  GGT TTTCTGA  GGCTTTTTCG  GTAACGTATT  TTT CATCGGG
151 GCGTTTGGAG  AGGCCGCTAGA  GTGGCAGCCT  CGCCTCGCCG  TCCACATAAT
201 CGATGACTTC  CTCGATACCG  ACTTCGCGACT  CGGCACTCAG  GCTGACGGTA
251 ACGTGC GAAC  GCTGGTTGTG  CGCGCCGTAT  TGGGAAATTT  CTTTGAACA
301 CCGGCAAGC  GAGGTTACGG  GAATCATGAC  CTTCACTACT  TGCCCGTATG
351 CCCGCTCTT  GATTTCGCCC  GTGACGACAGA  CATCATAATC  CAGTAA
```

```
m609.pep
1  MVVDRLEILA  LDDETLDAFV  GNQRSSDIAH  HIFNIEFRVFV  GFFGNVFFIG
51  AFEQAVELAA  LRLRLHIIDF  LDTDFGIGSG  ADGNVRTLVV  RAVLGNFFGT
101 RAKRGYGNHD  LHTVAVCPVF  DFARETDIII  Q*
```

	10	20	30	40	50	60
m609.pep	MVVDRLLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVVFVGGFNGVFFIGAFEQAVELAA					
g609	MVVDRLLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVVFVGLFGNVFFIGAFEQAVELAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m609.pep	RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRVLGNFGFTRAKRGYGNHDLHTVAVCVPVF					

```
a609.seq
  1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTCTGA
51  TCGCAATTCG GGCAATCAGC GAAGTAGCCG CATCGCGCAC CATATCTTCC
101 ACGAATTTCTG GATTTTCGTA GGCCTTTTTCG GTAACGTATT TTTCATCTGG
151 CGCTTTGAGC AGGCCGTAGA GTTGCCAGCT CGCTGCGGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGGTTTETG CGCGCCATAT TGGGAAATTT CTTTGGAAAC
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCATACTG TGGCCGTATG
351 CACCGTCTTT CATTTCGCCC GTGAGGCTGA CATCATAATC CAGTAA
```

a609.pep

1	MVVDRLEILA	LDDETLDFAV	GNQRSSDIAH	HIFHEFRVVFV	GFFGNVFFIG
51	AFEQAVELAA	RLRLHIIDCF	LDTDFGIGSQ	ADGNVRTLVV	RAILGNFFGT
101	RAKRGYGNHD	LHTVAVCTVF	HFAREADIII	Q*	

[illegible][illegible]

974

```
801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTA CCGACTTAIG
851 CCTATCAGGT TTCGGGCGAA TATGCGATGT TGCAGGCGGC GGTGCGCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTGT GAAAGCCTGC TGGCATTCAA
951 ACGTGC GGGT GCGGACGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1938; ORF 610.ng>:

```
g610.pep
1  MIGGLMQFPY RNPASRMRR MRRDDFSRRL MREHMLTADD LIYPVFVLEG
51  AAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTGRA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHQQ DGLTDENGYV
151 MNDETVEVLV KOALCHAEAG TQVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLKGAD KKTQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSCE YAMLQAAVAN
301 GWLDGGKVVL ESLLAFKRAG ADGILTYAI EAAKMLKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1939>:

```
m610.seq
1  ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTC CGGCTTCGCG
51  TATCGCCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCTG ATGCGCGAAC
101 ACACGCTGAC CGCCGATGAT TTGATTTATC CGGTGTTTCT ATTGGAGGGG
151 TCGCGCGCGG AGGAGGATGT GCCTTCTATG CCGGGGTGTA AGCGTCAAAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GCGGTAAG CTCGGTATTC
251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAACACAAAC CGAGCGTGGC
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT TCACGGTCAG GACGGGCTGA CCGACGAAA CCGTTATGTG
451 ATGAACGATG AAACCGTAGA GSTTTTGGTC AAGCAGGCTT TGTGCCACGC
501 TGAAGCGGGC GCGCAGGTGG TTGCCCTTTC CGATATGATG GACGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTAGGCGGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTGCACGA AGTGGCGTTG
751 GACATTTCAG AAGGTGCGGA TATGGTAATG GTCAGGCCG GTTGTCCGTA
801 TTTGGACGTT GTCCGCCGCG TAAAGGACGA GTTCGGTGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGT TCGAGGCGAG GATTGCGAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTGT GAAAGCCTGC TGGCATTCAA
951 ACGTGC GGGT GCGGACGGGA TTTTGACCTA TTACGCTATT GAGGCGGCAA
1001 AGATGTTGAA GCGTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1940; ORF 610>:

```
m610.pep
1  MIGGLMQFPY RNPASRMRR MRRDDFSRRL MREHMLTADD LIYPVFVLEG
51  SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHQQ DGLTDENGYV
151 MNDETVEVLV KOALCHAEAG AOVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLKGAD KKTQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSCE YAMLQAAIAN
301 GWLDGGKVVL ESLLAFKRAG ADGILTYAI EAAKMLKR*
```

m610/g610 98.5% identity in 338 aa overlap

	10	20	30	40	50	60
m610.pep	MIGGLMQFPYRNPASRMRRMRRDDFSRRLMREHMLTADDLIYPVFVLEGSAREEDVPSM					
g610	MIGGLMQFPYRNPASRMRRMRRDDFSRRLMREHMLTADDLIYPVFVLEGAAREEDVPSM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m610.pep	PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER					
g610	PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTGRAQEAYNPEGLVPSTVRALRER					
	70	80	90	100	110	120
	130	140	150	160	170	180
m610.pep	FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKOALCHAEAGAQQVAPSDMM					
g610	FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKOALCHAEAGTQVVAPSDMM					
	130	140	150	160	170	180
	190	200	210	220	230	240
m610.pep	DGRIGAIREALEDAGHIHTRIMAYSAKYSAFYGPFRDAVGSSGNLGRADKKTQMDPAN					

975

```

g610      CGRIGAI REALE DAGHIHTRIMAYS AKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
           190      200      210      220      230      240

           250      260      270      280      290      300
m610.pep  TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTYAYQVSGEYAMLQAAIAN
           |||||
g610      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTYAYQVSGEYAMLQAAVAN
           250      260      270      280      290      300

           310      320      330      339
m610.pep  GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           |||||
g610      GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1941>:

```

a610.seq
1   ATGATTGGAG  GGCTTATGCA  GTTTCCTTAC  CGCAATGTTT  CGGCTTCGCG
51  TATGCCCGGT  ATGCCGAGGG  ACGATTTTTC  ACGCCGCTTG  ATGCCGAGCG
101 ATACCGTGAC  TGCCGATGAT  TTGATTATAT  CCGTGTTCGT  ATTGGAGGGG
151 TCGGCGCGCG  AGGAGGATGT  GCCTTCTATG  CCGGCGGTGA  AGCGTCAGAG
201 TTTGGACAGG  CTGCTGTTTA  CGGCGGAAGA  GGCGGTAAAG  CTCGGTATTC
251 CGATGTTGGC  ACTGTTCCCC  GTGGTTACGG  CAAACAAAAC  CGAGCGTGCG
301 CAGGAGGCGT  ACAATCCCGA  AGGACTCGTG  CCGTCAACTG  TCCGCGCCTT
351 GCGCGAGAGG  TTTCCCGAAC  TGGGCATTAT  GACGGATGTC  GCGCTCGATC
401 CTTATACGGT  GCACGGTCAG  GACGGGTGTA  CGGACGAAAA  CGGTTATGTG
451 ATGAACGATG  AAACCGTAGA  GETTTTGGTC  AAGCAGGCTT  TGTGTCATGC
501 AGAGGCAGGC  GCACAGGTCG  TTGCTCCTTC  CGATATGATG  GATGGGCGTA
551 TCGGTGCGAT  TCGCGAGGCG  TTGGAGGATG  CCGGCGATAT  CCATACGCGG
601 ATTATGGCGT  ATTCGCCCAA  ATATGCTTCT  GCATTTTACG  GCCCTTCCG
651 TGATGCGGTA  GGCAGTTCGG  GCAATTTGGG  CAAGGCAGAT  AAAAGACCT
701 ACCAGATGGA  TCCGGCAAAT  ACCGATGAGG  CGTTGCACGA  ACTGGCGTTG
751 GACATTCAAG  AAGGTGCGGA  TATGGTGATG  GTCAAGCCCG  GTTTGCCGTA
801 TTTGGACGTT  GTCCGCCGCG  TGAAGGACGA  GTTCGGCGTG  CCGACTTATG
851 CCTATCAGGT  TTCCGGAGAA  TACGCGATGC  TGCAGGCGCG  GGTGCCCAAC
901 GGCTGGCTGG  ACGGCGGCAA  AGTGGTTTTG  GAAAGCCTGC  TGGCATTCAA
951 ACGTGCGGGT  GCGGATGGGA  TTTTGACCTA  TTACGCCATT  GAGGCGGCAA
1001 AGATGCTGAA  GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1942; ORF 610.a>:

```

a610.pep
1   MIGGLMQFPY  RNVSASRMRR  MRRDDFSRRL  MREHTLTADD  LIYPVFVLEG
51  SAREEDVPSM  PGVKRQSLDR  LLFTAEEAVK  LGIPMLALFP  VVTANKTERA
101 QEAYNPEGLV  PSTVRALRER  FPELGIMTDV  ALDPYTVHGQ  DGLTDENGYV
151 MNDETVEVLV  KQALCHAEAG  AQVVAPSDMM  DGRIGAIREA  LEDAGHIHTR
201 IMAYS AKYAS  AFYGPFRDAV  GSSGNLGKAD  KKTYQMDPAN  TDEALHEVAL
251 DIQEGADMVM  VKPGLPYLDV  VRRVKDEFV  PTYAYQVSSE  YAMLQAAVAN
301 GWLDGGKVV  LESLLAFKRAG  ADGILTYYAI  EAAKMLKR*

```

m610/a610 99.4% identity in 338 aa overlap

```

           10      20      30      40      50      60
m610.pep  MIGGLMQFPYRNVPASRMRRMRRDDFSRRLMREHTLTADLIYPVFVLEGSAREEDVPSM
           |||||
a610      MIGGLMQFPYRNVSASRMRRMRRDDFSRRLMREHTLTADLIYPVFVLEGSAREEDVPSM
           10      20      30      40      50      60

           70      80      90      100     110     120
m610.pep  PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           |||||
a610      PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           70      80      90      100     110     120

           130     140     150     160     170     180

```


976

```

m610.pep    FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVRQALCHAEAGAQQVAPSDMM
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a610        FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVRQALCHAEAGAQQVAPSDMM
              130      140      150      160      170      180

              190      200      210      220      230      240
m610.pep    DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a610        DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
              190      200      210      220      230      240

              250      260      270      280      290      300
m610.pep    TDEALHEVALDIQEGADMVMVVKPGLPYLDVVRVKDEFVPTAYAYQVSGEYAMLQAAIAN
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a610        TDEALHEVALDIQEGADMVMVVKPGLPYLDVVRVKDEFVPTAYAYQVSGEYAMLQAAVAN
              250      260      270      280      290      300

              310      320      330      339
m610.pep    GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a610        GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
              310      320      330

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1943>:

```

g611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCCCGGA CTCTGTCGAG
101 GCGGTGCTCTG CCGGGGCAGG TGCTTCGGTT TTTTCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT Ctcgcgcagg ttgtGGCtgt
201 tatcctTGGG CGGGCTGggt tgtttgcccg ccataaTTtc cagtacctgA
251 TcgcgGTCta tggtttcCCA ttCcatcagg gctttgcaca TCGTTTCCAT
301 cttgTCGCGG TTTTcatcga ggaTTTGTa ggcaacCTGA TACTgctcgt
351 ccaaaAtccg Gcggatttcc gcgtcgAtgt cctgctgggt tTTCTCGGAA
401 ATGTTTTCGG AACGGgttac gctGCGCCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTTgTc gTCAtgCG TAGCGCGTTA
501 CCATTTTCGG TGCCATTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1944; ORF 611.ng>:

```

g611.pep
1  MPSENGMKR QLAGCRLFGK LSLVFRLLPG LCRGGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVILG RAGLFARHNF QYLIAYVGFP FHQGFARHFH
101 LVAVFIEDFV GNLLLLVQNP ADFRVDVLLG FLGNVLRGTY AAPQEDFAFV
151 FRINHHAHFV AHAVARYHFA CHLGCAFKVV *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1945>:

```

m611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCGAA
101 GCGGTGCTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTGCCCC CCATGATTTC CAGTACCTGA
251 TCGCGGTCTGA TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTTGTGCGCG TTTTCATCGA GGATTTGTa GGCAACCTGA TATTGCTCGT
351 CCAAAATCCG GCGGATTTC GCGTCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTCGG AACGGGTtac GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTTgTc GTCATGCCG TAGCGCGTTA
501 CCATTTTCGG CGCCATTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1946; ORF 611>:

```

m611.pep
1  MPSENGMKR QLAGCRLFGK LSLVFRLLLG LCRSGVCRGR CFGFFPSRSV
51  KRVIKRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGFH FHQGFARHFH
101 LVAVFIEDFV GNLLLLVQNP ADFRVDVLLG FLGNVLRGTY AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/g611 96.1% identity in 180 aa overlap

10 20 30 40 50 60

977

```

m611.pep      NPSENGMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
               |||||
g611           NPSENGMGKRQLAGCRLFGKLSLVFRLLPGLCRGGVCRGRCFGFFPSRSVRRVIFRRVRI
               10      20      30      40      50      60

               70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFRHLVAVFIEDFVGNLILLVQNP
               |||||
g611           LAQVVAVILGRAGLFARHNFQYLIADVGFPHQGFARHFRHLVAVFIEDFVGNLILLVQNP
               70      80      90      100     110     120

               130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFAHRLGCAFKVV
               |||||
g611           ADFRVDVLLGFLGNVLRGTGYAAPQEDFAFVFRINHHAHFVAHAVARYHFACHLGCAFKVV
               130     140     150     160     170     180

m611.pep      X
               |
g611           X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1947>:

```

a611.seq
1  ATGCCGTCGTG AAAACAGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51 GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTGCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGCTGGGT TGTTCGCCG CCATGATTTT CAGTACCTGA
251 TCGCGGTCTGA TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTGTGTCGGG TTTTCATCGA GGATTTTGTG GGCAACCTGA TACTGCTCGT
351 CCAAAATCCG GCGGATTTCG GCATCGATGT CCTGCTGEGT TTTCTCGGAA
401 ATGTTTTGCG AACGGGTAC GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTGC GCTCATGCCG TAGCGCGTTA
501 CCATTTGCGG CGCCATTGCG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1948; ORF 611.a>:

```

a611.pep
1  MPSENRMGKR QLAGCRLFGK LSLVFRLLLG LCRSGVCRGR CFGFFPSRSV
51 RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGF PHQGFARHFR
101 LVAVFIEDFV GNILLVQNP ADFRIDVLLG FLGNVLRGTG AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/a611 98.9% identity in 180 aa overlap

```

               10      20      30      40      50      60
m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
               |||||
a611           MPSENRMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
               10      20      30      40      50      60

               70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFRHLVAVFIEDFVGNLILLVQNP
               |||||
a611           LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFRHLVAVFIEDFVGNLILLVQNP
               70      80      90      100     110     120

               130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFAHRLGCAFKVV
               |||||
a611           ADFRIDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFAHRLGCAFKVV
               130     140     150     160     170     180

m611.pep      X

```

a611 I
 X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1949>:

```
g612.seq
1  ATGGGcttcg gcggaatat tgcAAAAAAG CTGGCcgGgGg taGATGAAAT
51  AGCCTttgac tttgacggcA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCataG CGGCGTAATC AATGCTGCTG TCGCCGGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCGATTTTC
251 CAAATTGGG GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA TAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTTTAC GGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1950; ORF 612.ng>:

```
g612.pep
1  MGFGGNIKK LAGVDEIAFD FDGIVDFGR DDAVRHSGVI NAAVAGLHIV
51  GEVFADKAVE KCAENVLFKV PAIHRAAYFV GDFPNLAVQL GALLHFGHHR
101 NPYIKLNKSK SPDIFRRFFY GHSN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1951>:

```
m612.seq
1  ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51  AGCCTTTAAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTGGG GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA .AAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTTTAC GGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1952; ORF 612>:

```
m612.pep
1  MGFGGNIKK LAGVDEIAFN FDGIVDFGR DDAVRHSGVI NTAVACLHIV
51  GEVFADKAVE KCAENVLFKV PAIHRAAYFV GNFPNLAVQL GALLHFGHHR
101 NPYXLNLSK SPDIFRRFFY GHSN*
```

m612/g612 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m612.pep	MGFGGNIKKLAGVDEIAFNFDGIVDFGRDDAVRHSGVINTAVACLHIVGEVFADKAVE					
g612	MGFGGNIKKLAGVDEIAFDGIVDFGRDDAVRHSGVINAAGLHIVGEVFADKAVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m612.pep	KCAENVLFKVPPIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXLNLSKSPDIFRRFFY					
g612	KCAENVLFKVPPIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYIKLNLSKSPDIFRRFFY					
	70	80	90	100	110	120
m612.pep	GHSNX					
g612	GHSNX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1953>:

```
a612.seq
1  ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51  AGCCTTTGAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTAAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTGAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTGGG GGTGCAGTTG GCGCGTTGT TGTATTTCGG TCATCATCGA
301 AATCCATAT. AAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTT.AC GGCATTCAA ATTAA
```

979

This corresponds to the amino acid sequence <SEQ ID 1954; ORF 612.a>:

```

a612.pep
  1  MGFGGNIAKK LAGVDEIAFD FDGIVDFDGR DDAVRHSGVI NTAVACLHIV
 51  GKVFADKAVE KCAENVLFEV PAIHRAAYFV GNFPNLAVQL GALLYFGHHR
101  NPYXKLNKSK SPDIFRREFX GHSN*

m612/a612  96.0% identity in 124 aa overlap

              10      20      30      40      50      60
m612.pep    MGFGGNIAKKLAGVDEIAFNFDGIVDFDGRDDAVRHSGVINTAVACLHIVGEVFADKAVE
              |||||
a612        MGFGGNIAKKLAGVDEIAFDGIVDFDGRDDAVRHSGVINTAVACLHIVGKVFADKAVE
              10      20      30      40      50      60

              70      80      90      100     110     120
m612.pep    KCAENVLFKVP AIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRREFY
              |||||
a612        KCAENVLFEPV AIHRAAYFVGNFPNLAVQLGALLYFGHHRNPYXKLNKSKSPDIFRREFX
              70      80      90      100     110     120

m612.pep    GHSNX
              ||||
a612        GHSNX
  
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1955>:

```

g613.seq
  1  ATGTCGCGTT CGAGCCTGTC GAGGCGTTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTCTG CGAGGCAGTC ggcaagggct tegtgtccgg
101  tgtttGcgGA CTCGGGTTTCG CGGGAAAATC CGCCGATTTC TTCGGCGATG
151  TTCCTGCCGA TTTgtttGat GCCGTGTCCG ATGTCGGTGG CACGgttgcc
201  gatgcCTGCC TGCGTGCCGA AAATCCGTGC CAATTcgtCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CgATGCCGAG GATGAGGTCC
301  CCTTCGAGCC TGATGTCGCC AGCCCCGGGT TCGCCGCTT GGAGGATTTT
351  CCGTATCGCG CTGTTGCGGA AGGTAATTC GGTGTCTGCA AAGCCGTTTC
401  CGCCCGAGAG CAAACCGTCT TCTGTGATGC GTCCCGCCAG TTTCAGCCCG
451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGAGGTAA GTTCCGAGCG
501  GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551  ACATATTTTC TGATTGGGGC GGAGAATGCC TGTGTTGCT GTTGCCGCTT
601  ATTTTACAGG CTAA
  
```

This corresponds to the amino acid sequence <SEQ ID 1956; ORF 613.ng>:

```

g613.pep
  1  MSRSSLSRRS LRRSTPSRSL LISSROSARA SLPVFADSGS RENPPICSAM
 51  FLPICLMPCP MSVARLPMPA CVPKIRANSS DARERRLP SR DSTAMPRMRS
101  PSSLMSPAPG SPPWRIFRIA LLRKVISVSA KPFFPAESKPS SVMRPASFSP
151  AMFRVSVLPA KEVSSERLSG LCRIRRLMMG RRADIFSDWG GECLLLLLPL
201  ILQA*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1957>:

```

m613.seq
  1  ATGTCGCGTT CGAGCCGGTC GAGGCGTTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTCTG CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101  TGTTTGCGGA CTCGGATTTCG CGGGAAAATC CGCCGATTTC TTCGGCGATG
151  TTCCTGCCGA TTTGTTTGAT GCCGTGTCCG ATGTCGGCGG CACGCTGCC
201  GATGTCTGCC TGCGTGCCGA AAATCCGTGC CAATTCGTCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCC
301  CCTTCGAGCC CGATGTCGCC CGCCCCGGGT TCGCCTCCTT GGAGGATTTT
351  CTGTACCGCG CTGTTGCGGA AGGTAATTC GGTGTCTGCA AAGCCGTTTC
401  CGCCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCAGCCCG
451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGCGCAA CTTCCGAGCG
501  GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551  ACATATTTTC TGATCGGGGC GGAGAATGCC TGTGTTGCT GTTGCCGCTT
  
```

980

601 ATTTTACAGG CTAA

This corresponds to the amino acid sequence <SEQ ID 1958; ORF 613>:

m613.pep

```
1  MSRSSRSRRS LRRSTPSRSL LISSRQSARA SLEMFADSDS RENPPICSAM
51  FLPICLMPCP MSAARLPMSA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101 PSSPMSPAPG SPPWRIFCTA LLRKVISVSA KPFPAESKPS SYMRPASFSF
151 AMFRVSVLPA KAASSERLSG LCRIRRLMMG RRADIFSDRG GECLLLLLPL
201 ILQA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m613/g613 94.6% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSL	LISSRQSARASLEMFADSDS	RENPPICSAMFLPICLMPCP			
g613	MSRSSLSRRSLRRSTPSRSL	LISSRQSARASLPVFADSGS	RENPPICSAMFLPICLMPCP			
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVPKIRANSS	DARERRLPSRDSTAMPRMRS	PSSPMSPAPGSPPWRIFCTA			
g613	MSVARLPMPACVPKIRANSS	DARERRLPSRDSTAMPRMRS	PSSLMSPAPGSPPWRIFRIA			
	70	80	90	100	110	120

981

	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFSPAMFRVSVLPAAKASSERLSGLCRIRRLMMG					
g613	LLRKVISVSAKPFPAESKPSSVMRPASFSPAMFRVSVLPAAKEVSSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
g613	RRADIFSDWGGECLLLLLPLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1959>:

```

a613.seq
1  ATGTCGCGTT  CGAGCCGCTC  GAGGCGTTCG  TTGAGGCGTT  CCACGCCGTC
51  GCGCAGTCTG  CTTATTTTCG  CGAGGCAGTC  GGCAAGGGCT  TCGTTGCCGA
101 TGTTTGGCGA  CTCGGGTTCG  CGGGAAAATC  TGCCGATTTC  TCGGCGATG
151 TTCTGCCGA  TTGTTTGAT  GCCGTGTCCG  ATGTCGGCGG  CACGGCTGCC
201 GATGTCTGCC  TGCSTGCCGA  AAATCCGTGC  CAATTCGTCC  GATGCGCGGG
251 AACGCAGGCT  GCCSAGCAGG  GACAGTACCG  CGATGCCGAG  GATGAGGTCG
301 CCTTCGAGCC  CGATGTCGCC  CGCCCCGGGT  TCGCCGCCTT  GGAGGATTTT
351 CTGTACCGCG  CTGTTGCCGA  AGGTGATTTC  GGTGTCTGCA  AAGCCGTTTC
401 CCGCCGAGAG  CAAACCGTCT  TCCGTGATGC  GTCCCGCCAG  TTTCAACCCG
451 GCAATGTTCA  GGGTCAGTGT  TTGCCTGCG  AAGGCGGCAA  GTTCCGAGCG
501 GCTGTCCGGG  CTTTGAGAAA  TCAGGCGGTT  GATGATGCGG  AGGAGGCGG
551 ACATATTTTC  TGATCGGGGC  GGAGAATGCC  TGTGTGCTCT  GTTGACGCTT
601 ATTTTACAGG  CTAA

```

This corresponds to the amino acid sequence <SEQ ID 1960; ORF 613.a>:

```

a613.pep
1  MSRSSRSRRS  LRRSTPSRSL  LISSRQSARA  SLPMFADSGS  RENLPICSAM
51  FLPICLMPCP  MSAARLPMSA  CVPKIRANSS  DARERRLPSR  DSTAMPRMRS
101 PSSPMSPAPG  SPPWRIFCTA  LLRKVISVSA  KPFPAESKPS  SVMRPASFNP
151 AMFRVSVLPA  KAASSERLSG  LCRIRRLMMG  RRADIFSDRG  GECLLLLLTL
201 ILQA*

```

m613/a613 98.0% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP					
a613	MSRSSRSRRSLRRSTPSRSLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPPWRICTA					
a613	MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPPWRICTA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFSPAMFRVSVLPAAKASSERLSGLCRIRRLMMG					
a613	LLRKVISVSAKPFPAESKPSSVMRPASFNPAMFRVSVLPAAKASSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
a613	RRADIFSDRGGECLLLLLTLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1961>:

982

g614.seq

```

1   AtggcTgcgt  tcAacgccltt  ggacggcaaa  aaagaagaca  acgggcaaat
51  cgaaTATCT  CAGTTCATCC  GACAGGTCAA  CAACGGCGAA  GTATCCGGCG
101 TCAACATCGA  AGGATCCGTC  GTCAGCGGTT  ACCTGATTAA  AGGCGAGCGC
151 ACCGACAAAA  GCACCTTCTT  CACCAACGCG  CCCTTGGATG  ACAACCTGAT
201 TCAAACCTT  TTGAACAAAA  ACGTCCGCGT  AAAAGTAACG  CCGGAAGAAA
251 AACCGAGCGC  GCTGACTGCC  CTGTTTACA  GCCTGCTGCC  CGTCTGCTG
301 CTGATTGGCG  CATGGTTCTA  CTTTATGCGT  ATGCAGGCGG  GCGGCGGCGG
351 AAAAGGCGGC  GCATTCTCCT  TCGGCAAAAG  CCGCGCCCGC  CTGCTGGACA
401 AAGATGCCAA  CAAAGTTACC  TTTGCCGATG  TCGCCGGCTG  CGACGAAGCC
451 AAAGAAGAAG  TGCAGGAAAT  CGTCGATTAC  CTCAAAGCAC  CGAACCGCta
501 tcaAAGcctc  ggcggccgtg  ttcCGCGCGG  CATCCTgCtg  gcgGgcagcc
551 CGGGAaccgg  taaAACACTC  TTGGCGAAAG  CCATTGCAGG  CGAGGCCGCG
601 GTGCCGTCT  TCAGCATTTT  CGGTTCCGAT  TTTGTGCAAA  TGTTCGTCGG
651 TGTCCGTGCA  AGCCGCGTCC  GCGATATGTT  CGAGCAGGCA  AAGAAAAACG
701 CCCCATGCAT  TATCTTTATC  GACGAGATTG  ACGCGGTAGG  CCGCCAACGC
751 GGCGCAGgTT  TGGGCGGCGG  CAATGATGAG  CGCGAGCAAA  CATTAAACCA
801 ATTATTGGTT  GAAATGGACG  GTTTTGAAG  CAATCAGACT  GTAATTGTGA
851 TTGCGGCAAC  CAACCGCCCC  GACGTACTCG  ATCCTGCGCT  GCAACGCCCC
901 GGCCGCTTCG  ACCGCCAAGT  CGTCGTCCCC  CTGCCGGACA  TCCGGGGGCG
951 CGAACAGatn  ttGAACGTCC  ATTCTaaAAA  AGTGCcttTG  gacgaATCTg
1001 tggattTTATT  GTCCCTCGCG  CGCGGCACGC  ccggtttTtc  cggcgcgat
1051 tTggcgaaac  tgggtcaacga  agccccctg  tttgcccggc  gccgcaacaa
1101 agtgaaagtc  gatcaaagcg  attTGAAGAC  GCCAAAGACA  AAATCTATAT
1151 GGGTCCGAA  CGCCGAGTA  TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1962; ORF 614.ng>:

g614.pep

```

1   MAAFNALDGK  KEDNGQIEYS  QFIRQVNNGE  VSGVNIIEGSV  VSCYLIKGER
51  TDKSTFTFNA  PLDDNLIQTL  LNKNVVRVKV  FEEKPSALTA  LFYSLLPVLL
101 LIGAWFYFMR  MQAGGGGKGG  AFSFGKSRAR  LLDKDANKVT  FADVAGCDEA
151 KEEVQEIVDY  LKAPNRYQSL  GGRVPRGILL  AGSPGTGKTL  LAKAIAEGAG
201 VPFFSISGSD  FVEMFVGUGA  SRVRDMFEQA  KKNAPCIIFI  DEIDAVGRQR
251 GAGLGGGNDE  REQTLNQLLV  EMDGFESNQT  VIVIAATNRP  DVLDPALQRP
301 GRFDRQVVVP  LPDIRGREQX  LNVHSKVKPL  DESVDLLSLA  RGTPGFSGAD
351 LAKLVNEAPL  FAGRRNKVKV  DQSDLKTPKT  KSIWVRNAAV  W*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1963>:

m614.seq

```

1   ATGGCTGCGT  TCAACGCTTT  AGACGGTAAA  AAAGAAGACA  ACGGGCAAAT
51  CGAATACTCT  CAGTTCATCC  AACAGGTCAA  CAACGGCGAA  GTATCCGGCG
101 TCAACATCGA  AGGATCCGTC  GTCAGCGGCT  ACCTGATTAA  GGGCGAGCGC
151 ACCGACAAAA  GCACCTTCTT  CACCAACGCG  CCTTTGGACG  ACAACCTAAT
201 TAAAACACTG  CTCGACAAAA  ACGTCCGCGT  AAAAGTAACG  CCGGAAGAAA
251 AACCGAGCGC  GCTGGCTGCC  CTGTTTACA  GCCTGCTGCC  CGTCTGCTG
301 CTGATTGGCG  CATGGTTCTA  CTTTATGCGT  ATGCAGACGG  GCGGCGGCGG
351 AAAAGGCGGC  GCATTCTCAT  TCGGTAAAAG  CCGCGCCCGC  CTGCTGGACA
401 AAGATGCCAA  CAAAGTGACC  TTTGCCGATG  TCGCCGGCTG  CGACGAAGCC
451 AAAGAAGAAG  TACAGGAAAT  CGTCGATTAC  CTCAAAGCGC  CGAACCGCTA
501 TCAAAGCCTG  GCGGGGCGCG  TGCCGCGCGG  CATCCTGCTG  GCGGCGAGCC
551 CGGGTACGGG  TAAGACGCTT  TTGGCGAAAG  CGATTGCAGG  CGAAGCCGGC
601 GTGCCGTTCT  TCAGCATTTT  AGGTTCCGAC  TTTGTGCAAA  TETTCGTCGG
651 TGTCCGTGCG  AGCCGCGTCC  GCGATATGTT  CGAGCAGGCG  AAGAAAAACG
701 CCCCTGCAT  CATCTTTATC  GACGAGATTG  ACGCAGTCGG  CCGCCAACGC
751 GGCGCAGGTT  TGGGCGGCGG  CAATGATGAG  CGCGAGCAAA  CATTAAACCA
801 ATTGTTGGTT  GAAATGGACG  GTTTTGAAG  CAATCAGACT  GTAATTGTGA
851 TTGCGGCAAC  CAACCGCCCC  GACGTACTCG  ATCCTGCGCT  GCAACGCCCC
901 GGCCGTTTCG  ACCGCCAAGT  GGTGTCCCC  CTGCCGGACA  TCCGAGGGCG
951 CGAACAGATT  TTGAACGTCC  ATTCTAAAAA  AGTGCCTTTG  GACGAATCTG
1001 TGGATTATT  GTCCCTCGCG  CGCGGCACGC  CGGGTTTTTC  CGGCGCGGAT
1051 TTGGCGAACT  TGGTCAACGA  AGCCGCCCTG  TTTGCCGGCC  GCCCAATAA
1101 AGTCAAAGTC  GATCAGAGCG  ATTTGAAGAC  GCCAAAGACA  AAATCTATAT
1151 GGSTCCGAA  CGCCGAGTA  TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1964; ORF 614>:

983

```

m614.pep
  1  MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIEGSV VSGYLIKGER
 51  TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101  LIGAWFYEMR MQTGGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151  KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIIAGEAG
201  VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251  GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301  GRFDRQVVVP LPDIRGREQI LNVHSHKVPL DESVDLLSLA RGTPGFGSAD
351  LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m614/g614 98.0% identity in 391 aa overlap

	10	20	30	40	50	60
m614.pep	MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIEGSVVSGYLIKGERTDKSTFFTNA					
g614	MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIEGSVVSGYLIKGERTDKSTFFTNA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m614.pep	PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMRMQTGGGGKGG					
g614	PLDDNLIQTLLNKNVRVKVT PEEKPSALTALFYSLPVLL LIGAWFYFMRMQAGGGGKGG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m614.pep	AFSEFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDY LKAPNRYQSLGGRVPRGILL					
g614	AFSEFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDY LKAPNRYQSLGGRVPRGILL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m614.pep	AGSPGTGKTL LAKAIIAGEAGVPFFSISGSD FVEMFVGASRVRDMFEQA KKNAPCIIFI					
g614	AGSPGTGKTL LAKAIIAGEAGVPFFSISGSD FVEMFVGASRVRDMFEQA KKNAPCIIFI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m614.pep	DEIDAVGRQRGAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP					
g614	DEIDAVGRQRGAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m614.pep	GRFDRQVVVPLPDIRGREQILNVHSHKVPLDESVDLLSLARGTPGFGSADLANLVNEAAL					
g614	GRFDRQVVVPLPDIRGREQILNVHSHKVPLDESVDLLSLARGTPGFGSADLAKLVNEAPL					
	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
g614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1965>:

```

a614.seq
  1  ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
 51  CGAATATTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
101  TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
151  ACCGACAAAA GCACCTTCTT CACCAACGCG CCTTGGACG ACAACCTGAT
201  TAAACACTG CTCGACAAAA ACGTCCGTGT AAAAGTAACG CCGGAAGAAA
251  AACCGAGCGC GCTGGCTGCC CTGTTTACG GCCTGCTGCC CGTCCTGCTG

```


984

```

301 CTGATTGGCG CGTGGTTCTA CTTTATGCGT ATGCAGACGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCAT TCGGCAAAAG CCGCGCCCGC CTAAGGACAA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCGCTA
501 TCAAAGCCTG GCGGGGCGCG TCGCGGCGCG CATCCTGCTG GCGGGCAGCC
551 CCGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
601 GTGCCGTTCT TCAGCATTTC AGGTTCCGAC TTTGTGCGAA TGTTCTGTCG
651 TGTCGGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGCGC AAGAAAAACG
701 CCCCTGTCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
751 GCGCGAGGTT TGGGCGGCGG TAATGATGAG CGCGAGCAAA CATTAAACCA
801 ATTGTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACCGCCCC GACGACTCG ATCCTGCGCT GCAACGCCCC
901 GGCGGTTTCG ACCGCCAAGT GGTGTGTCCTG CTGCGGGACA TCCGGGGGCG
951 CGAACAGATT TTGAACGTCC ACTCTAAAAA AGTGCTTTG GACAAATCTG
1001 TGGATTTATT GTCCCTCGCG CGCGGCACGC CGGGTTTTTC CGGCGCGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTGCGCGGCC GCCGCAATAA
1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGTCCGGAA CGCCGCAGTA TGTGTA

```

This corresponds to the amino acid sequence <SEQ ID 1966; ORF 614.a>:

```

a614.pep
1  MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIIEGVS VSCYLIKGER
51  TDKSTFFFTNA PLDDNLIKTL LKNVRVKVT PEEKPSALAA LFYSLLPVLL
101 LIGAWFYFMR MQTGGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAEAG
201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQI LNVHKKVPL DKSVDLLSLA RGTGPGFSGAD
351 LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

m614/a614 99.7% identity in 391 aa overlap

          10      20      30      40      50      60
m614.pep  MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKERTDKSTFFFTNA
a614      MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKERTDKSTFFFTNA
          10      20      30      40      50      60

          70      80      90      100     110     120
m614.pep  PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGGKGG
a614      PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGGKGG
          70      80      90      100     110     120

          130     140     150     160     170     180
m614.pep  AFSFGKSRAR LLDKDANKVT FADVAGCDEA KEEVQEIVDY LKAPNRYQSL GGRVPRGILL
a614      AFSFGKSRAR LLDKDANKVT FADVAGCDEA KEEVQEIVDY LKAPNRYQSL GGRVPRGILL
          130     140     150     160     170     180

          190     200     210     220     230     240
m614.pep  AGSPGTGKTL LAKAIAEAG VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI
a614      AGSPGTGKTL LAKAIAEAG VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI
          190     200     210     220     230     240

          250     260     270     280     290     300
m614.pep  DEIDAVGRQR GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
a614      DEIDAVGRQR GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
          250     260     270     280     290     300

          310     320     330     340     350     360
m614.pep  GRFDRQVVVP LPDIRGREQI LNVHKKVPL DESVDLLSLARGT GPGFSGAD LANLVNEAAL
a614      GRFDRQVVVP LPDIRGREQI LNVHKKVPL DESVDLLSLARGT GPGFSGAD LANLVNEAAL

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	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
a614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1967>:

```

g615.seq
1  ATGTGGAAC  GGCGGCGGCG  CGGTGtcggC  AGCTTtgaag  agcagcGaAT
51  agatgCCGCC  GGCAAACAC  AATGCGGAAa  gcaggCtgaa  gcGGTTgcgC
101  GGCagcTTca  tGCCGCCTCC  TcGTCCaGCC  ACgtttGgca  gattttggac
151  agggcgAGga  ATTTGCcgCc  gcgtgcggCA  agtatgtcgc  gcCAttgtgc
201  cacttcttcg  gcggacggTG  cttcgtcgaT  gctgCATTCG  TACagcagga
251  aatcgagggT  ttcttcgatg  acggGgatgg  AttccgTTTG  GataAgCTgc
301  ttgagttcgt  tcatgactGt  TCgGATAcgg  aaatcgggaa  aatgccgtct
351  gAaagggctt  CAGACGGCat  tggATTATTT  GCTGTGCAGG  AAgcgcgttg
401  cctcttccca  tttgcCGGAA  AtgATGTCGg  gtacggcctg  cAGGGATttg
451  gCGACGGcat  cgtcgatttg  ccgGcggtgc  ttCgcgcctc  ggtttGTTca
501  agacgtagcc  gaCGACGagg  ttgcggtcGC  CGGGGtggcC  GATGCGGAGG
551  CGCAGGCGGt  aatagtcgtC  CGTGCCGAGT  TTTGCctgAA  TGTCTTTCAA
601  GCCGTTGTGT  CcgCGGtgc  cgcCGCCGAG  TTTGAATTtg  ATCCGTCCGC
651  AAGGGATGTC  GAGTTCGTGC  TGGACGACGA  GGATTCTTTC  GGGTTTGATT
701  TTGTAGAACT  GTGCAAGCGC  GGCAACCGCC  TGTCCGGAAC  GGTTCATGAA
751  CGTGGCCGGT  TTGAGCAGCC  AAACATCGCC  GTCGGGCAGG  GCGGCGCGGG
801  CAACTTCGCC  GAAGAATTTT  TTTTCTTCTT  TAAACGAAGC  CTTCCATTTC
851  CACGCCAGTT  CGTCGAGGAA  CCAAAAGCCC  GCATTGTGGC  GGGTCTGTTC
901  GTATTCTTTG  CCCGGGTTGC  CCAAGCCGAC  AACCATTTTG  ATTGTGttcg
951  acatgataTT  TtccgtgTTT  CTgTCGaag  cggtCtgaAG  GCTTCAGacg
1001  gcatggTtaT  TCTTCTTgaT  TttgaACgcg  tgtgcggCGC  GCTTCTTTGG
1051  GGTTCGATCAA  CAGCGGGCGG  TACACTTCGA  TGCGGTCECC  GTCGCGCAGC
1101  GCGGTGTCGT  CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1968; ORF 615.ng>:

```

g615.pep
1  MWKRRRRGVG  SFEEQRIDAA  GKPOCGKQAE  AVARQLHAAS  SSSHVWQILD
51  RRRNLPPRAA  SMSRHCATSS  ADGASSMLHS  YSRKSRVSSM  TGMDSVWISC
101  LSSFMTVRIR  KSGKCRLLKGL  QTALDYLLCR  KRVASSHLPE  MMSGTACRDL
151  ATASSICRRR  FRARFVQDVA  DDEVAVAGVA  DAEAQAVIVC  RAEFCLNVFQ
201  AVVSAVAAAE  FEFDPsARDV  EFVVDDEDFE  GFDFVELCKR  GNRLSGTVHE
251  RGRFEQPNIA  VQGCGAGNFA  EEEFFFFKRS  LPFPRQFVEE  PKARIVAGLF
301  VEFARVAQAD  NHFDCVRHDI  FRVSVECGLK  ASDGMVILLD  FERVCGALLW
351  GRSTAGGTLR  CGRRRAAACR  L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1969>:

```

m615.seq  Length: 1116
1  ATGCGGAAAA  GGCGGTGGCG  CGGTTTCGGC  AGCTTTGAAA  AGCAGTGAGT
51  AAATGCTGCC  TGCAAACAC  AATGCCGAGA  GCAGGATAAA  GCGGTTGCGT
101  GGCAGATTCA  TGCTTGTTC  TCTTCAAGCC  ATGTCTGGCA  TAGTTTGGAT
151  AGGCGCAGGA  ATTTTCGGCC  GCGTGCGGCC  AGCATATCGC  GCCAAACGGC
201  AATTTCTTCG  GCGGAGGGGG  CATCGTCTAT  GCTGCATTTC  TAGAGCAGGA
251  AATCGAGGGT  TTCTTCGATG  ACGGGGATGG  ATTCCGTTTG  GATAAGCTGC
301  TTGAGTTCGG  TCATGACTGT  TCGGATATGG  AAATCGGGAA  CATGCCGTCT
351  GAAAGGGCTT  CAGACGGCAT  CGGGTCATT  GCTGTGCAGG  AAGCGGGTTG
401  CTTCTTCCCA  TTTGCCGGCA  AGGATGTCGG  GTATGGCTTG  CAGGGATTTC
451  GCGACGGCAT  CGTCAATCTG  TCGGCGGTGT  .TCCGTA CTG  GGTTTGTTC
501  GGACATAGCC  GACGACGAGG  TTGCGGTCGC  CCGGGTGGCC  GATGCCGAGG
551  CGCAGGCGGT  AATAGTCTGC  CGTGCCGAGT  TTTGCCTGAA  TGTCTTTCAA
601  GCCGTTGTGT  CCGCCGTTGC  CGCCGCCGAG  TTTGAATTTG  ATCCGTCCGC
651  AGGGAATGTC  GAGTTCGTGC  TGGACGACGA  GGATTCTTTC  GGGTTTGATT
701  TTGTAGAACT  GTGCAAGCGC  GGCAACTGCC  TGTCCGGAAC  GGTTCATGAA
751  CGTGGCAGGT  TTGAGCAGCC  AAACGTCGCC  GTCGGGCAGG  GCGGACGGG

```

986

```

801 CGACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCATTTC
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTC
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATGTGTGTTG
951 ACATGATATT TTCCGTGTTT CTGTCGAATG CTGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTGAACGCG TTGCGGCGC GCTTCTTTGG
1051 GGTGATCAA CAGCGGCGG TACACTTCGA TGCGGTCGCC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1970; ORF 615>:

```

m615.pep Length: 372
1 MRKRRWRGFG SFEKQXVNA CXPQCREQDK AVAQIHACS SSSHVWHS LD
51 RRRNFPPRAA SISRQTAISS AEGASSMLHS XSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRC XRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVSAVAAAE FEFDPSAGNV EFVDDEDFF GFDFVELCKR GNCLSGTVHE
251 RGRFEQPNVA VGQGGTGDEA EEEEEFFKXS LPFPRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCVXHDI FRVSVECLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAACRLX L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m615/g615 86.8% identity in 371 aa overlap

m615.pep	10	20	30	40	50	60
	MRKRRWRGFGSFEKQXVNAACKPQCREQDKAVAQIHACSSSSHVWHS LD	RRRNFP	PPRAA			
g615	10	20	30	40	50	60
	MWKRRRRGVGSFEEQRIDAAGKPQCGKQAEAVARQLHAASSSSHVWQILD	RRRNLP	PPRAA			
m615.pep	70	80	90	100	110	120
	SISRQTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
g615	70	80	90	100	110	120
	SMSRHCATSSADGASSMLHSYSRKSRSVSSMTGMDSVWISCLSSFMVTRIRKSGKCR	RLKGL				
m615.pep	130	140	150	160	170	180
	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRCXRTGFVQDIADDEVAVARVA					
g615	130	140	150	160	170	180
	QTALDYLLCRKRVASSHLPEMMSGTACRDLATASSICRRCFRARFVQDVADDEVAVAGVA					
m615.pep	190	200	210	220	230	240
	DAEAQAVIVCRAEFC	LNVFQAVVSAVAAAEFEFDPSAGNVEFVDD	EDFFGFDFVELCKR			
g615	190	200	210	220	230	240
	DAEAQAVIVCRAEFC	LNVFQAVVSAVAAAEFEFDPSARDVEFVDD	EDFFGFDFVELCKR			
m615.pep	250	260	270	280	290	300
	GNCLSGTVHERGRFEQPNVAVGQGGTGDFAE	EEEEFFFKXSLPFPRQFVEE	PKTRIVACLF			
g615	250	260	270	280	290	300
	GNRLSGTVHERGRFEQPNIAVGQGGAGNFAE	EEEEFFFKRSLPFPRQFVEE	PKARIVAGLF			
m615.pep	310	320	330	340	350	360
	VFFARVAQADNHFDCVXHDI	FRVSVECLKASDGMVILLDFE	RVCGALLWGRSTAGGTLR			
g615	310	320	330	340	350	360
	VFFARVAQADNHFDCVRHDI	FRVSVECLKASDGMVILLDFE	RVCGALLWGRSTAGGTLR			
m615.pep	370					
	CGRRRAACRLX					
g615	370					
	CGRRRAACRLX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1971>:

```
a615.seq
1  ATGCGGAAAC GCGGCGGCG CGGTGTCGGC AGCTTTGAAG AGCAGCGAAT
51  AGATGCCGCC GGCAAACCAC AATGCGGAAA GCAGGCTGAA GCGGTTGCGC
101 GGCAGCTTCA TGCCGCTCC TCGTCCAGCC ACGTTTGGCA GATTTTGGAC
151 AGGCGCAGGA ATTTGCCGCC CGGTGCGGCA AGTATGTCGC GCCATTGTGC
201 CACTTCTTCG GCGGATGCTG CGTCGTCGAT GCTGCATTTC TACAGCAGGA
251 AATCGAGGGT TTCTTCGATG ACGGGGATGG ATTCGGTTTG GATAAGCTGC
301 TTGAGTTCCG TCATGACTGT TCGGATATGG AAATCGGGAA CATGCCGTCT
351 GAAAGGGCTT CAGACGGCAT CGGTCATTG GCTGTGCAGG AAGCGGGTTG
401 CCTCTTCACA TTTGCCGSCA AGGATGTCGG GTATGGCTTG CAGGGATTTC
451 GCGACGGCAT CGTCAATCTG TCGGCGGTG. TTCCGTACTG GGTTCGTTCA
501 GGACATAGCC GACGACGAGG TTGCGGTGCG CCGGGTGGCC CATGCCGAGG
551 CGCAGGCGGT AATAGTCTGC CGTGCCGAGT TTTGCCGTA TGTCTTTCAA
601 GCCGTTGTGT CCACCGTTGC CGCCGCCGAG TTTGAATTTC ATCCGTCGCG
651 AGGGAATGTC GAGTTCGTCG TGGACGACGA GGATTCTTC GGGTTTGATT
701 TTATAAAACT GCGCAAGGGC GGCAACTGCC TGTCGGGAAC GGTTCATGAA
751 CGTGGTCGGC TTGAGCAGCC AGACATCGCC GTCGGGCAGG GTAGCAGGGG
801 CGACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCATTTC
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTC
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGCCGAATG CCGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGT TTTGAACGCG TTTGCGGCGC GCTTCTTTGG
1051 GGTGATCAA CAGCGGGCGG TACACTTCGA TGGGTCGCC GTGCGCAGC
1101 GGC GTGTCGT CTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1972; ORF 615.a>:

```
a615.pep
1  MRKRRRRGVG SFEEQRIDAA GKPCQCKQAE AVARQLHAAS SSSHVWQILD
51  RRRNLPPRAA SMSRHCATSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRX FRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSTVAAAE FEFDPAGNV EFVVDDEDF GFDIFKLRKG GNCLSGTVHE
251 RGRLEQPDIA VGQSTGDEA EEEFFFK*S LPFPRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCV*HDI FRVSAECLRK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CRRRAAACR L*
```

m615/a615 90.3% identity in 371 aa overlap

m615.pep	10	20	30	40	50	60
	MRKRRWRGFGSFEKQXVNAACKPQCREQDKAVAWQIHACSSSSSHVWHSIDRRRNFPRAA					
a615	10	20	30	40	50	60
	MRKRRRRGVGSFEEQRIDAAAGKPCQCKQAEAVARQLHAASSSSHVWQILDRRRNLPRAA					
m615.pep	70	80	90	100	110	120
	SISRQTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
a615	70	80	90	100	110	120
	SMSRHCATSSADGASSMLHSYSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
m615.pep	130	140	150	160	170	180
	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXRTGFVQDIADDEVAVARVA					
a615	130	140	150	160	170	180
	QTASGHL.LCRKRVASSHL.PARMSGMACRDLATASSICRRXRTGFVQDIADDEVAVARVA					
m615.pep	190	200	210	220	230	240
	DAEAQAVIVCRAEFCLNVFQAVVSAVAAAEFEFDPAGNVFVVDDEDFGDFVELCKR					
a615	190	200	210	220	230	240
	DAEAQAVIVCRAEFCLNVFQAVVSTVAAAEFEFDPAGNVFVVDDEDFGDFIKLRKG					
	250	260	270	280	290	300

988

```

m615.pep  GNCLSGTVHERGRFEQPNVAVQGSGTGF AEEFFFFFKXSLPFPRQFVEEPKTRIVACLF
          |||||:||||:||||:|||||
a615       GNCLSGTVHERGRLEQPDIAVGQSGTGF AEEFFFFFKXSLPFPRQFVEEPKTRIVACLF
          250      260      270      280      290      300

          310      320      330      340      350      360
m615.pep  VFFARVAQADNHFDVCXHDIFRVSV EECCLKASDGMVILLDFERVCGALLWGRSTAGGTLR
          |||||:||||:||||:|||||
a615       VFFARVAQADNHFDVCXHDIFRVSA ECRCLKASDGMVILLDFERVCGALLWGRSTAGGTLR
          310      320      330      340      350      360

          370
m615.pep  CGRRRAAACRLX
          |||||
a615       CGRRRAAACRLX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1973>:

```

g616.seq
1  atgtcgaaCA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACCCGCCACA ATGCGGGCTT TTGGTTCCTC GACGAACTGG
101 CGTGGAATG GAAGGCTTCG TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTTGCCCGCG CCGCCCTGCC CGACGGCGAT GTTGGCTGC TCAAACCGGC
201 CACGTTTCATG AACCGTTCCG GACAGGCGGT TGCCGCGCTT GCACAGTTCT
251 ACAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATC
301 CCTTGGCGGAC GGATCAAAAT CAAACTCGGC GcgggcaaCG gcgGACACAA
351 CGGCTTGAAA GACATTcagC CAAACTCGG CACGGcagac tattaCCGCC
401 TGCGCCTCGG CATCGgccaC CCGGGCgacc gcaacctCGT CGtcggctac
451 gtcttgAACA aaccgagcgc gGaagcaccg Ccggaatc gacgatgCCG
501 TCGccaaATC CCTGcaggcc gtaccCGACA TcaTTTCCGg caaatgggaa
551 gaggcaacgc gCTTCCTGCA CAGCAAAATA TccaatGCCG TCTGaagccc
601 ttTcagacgg cattttcccg atttccgTAT CcGAaCagtc atgaacgaac
651 tcaagcAGcT tatCCAAAcg gaatccatcc ccgcatcga agaaaccttc
701 gatttcctgc tGTACGAATG cagcAtcgac gaagCACCgt ccgccgaaga
751 agtggcacia TGgcgcgaca tactTGccgc acgcgGcgGC AAATtcCTgc
801 gcctgtccaa aatctgcCaa aCGTGGCTGG AcgAGGAGGC GGCatgAAgc
851 tGCGGcgCAA CcgcttcaGc ctgctTTCCG CATGTGTGGT TGCCGGCGGc
901 atcATtCgc tgctettcaa AGCTGcgaC ACCGCGCGCG CGCCGTTTCC
951 ACATTTtcga AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAaatCTTgt
1001 tTctGGCCAA AGCATTCAA ACCGGAAGAA ITCCCATCCC CTACCCGAGC
1051 CTGATTGCGT TCGCCTTCTG TTTTGCCGTC GGCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGCGAA CCGGCAGTTT GGGCGATGTC CTTGCCgACC
1151 TGACSGGCGC AGCCCTTGCC CTCTTTGCCG CGGTTTCTGC CTGCCGccc
1201 gactaa

```

This corresponds to the amino acid sequence <SEQ ID 1974; ORF 616.ng>:

```

g616.pep
1  MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKFFGE
51  VARAALPDGD VWLLKPATFM NRSQAVAAAL AQFYKIKPEE ILVHUELDI
101 PCGRIKFKLG GNGGHNGLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVG
151 VLNKPSAEAP PANRRRCRQI FAGRTRHHFR QMGRGNALPA QQIIQCR LKP
201 FQTAFSRFPY PNSHRTQAA YPNGIHPRHR RNPFPFAVRM QHRRSTVRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRGG GMKLPRNRFS LLSALWFAGG
301 IYSLLFKAAD TAPPFFPHFD KAAHLALFFA QILFLAKAFK TGKLP IPYRS
351 LIAFAFCFAV GSECAQAWFT ATRTGS LGDV LADLTGAALA LFAARSACRP
401 D*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1975>:

```

m616.seq
1  ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAACTGG
101 CGTGGAATG GAAGGCTTCA TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTCGCCCCTG CCGCCCTGCC CGACGGCGAC GTTGGCTGC TCAAACCTGC
201 CACGTTTCATG AACCGTTCCG GACAGGCGAGT TGCCGCGCTT GCACAGTTCT
251 ACAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCCTGCGGAC GGATCAAAAT CAAACTCGGC GCGGGCAACG GCGGACACAA
351 CGGCTTGAAA GACATTcagC CAAACTCGG CACGGCAGAC TATTACCGCC
401 TGCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCTGAACA AACCCAGTAC GGAACA.CCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CTGCAAGACC ATACCCGACA TCCTTGCCCG CAAATGGGAA

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989

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551 GAAGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTCAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCCTC
701 GATTTCTTGC TCTACGAATG CAGCATAGAC GATGCCCCCT CCGCCGAAGA
751 AATTGCCGTT TGGCGCGATA TGCTGGCCGC ACGCCGCCGA AAATTCCTGC
801 GCCTATCCAA ACTATGCCAG ACATGGCTTG AAGAGGAACA AGCATGAATC
851 TGCCACGCAA CCGCTTTATC CTGCTCTCGG CATTGTGTT TGCAGGCAGC
901 ATTTACTCAC TGCTTTTCAA AGCTGCCGAA ACCGCCGCAC CGCCTTTTCC
951 GCATTTTGAC AAAGTGGCGC ACCTGCCCTT GTTTTTCGCA CAAATCTGGC
1001 TTCTGACCAA AGCATTGAGA ACCGACAACC GCCCATCCC CTATCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTCGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTC CTTGCCGACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTACCG CGCGAGCTGC CTGCCGCCCG
1201 GACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1976; ORF 616>:

```

m616.pep
1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51 VARAALPDGD VWLLKPATFM NRSQQAVAL AQFYKIKPEE ILVVHDELDI
101 PCGRKFKFLG GNGGHNGLK DIQALGTAD YYRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTDXRRCRQI PASHTRHPCR CMGRSNPLPA QMTRCRLKP
201 FQTACSRFPY PSHDRTQAA YPNRIHPRHR RNPRFPALRM QHRRCPLERR
251 NCRLARYAGR TRRKIPAPIQ TMPDMAXRGT SMNLPNRNFI LLSALWFAGS
301 IYSLLFKAAE TAPPPPHFD KVAHLALFFA CIWLLTKAFR TDNRPIPYRS
351 LMVFALCFAL FSECAQAWFT ATRTGLGSDV LADLTGAALA LFTARAACRP
401 D*

```

m616/g616 86.0% identity in 401 aa overlap

m616.pep	10	20	30	40	50	60
	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
g616	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
	10	20	30	40	50	60
m616.pep	70	80	90	100	110	120
	VWLLKPATFMNRSQQAVALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHNGLK					
g616	VWLLKPATFMNRSQQAVALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHNGLK					
	70	80	90	100	110	120
m616.pep	130	140	150	160	170	180
	DIQALGTADYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRCRQIPASHTRHPCR					
g616	DIQALGTADYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRCRQIPASHTRHPCR					
	130	140	150	160	170	180
m616.pep	190	200	210	220	230	240
	QMGRSNPLPAQMTRCRLKPFQTACSRFPYPNSHDRTQAAYPNRIHPRHRNPRFPALRM					
g616	QMGRSNPLPAQMTRCRLKPFQTACSRFPYPNSHDRTQAAYPNRIHPRHRNPRFPALRM					
	190	200	210	220	230	240
m616.pep	250	260	270	280	290	300
	QHRRCPLERRNCRLARYAGRTRRKIPAPIQTMPDMAXRGTSMNLPNRNFI LLSALWFAGS					
g616	QHRRCPLERRNCRLARYAGRTRRKIPAPIQTMPDMAXRGTSMNLPNRNFI LLSALWFAGS					
	250	260	270	280	290	300
m616.pep	310	320	330	340	350	360
	IYSLLFKAAETAPPPPHFDKVAHLALFFAQIWLTKAFRTDNRPIPYRSLMVFALCFAL					
g616	IYSLLFKAAETAPPPPHFDKVAHLALFFAQIWLTKAFRTDNRPIPYRSLMVFALCFAL					
	310	320	330	340	350	360
m616.pep	370	380	390	400		
	FSECAQAWFTATRTGLGSDVLADLTGAALALFTARAACRPDX					
g616	FSECAQAWFTATRTGLGSDVLADLTGAALALFTARAACRPDX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1977>:

990

a616.seq
1 ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CSGGCAAAGA
51 ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCCTC GACGAACTGG
101 CGTGGAAATG GAAGGCTTCA TTAAAGAAAG AAAAAAATT CTTCGGCGAA
151 GTCGCCCCGTG CTACCTTGCC CGACGGCGAT GTCTGGCTGC TCAAGCCGAC
201 CACGTTTCATG AACCGTTCCG GACAGGCAGT TGCCGCCCTT GCGCAGTTT
251 ATAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCCTGCGGAC GGATCAAATT CAAACTCGGC GCGGGCAACG GTGGACACAA
351 CGGCTTGAAA GACATTCAGG CAAACTUGG CACGGCAGAC TATTACCGCC
401 TGCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCCAGTAC GGAA.CACCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGTGAA
551 GAGGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTTCAGACG CATGTTCCCG ATTTCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCTC
701 GATTTCCTGC TGTACGAATG CAGCATCGAC GACGCACCAT CCGCCGAGAA
751 AGTGGCACAA TGGCGCGACA TACTTGCCGC ACGCGGCGGC AAATTCCTGC
801 GCCTGTCCAA AATCTGCCAA ACGTGGCTGG ACGAGGAGGC GGCATGAAGC
851 TGCCGCGCAA CCGCTTCAGC CTGCTTCCG CATTGTGGTT TGCCGCGCGC
901 ATCTATTGCG TGCTCTTCAA AGCTGCCGAC ACGCGCGCGC CGCCGTTTCC
951 GCATTTTCGAC AAAGCAGCAC ACCTTGCCCT*GTTTTTCGCA CAAATCTGGC
1001 TTTTGACCAA AGCATTCAA AC CGGAAAAC TTCCCATCCC CTACCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTCGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGATTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTT CTTGCCGATA
1151 TGGCAGGTAC GGTCTCGCA CTCTTGCCG CCCGCGCCG CGACCGCCG
1201 GACTGA

This corresponds to the amino acid sequence <SEQ ID 1978; ORF 616.a>:

a616.pep
1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51 VARATLPDGD VWLLKPTTFM NRSGQAAVAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGHNELK DIQAKLTAD YYRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTD*RCRRQI PASHTRHPCR QM*RGNPLPA QMTRCRLKP
201 FQTACSRFPY PNSHRTCAA YPNRIHPRHR RNPRFPAVRM QHRRRTIRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRG GMKLPNRFS LLSALWFAGG
301 IYSLLFKAAD TAPPPFPHFD KAAHLALFFA QIWLTKAFK TGKLPYPYRS
351 LMVFALCFAL FSECAQA*FT ATRTGS LGDV LADMAGTVLA LFAARAADRP
401 D*

m616/a616 90.0% identity in 401 aa overlap

	10	20	30	40	50	60
m616.pep	MSNTIKMVVGLG	NPGKEYEQTRH	NAGFWFLDEL	AWKWKASFKE	EKKFFGEVAR	AALPDGD
a616	MSNTIKMVVGLG	NPGKEYEQTRH	NAGFWFLDEL	AWKWKASFKE	EKKFFGEVAR	ATLPDGD
	10	20	30	40	50	60
	70	80	90	100	110	120
m616.pep	VWLLKPATFMNR	SGQAAVALAQ	FYKIKPEEIL	VVHDELDIPC	GRIKFKLGG	GNGGHNELK
a616	VWLLKPTTFMNR	SGQAAVALAQ	FYKIKPEEIL	VVHDELDIPC	GRIKFKLGG	GNGGHNELK
	70	80	90	100	110	120
	130	140	150	160	170	180
m616.pep	DIQAKLTADYY	RLRLGIGHPG	DRNLVVGYY	VLNKPSTEXP	PTDXRCRRQI	PASHTRHPCR
a616	DIQAKLTADYY	RLRLGIGHPG	DRNLVVGYY	VLNKPSTEXP	PTDXRCRRQI	PASHTRHPCR
	130	140	150	160	170	180
	190	200	210	220	230	240
m616.pep	QMG	RSNPLPAQ	QMTRCRLKPF	QTACSRFPY	PNSHRTQAAY	PNRIHPRHRRNPRFPALRM
a616	QMX	RGNPLPAQ	QMTRCRLKPF	QTACSRFPY	PNSHRTQAAY	PNRIHPRHRRNPRFPVRM
	190	200	210	220	230	240
	250	260	270	280	290	300

901 GCAGTGTGA GCGTAGTAGT AGAATTGCC GCGGACTCG TTTCTCTTA
951 TCTCGTTTAA AACACAAAA AATGA

This corresponds to the amino acid sequence <SEQ ID 1982; ORF 619>:

m619.pep
1 MPSEKNIGFM AGSSRPLWVA FALLLVSCVL FMTLNVKGDW DFVLQRLTK
51 LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLTVF LQTLVETFG
101 GVGYASLPT GKFGFELVVM MGGSLLLFYT LIKQGRDLS RMILIGVIFG
151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
201 VVWRERYRLD VYLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVG
251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC GIGILLVGGQ TVFEHLLGMQ
301 AVLSVVVEFA GGLVFLYLV KKKK*

m619/g619 95.1% identity in 324 aa overlap

	10	20	30	40	50	60
m619.pep	MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQRLTKLAALLMVAYA					
g619	MPSEKNIGFMAGSSRPLRVAFALLLVSCILFMTLNVKGDWDFVLHLRLTKLAALLMVAYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m619.pep	VGSTQLFQTLTNNPILTPSILGFDSLTVFLQTLVETFGVGYSPLTGKFGFELVVM					
g619	VGSTQLFQTLTNNPILTPSILGFDSLTVFLQTLVETFGVGYSPLTGKFGFELVVM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m619.pep	MGGSLLLFYTLIKQGRDLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
g619	MGGSLLLFYTLIRQGRDLPHMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m619.pep	NTVHSELLGIGALILLVSAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
g619	NTVHSELLGIGALILLVSAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m619.pep	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGILLVGGQTVFEHLLGMQ					
g619	VATATAVVGVPVSFFGLLAASLANHFSPSVRHSVRLPMTVCIGILLVGGQTVFEHLLGMQ					
	250	260	270	280	290	300
	310	320				
m619.pep	AVLSVVVEFAGGLVFLYLVLKHKKK					
g619	AVLSVVVEFAGGLVFLYLVLKHKKK					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1983>:

a619.seq
1 ATGCCGTCTG AAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGTCCGTT
51 GTGGGTTGCC TTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
101 TCAACGTCAA AGGCGATTGG GATTTTGTTC TGCACCTCCG CCTGACCAAG
151 CTGCGCGCGC TGCTGATGGT CGCCTATGCG GTCGCGGTTT CGACCCAGCT
201 TTTTCAAACG CTGACCAACA ATCCGATTCT GACCCCTTCG ATTTTGGGTT
251 TCATTTCGCT GTATGTGTTT TTGCAGACCT TGCTGGTGTT TACGTTCGGC
301 GCGGTGGGCT ATGCTTCCCT GCCGTGACG GGCAAAATCG GCTTTGAACT
351 GGTCGTTATG ATGGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCAAAC
401 AGGGCGGGCG CGATTGCGG CGTATGATTT TAATCGGCGT GATTTTCGGG
451 ATTTTGTTCG GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGACCCCGA
501 AGAATTTACG GCGGCGCAGG CGAATATGTT TGCCGATTTC AATACCGTCC
551 ACAGCGAGCT TTTAGGCATA GGCGCGCTGA TTCTGCTCGT CAGCGCGGCG
601 GTCGTTTGGC GCGAACGCTA CCGCTTGGAC GTACACCTTT TGGGCGCGCA
651 CCAAGCCATA AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
701 TGCTTTGGAT TGCCGCGCTG GTGGCGACGG CGACCGCCGT TGTGCGCCCG

993

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751  GTAAGCTTTT TCGGGCTTCT CGCGCCTCG CTGCCAACC ACTTTTCCCC
801  GTCGGTCAAA CATTCCGTC GCTGCGGAT GACGGTTGT GTCGGCGGCA
851  TCCTCTTGGT CGGCGGACAG ACCGTATTCG AACACTTCTT GGGCATGAAG
901  GCGGTATTAA GCGTGGTGGT CGAATTTCG GCGGGACTCG TTTCTCTCTA
951  TCTCGTTTTA AGACACAAAA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 1984; ORF 619.a>:

```

a619.pep
1  MPSEKNIGFM AGSSRPLWVA FALLLVSCIL FMTLNVKGDW DFVLHLRLTK
51  LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLTVF LQTLVFTFG
101 GVGYASLPLT GKFGFELVVM MGSLLLFYT LIKQGGRLP RMILIGVIFG
151 ILFRSLSSL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
201 VVWRERYRLD VHLLGRDQAI NLGISYTRNT LWILLWIAAL VATATAVVG
251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
301 AVLSVVVEFA GGLVFLYLVL RHKK*

m619/a619 97.2% identity in 324 aa overlap

m619.pep      10      20      30      40      50      60
MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQRLTKLAALLMVAYA
|||||
a619          10      20      30      40      50      60
MPSEKNIGFMAGSSRPLWVAFALLLVSCILFMTLNVKGDWDFVLHLRLTKLAALLMVAYA
|||||

m619.pep      70      80      90     100     110     120
VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLVFTFGGVGYASLPLTGKFGFELVVM
|||||
a619          70      80      90     100     110     120
VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLVFTFGGVGYASLPLTGKFGFELVVM
|||||

m619.pep     130     140     150     160     170     180
MGSLLLFYTLIKQGGRLDSRMILIGVIFGILFRSLSSLSRMIDPEEFTAAQANMFAGF
|||||
a619         130     140     150     160     170     180
MGSLLLFYTLIKQGGRLDPRMILIGVIFGILFRSLSSLSRMIDPEEFTAAQANMFAGF
|||||

m619.pep     190     200     210     220     230     240
NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL
|||||
a619         190     200     210     220     230     240
NTVHSELLGIGALILLVSAAVVWRERYRLDVHLLGRDQAINLGISYTRNTLWILLWIAAL
|||||

m619.pep     250     260     270     280     290     300
VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ
|||||
a619         250     260     270     280     290     300
VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCVGGILLVGGQTVFEHFLGMK
|||||

m619.pep     310     320
AVLSVVVEFAGGLVFLYLVLKHKXX
|||||
a619         310     320
AVLSVVVEFAGGLVFLYLVLKHKXX
|||||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1985>:

```

g620.seq
1  ATGAAGAAAA CCCTGTTGGc AATTGTTGCC gttttCGCCT TAAGTGCCCTG
51  CCGGcAggcg gaAGaggcac cgccgCCTTT ACCCCGGCAG AtTAGCGacc
101 gttegggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga ttttttgaa cGGCAAAACC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGI
351 CATCGACAGC GGCTTTATCG GCGGTA?GGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1986; ORF 620.ng>:

```
g620.pep
1  MKKTLAIVA VFALSACROA EEAPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAOIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1987>:

```
m620.seq
1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGCG AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTCC GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 1988; ORF 620>:

```
m620.pep
1  MKKTLAIVA VSALSACROA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*
```

m620/g620 97.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTLAIVAVSALSACROAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
g620	MKKTLAIVAVFALSACROAEEAPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS					
g620	DQPVWFSTVKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GFIGGMAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDTYIFKX					
g620	GFIGGMAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDAYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1989>:

```
a620.seq
1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGCG AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTCC GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 1990; ORF 620.a>:

```
a620.pep
1  MKKTLAIVA VSALSACROA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*
```

995

m620/a620 100.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTLIAIVAVSALSACRQAEEGPPPLRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
a620	MKKTLIAIVAVSALSACRQAEEGPPPLRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQPVWFSTIKQMFYTKLPPEPKGIRVIYVTDMGNVTDWTPNADTEWMDAKKAFYVIDS					
a620	DQPVWFSTIKQMFYTKLPPEPKGIRVIYVTDMGNVTDWTPNADTEWMDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
a620	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1991>:

g622.seq

```

1  ATGCAactta  ccgctgtcgg  ACTCAATCAT  CAAACCGCAC  CTTTAAGCAT
51  ACGGGAAAag  ctggCGTTTG  CCGCCGCCGC  CCTGCCAGAA  gccgTccgCA
101 ATCTTGCCCG  AAGCAATGCG  GCAACGGAGG  CGGTAATCCT  TTCTACCTGC
151 AACCGCACCG  AGCTTTACTG  CGTCGGCGAT  TCGGAAGaaa  TCATCCGATG
201 GCTTGCCGAT  TACCACAGTT  TGCCGATTGA  AGAAATCCGT  CCGTATCTGT
251 ACACGCTGGA  TATGCAGGAA  ACCGTGCGCC  ACGCCTTCCG  CGTTGCCTGC
301 GGCTTGGAAT  CGATGGTTT  GGGCGAGCCG  CAGATTTTGG  GGCAGATTAA
351 AGATGCGGTG  CGTGCGGCTC  AAGAACAGGA  AAGTATGGGG  GCAAAACTCA
401 ATGCCCTGTT  CCAAAAAACC  TTTTCCGTG  CTAAGAAGT  CCGTACCGAT
451 ACCGCTGTGC  GCGAAAATTC  GGTTCGATG  GCTTCCCGGT  CCGTCAAGTT
501 GCGGGAACAG  ATTTTCCCG  ACATCGGCGA  TTTGAACGTA  TTGTTATCG
551 GCGCAGGCGA  AATGATTGAG  CTGGTTGCCA  CTTATTTTGC  CGCCAAAAAT
601 CCCC GGCTGA  TGACGGTTGC  CAACCGGACG  CTGGCGCGTG  CACAGGAGTT
651 GTGCGACAAG  CTCGGTGTTA  ACGCCGAACC  GTGCCTGCTG  TCCGATCTGC
701 CTGCCATTCT  GCACGATTAC  GACGTGGTGG  TTTCTTCAAC  GGCGAGCCAG
751 CTTCCGATAG  TCGGCAAAGG  CATGGTCGAA  CGCGCATTTA  AACAGCGTCA
801 GAGTATGCCG  TTGTTTATGC  TTGACTTGGC  CGTCCCGCGC  GATATTGAAG
851 CGGAAGTCGG  CGATTGTAAC  GATGCGTATC  TTTATACGGT  GGACGATATG
901 GTCAACATCG  TCCAAAGCGg  caaggaggca  aggcagaaag  ccgccgcCgc
951 cgccgaaacg  ctggTGTCGG  AAAAGGTTGC  CGAATTGTGC  AGGCAGCAGC
1001 AGGGCAGGCA  gagcgttcCG  CTGATTAAGG  CCTTCCGGGA  CGAGGGCGAG
1051 AAAGCGCGCA  AGCAGGTGTT  GGAAATATCG  ATGAAACAGC  TTGCCAAAGG
1101 CGcaacGGCG  GAAGagggtt  TGgaacggct  gtccgtcCAA  CTGACCAACA
1151 AGCTGCTGCA  TTCGCCAACT  CAAACCTTGA  ATAAGCGGGG  GGAAGAAGAT
1201 AAAGatttGG  TTCATGCCgt  cGCGCAGATt  tatcatttGG  ACAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1992; ORF 622.ng>:

g622.pep

```

1  MQLTAVGLNH  QTAPLSIREK  LAFAAAAALPE  AVRNLARSNA  ATEAVILSTC
51  NRTELYCVGD  SEEIIRWLAD  YHSLPIEEIR  PYLYTLDMQE  TVRHAFRVAC
101 GLDSMVLGEP  QILGQIKDAV  RAAQEQESMG  AKLNALFQKT  FSVAKEVRTD
151 TAVGENSVSM  ASASVKLAEO  IFPDIGDLNV  LFIGAGEMIE  LVATYFAAKN
201 PRLMTVANRT  LARAQELCDK  LGVNAEPCLL  SDLPAILHDY  DVVVSSTASQ
251 LPIVGKGMVE  RALKQROQSM  LFMLDLAVPR  DIEAEVGLDN  DAYLYTVDDM
301 VNIVQSGKEA  RQKAAAAAET  LVSEKVAEFV  RQQQGRQSV  LIKALRDEGE
351 KARKQVLENA  MKQLAKGATA  EEVLERLSVQ  LTNKLLHSPT  QTLNKAGEED
401 KDLVHAVAQI  YHLDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1993>:

m622.seq

```

1  ATGCAACTTA  CCGCTGTCCG  ACTCAATCAT  CAAACCGCAC  CTTTAAGCAT
51  ACGGGAAAAG  CTGGCGTTTG  CCGCCGCCGC  CCTGCCATAA  GCCGTCCGCA
101 ATCTTGCCCG  AAGCAATGCG  GCAACGGAGG  CGGTAATCCT  TTCTACCTGC
151 AACCGCACCG  AGCTTTACTG  CGTCGGTGAT  TCGGAAGAAA  TCATCCGATG
201 GCTTGCCGAT  TACCACAGTT  TGCCGATTGA  AGAAATCCGT  CCGTATCTGT
251 ACGCGCTGGA  TATGCAGGAG  ACTGTGCGCC  ATGCTTTCCG  CGTCGCTGTC

```

```

301 GGGCTGGATT CGATGGTGT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCCGTT AGGGTTGCTC AAGAGCAGGA AACTATGGGT AAGAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCCGTTG CTAAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAACTC GGTTCATG GCTTCGCTT CCGTCAAAAT
501 GGCAGAACAG ATTTTCCCG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GCGCAGCCGA AATGATTGAG CTGGTIGCCA CTATTITGTC CGCCAAAAGT
601 CCCCAGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTAGTGG TTCTTCAAC GGCAAGCCAG
751 TTGCCATTG TCGGCAAAGG CATGGTGGAG CGTGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTATGC TTGATTGGC AGTGCCGCGT GACATTGAAG
851 CGGAAGTCGG CGATTGAAT GATGCCTATC TTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAG CCGCCGCCG
951 CGCCGAAACG CTGGTGTCCG AGAAAGTTGC CGAATTGTG AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCCC TTGATTAAAG CGTTGCGGGA CGAGGGCGAG
1051 AAAGCGCGCA AACAGGTGTT GGAAATGCC ATGAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGGAACGGCT GTCCGTCCTA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTGG TTCATGCCGT CGCGCAGATT TATCATTGG ACAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1994; ORF 622>:

```

m622.pep
1  MQLTAVGLNH QTAPLSIREK LAFAAAAALPK AVRNLARSNA ATEAVILSTC
51  NRETELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYALDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SLPAILHDY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMPLFMLDLAVPR DIEAEVGDND DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQOQGRQSVPLIKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*

```

m622/g622 98.8% identity in 415 aa overlap

m622.pep	10	20	30	40	50	60
	MQLTAVGLNHQTAPLSIREKLAFAAAAALPKAVRNLARSNAATEAVILSTCNRETELYCVGD					
g622	10	20	30	40	50	60
	MQLTAVGLNHQTAPLSIREKLAFAAAAALPEAVRNLARSNAATEAVILSTCNRETELYCVGD					
m622.pep	70	80	90	100	110	120
	SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
g622	70	80	90	100	110	120
	SEEIIRWLADYHSLPIEEIRPYLYTLDQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
m622.pep	130	140	150	160	170	180
	RVAQEESMGKKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
g622	130	140	150	160	170	180
	RAAQEESMGAKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
m622.pep	190	200	210	220	230	240
	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
g622	190	200	210	220	230	240
	LFIGAGEMIELVATYFAAKNPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
m622.pep	250	260	270	280	290	300
	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNDAYLYTVDDM					
g622	250	260	270	280	290	300
	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNDAYLYTVDDM					
m622.pep	310	320	330	340	350	360
	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQOQGRQSVPLIKALRDEGEKARKQVLENA					
g622	310	320	330	340	350	360
	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQOQGRQSVPLIKALRDEGEKARKQVLENA					
m622.pep	370	380	390	400	410	
	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
g622	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					

370 380 390 400 410

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1995>:

```
a622.seq
1   ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGAAAAAG CTGGCGTTTG CCGCGGCCTG CCTGCCCGAA GCCGTCCGCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGTACCG AGCTTTACTG TGTAGGTGAT TCGGAAGAAA TCATCCGTG
201 GCTCGCAGAC TATCACAGCC TTCCCATAGA AGAAATCAGC CCCTACCTTT
251 ATACTTTGGG GATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTCGCCTGC
301 GGCTTGATT  CGATGGTGT  GSGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCGGTC AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCTGTG  CTAAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAACTC GGTTCCTATG GCTTCCGCTT CCGTCAAGTT
501 GGCAGAGCAG ATTTTCCCG  ACATCGGCGA TTGAATGTC  TTGTTTATCG
551 GTGCGGGTGA GATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCCGGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTTT GCATGAGTAC GACGTGGTGG TTTCTTCAAC GSCAAGCCAG
751 TTGCCCATTT TCGGCAAAGG TATGGTGGAG CGCGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGA GACATTGAGG
851 CGGAAGTCGG AGATTTGAAC GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCGCG
951 CGCCGAAACG CTGGTGTCCG AGAAGGTTGC CGAATTGTGC AGGCAGCAGC
1001 AGGCGAGGCA GAGTGTCCCG TTAATCAGGG CATTGAGGGA TGAGGGAGAG
1051 AAAGCGCGCA AACAGGTCTT GGAAATGCG  ATGAAACAGC TTGCCAAAGG
1101 CGCAACGCGA GAAGAGGTTT TGGAAAGGCT GTCGATCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTGG  TTCACGCCGT CGCGCAGATT TATCATTGG  ACAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1996; ORF 622.a>:

```
a622.pep
1   MQLTAVGLNH QTAPLSIREK LAFAAACLPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIS PYLYTLGMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEQESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHEY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMF LFMLDLAVPR DIEAEVGLN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSV LIRALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSIQ LTNKLLHSPT QTLNKAGEED
401 KDLVHVAQI YHLDK*
```

m622/a622 98.1% identity in 415 aa overlap

	10	20	30	40	50	60
m622.pep	MQLTAVGLNHQTAPLSIREKLAFAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD					
a622	MQLTAVGLNHQTAPLSIREKLAFAAACLPEAVRNLARSNAATEAVILSTCNRTELYCVGD					
	10	20	30	40	50	60
m622.pep	SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
a622	SEEIIRWLADYHSLPIEEISPYLYTLGMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
	70	80	90	100	110	120
m622.pep	RVAQEQESMGKKLNALEFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEIFPDIGDLNV					
a622	RVAQEQESMGKKLNALEFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEIFPDIGDLNV					
	130	140	150	160	170	180

998

	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
a622	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHEY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDLDNDAYLYTVDDM					
a622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDLDNDAYLYTVDDM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
a622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIRALRDEGEKARKQVLENA					
	310	320	330	340	350	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
a622	MKQLAKGATAEEVLERLSIQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1997>:

g624.seq
 1 ATGATCCGTT ATCTTTTAAT TGCCTGCGGC GGCATCTCCC TGCTGTTGGG
 51 GATAATCGGC ATTTTTTTCG CGCTGTTGCC GACCACGCCG TTCGTAATAC
 101 TCTCCGCCCG CTGCTGGGCA AAGGCATccc cgcgcTTTCa ccgCTGGCTG
 151 CACcgGCacc gCTATTTCGG CCGATGGTT CATAACTGGG AACAAAACGG
 201 CGCAGTGCCG CGCAAAGCCA AGATTTCGCG CATCAGCATG AtaaccgcAt
 251 cctgcctcat gatctTTtg CatTTTCccc aacnctggtg ggtcGGGGCG
 301 GTTTCATCGG TTTTGTGTC CCTGTGcAc ATacggatgt gGcacAGAcC
 351 cgaatCTTGA

This corresponds to the amino acid sequence <SEQ ID 1998; ORF 624.ng>:

g624.pep
 1 MIRYLLIACG GISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
 51 HRHRYFGPMV HNWEQNGAVP RKAKIFAISM ITASCLMIFW HFQXWWVGA
 101 VSSVFCSLVT IRMWRPES*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1999>:

m624.seq
 1 ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTCCC TACTGTTGGG
 51 TATCATCGGC ATTTTTTTCG CGCTGTTGCC GACCACGCCG TTCGTAATGC
 101 TCTCCGCCCG CTGCTGGGCA AAGGCATCCC CGCGCTTTTA CCGCTGGCTG
 151 CACCGGCACC GCTATTTCGG CCGATGGTT CATAACTGGG AACAAAACGG
 201 CGCAGTGCCG CGCAAAGCCA AAATATTCG CATCAGTATG ATGACCGCAT
 251 CCTGCCTGAT AATGTTTGG CAGTTTCCC AACGCTGGTG GGTGCGGGCG
 301 GTTTCATCGG TTTTGTGTC CCTGTGCGC ATATGGATGT GGCAGAGGCC
 351 CGAATCTTGA

This corresponds to the amino acid sequence <SEQ ID 2000; ORF 624>:

m624.pep
 1 MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFYRWL
 51 HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
 101 VSSVFCSLVA IWMWRPES*

m624/g624 91.6% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACGCISLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV					
g624	MIRYLLIACGCISLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV					
	10	20	30	40	50	60

999

	70	80	90	100	110	120
m624 . pep	HNWEQNGAVPRKAKIFAISM	MTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX				
g624	HNWEQNGAVPRKAKIFAIS	MITASCLMIFWHFPQXWWVGAVSSVFCSLVTIRMWHRPESX				
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2001>:

```
a624 . seq
1  ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCC TGCTGTGGG
51  TATCATCGGC ATTTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTACTGC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTCA CCGCTGGCTG
151 CACCGGCACC GCTATTTCCG TCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
251 CCTGCCTGAT AATGTTTGG CAGTTTCCCC AACGCTGGTG GGTCCGGGGC
301 GTTTCATCGG TTTTGTTC CCTTGTGCC ATATGGATGT GGCGCAGGCC
351 CGAATCTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2002; ORF 624.a>:

```
a624 . pep
1  MIRYLLIACG CISLLGLIIG IFLLPLPTTP FVLLSAACWA KASPRFHRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRRPES*
```

m624/a624 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
m624 . pep	MIRYLLIACGCISLLGLIIGIFLPLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV					
a624	MIRYLLIACGCISLLGLIIGIFLPLPTTPFVLLSAACWAKASPRFHRWLHRHRYFGPMV					
	10	20	30	40	50	60

	70	80	90	100	110	120
m624 . pep	HNWEQNGAVPRKAKIFAISM	MTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX				
a624	HNWEQNGAVPRKAKIFAISM	MTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX				
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2003>:

```
a625 . seq
1  ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGTTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2004>:

```
g625 . seq
1  atgTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGtTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC AttgCCGCGC
101 CGGtcgttcC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAGGGG ATATATICTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TGATTTTGCC
351 gtAA
```

This corresponds to the amino acid sequence <SEQ ID 2005; ORF 625.ng>:

```
g625 . pep
1  NFATRKMKKM TMCTRVRVSW LAFSSGRIIS IAAPVVPmie ASAVPTASRA
```


1000

51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2006>:

m625.seq
1 ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51 ACGGTTTTCG TTGGCTTTCA GCACCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGCGGACGC GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA

This corresponds to the amino acid sequence <SEQ ID 2007; ORF 625>:

m625.pep
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA
51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

m625/g625 98.3% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFW	LAFSSGRIISIAAPVVPMIE	ASAVPTASRAVLSLGVPFKS			
g625	MFATRKMKKMTMCTRRVRFW	LAFSSGRIISIAAPVVPMIE	ASAVPTASRAVLSLGVPFKS			
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTKMPPEMVYRASSSRMKG	MYSSTSACATVWIPADAPKT	KLNGMRKSNVQKAVILPX			
g625	PQTKMPPEMVYRASSSRMKG	IYSSTSACATVWIPADAPKT	KLNGMRKSNVQKAVILPX			
	70	80	90	100	110	

This corresponds to the amino acid sequence <SEQ ID 2008; ORF 625.a>:

a625.pep
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA
51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

m625/a625 100.0% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFW	LAFSSGRIISIAAPVVPMIE	ASAVPTASRAVLSLGVPFKS			
a625	MFATRKMKKMTMCTRRVRFW	LAFSSGRIISIAAPVVPMIE	ASAVPTASRAVLSLGVPFKS			
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTKMPPEMVYRASSSRMKG	MYSSTSACATVWIPADAPKT	KLNGMRKSNVQKAVILPX			
a625	PQTKMPPEMVYRASSSRMKG	MYSSTSACATVWIPADAPKT	KLNGMRKSNVQKAVILPX			
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2009>:

g627.seq
1 ATGTCCGCC TTTGGAACCG CGAACACCCG GGATTGAAA TCCTCGGCAG
51 CCGTTACGCC CTGCAAAACC TTGTCCGCGA TGTCATCCTG ATTACATTEA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCGCGC AGGCAACGAA
151 TTCAACTTTG AATCCATCGC CGAAGTGGGC AAATCTTCC TCGGCATCTT
201 CATCACCATC TTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATACGATGT ATTTCTGGAT GAGCGGCATA TTGTCGGCAT TCTTGATATA
351 CGCGCCCACT TATCTCGTGT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTAATGAC GGGTCCCTCG TTTTCATTcg TGCTGGCGGT TTCTAtgggT
451 tCGGTATTCA TGGGCGCACT GaccTACATc gGCAAcgcac cgaactTCAT

1001

501 GGtcaaggcc aTTGCCGaaC agcgcgGCgt accgaTGCcg actTTCTTcc
 551 ggtaTAtgat gtggtcggtc gcCTTCCTGa caCCCGTCTT CAtcgTACAT
 601 ACCCTcgtCT TTTTcgTTtt cAAACTACTg taa

This corresponds to the amino acid sequence <SEQ ID 2010; ORF 627.ng>:

g627.pep
 1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL ITLTAVSMAI TPKQVRAGNE
 51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
 101 NTMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGPL FHSLLAVSMG
 151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFRYMMWSV AFLTPVFIVH
 201 TLVFFVFKLL *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2011>:

m627.seq
 1 ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTGAAA TCCTCGGCAG
 51 CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
 101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
 151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAATCTTTC TCGGCATCTT
 201 CATCACCATC TTTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
 251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
 301 AATGTGATGT ATTTTGGAT GAGCGGCATA TTGTCCGCAT TCTTGGATAA
 351 CGCCCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
 401 CCTTGATGAC GGGTACCCTG TTTCAATCGC TGCTGGCGGT TTCTATGGGT
 451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
 501 GGTCAAGGCC ATTGCCGAAC AGCGCGGCGT ACCGATGCCG ACTTCTTCG
 551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
 601 ACCCTTATCT TTTTCGTTTT CAACTGCTG TAA

This corresponds to the amino acid sequence <SEQ ID 2012; ORF 627>:

m627.pep
 1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
 51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
 101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGTL FHSLLAVSMG
 151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
 201 TLIFFVFKLL *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m627/g627 97.6% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGLWKPEHPGFEILGSRYALQNLVRDVIL	IALTAVSMAITPKQVRAGNEFNFEPIAEVG				
g627	MSGLWKPEHPGFEILGSRYALQNLVRDVIL	ITLTAVSMAITPKQVRAGNEFNFEPIAEVG				
	10	20	30	40	50	60

1002

	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVSVLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
g627	KLFLGIFITIFPVLSILKAGEAGALGGVSVLVHDTAGHPINTMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSVMGALTYIGNAPNFMVKAIAEQRGVPMP					
g627	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSVMGALTYIGNAPNFMVKAIAEQRGVPMP					
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					
g627	TFFRYMMWSVAFLTPVFIVHTLVFVFKLLX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2013>:

```

a627.seq
1  ATGTCCGCC  TTGGAAACC  CGAACACCCG  GGATTGAAA  TCCTCGGCAG
51  CCGTTACGCC  CTGCAAAACC  TCGTCCGCGA  TGTCATCCTG  ATTGCATTGA
101 CCGCCGTATC  TATGGCAATC  ACGCCCAAAC  AAGTCCGCGC  AGGCAACGAA
151 TTCAACTTGT  AATCCATCGC  CGAAGTGGGC  AAACCTTCC  TCGGCATCTT
201 CATCACCATC  TTTCCCGTCC  TGAGCATTCT  GAAAGCAGGC  GAGGCAGGCG
251 CGCTGGGCGG  GGTGGTATCG  CTGGTTCACG  ATACGGCAGG  TCATCCGATT
301 AATGTGATGT  ATTTTGGAT  GAGCGGCATA  TTGTCGGCAT  TCTTGGATAA
351 CGCGCCCACT  TATCTCGTTT  TTTTCAATAT  GGCGGCGGCG  GATGCCCAAG
401 CCTTGATGAC  GGGTTCCTCG  TTTCAATCGC  TGCTGGCGGT  TTCTATGGGT
451 TCGGTATTCA  TGGGCGCACT  GACCTACATC  GGCAACGCAC  CGAACTTCAT
501 GGTCAAGGCC  ATTGCCGAAC  AGCGCGGCGT  ACCGATGCCG  ACTTCTCTCG
551 GCTATATGAT  GTGGTCGGTC  GCCTTCTCTG  CACCCGTCTT  CATCGTACAT
601 ACCCTTATCT  TTTTCGTTTT  CAAACTGCTG  TAA

```

This corresponds to the amino acid sequence <SEQ ID 2014; ORF 627.a>:

```

a627.pep
1  MSGLWKPEHP  GFEILGSRYA  LQNLVRDVIL  IALTAVSMAI  TPKQVRAGNE
51  FNFEPIAEVG  KLFLGIFITI  FVLSILKAG  EAGALGGVVS  LVHDTAGHP
101 NVMYFWMSGI  LSAFLDNAPT  YLVFFNMAGG  DAQALMTGSL  FHSLLAVSMG
151 SVFMGALTYI  GNAPNFMVKA  IAEQRGVPMP  TFFGYMMWSV  AFLTPVFIVH
201 TLIFFVFKLL  *

```

m627/a627 99.5% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
a627	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVSVLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
a627	KLFLGIFITIFPVLSILKAGEAGALGGVSVLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSVMGALTYIGNAPNFMVKAIAEQRGVPMP					
a627	YLVFFNMAGGDAQALMTGSLFHSLLAVSMGVSVMGALTYIGNAPNFMVKAIAEQRGVPMP					
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					

1003

a627 TFFGYMMWSVAFLTFVFIVHTLIFFVFKLLX
190 200 210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2015>:

g628.seq
1 ATGTGCGTGC CACTCAAGCC GGCAGGATGC GGGCCGCCAA ATTCATGTGT
51 TTCGATATTG GCAGCATTTT CAGACGGCAC GTCTGCCCTT GCTGCTTTAC
101 ACACATGGAT TTTACGTTTC GTACGGCGGC TCAATACCAA CAGGCCGCGT
151 TTGAAGTCTT CGGCGGCTTC TTTGATGATG ACCGTACGGT CGGCAGCCAG
201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCTA
251 CGGCAGGGAT TTTGCTGAAC GGACGGGTGC GAAGCGCAGT CCATAAGCCT
301 GATTGAATCA GGTTGCGGCG CACTTTTTCG CTGCTCAATT TTGCCAGCGC
351 TTCAGGTacg TAG

This corresponds to the amino acid sequence <SEQ ID 2016; ORF 628.ng>:

g628.pep
1 MCVPLKPAGC GPPNSCVSIL AAFSDGTSAP AALHTWILRS VRRNTNRP
51 LKSSAASLMM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP
101 D*IRLRRTFS LLNFASASGT *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2017>:

m628.seq
1 ATGTGCGTGC CACTCAAACC GGCAGGATGC GGGCCGCCGA ATTCATGTGT
51 TTCGATGTTG GCAGCATTTT CAGACGGCAC GTCTGCCCCA GCTGCCTTAC
101 AACATGGAT TTTGCGTTTC GTCAAACGGC TCAATACCAA CAGGCCGCGT
151 TTGAAATCCT CGGCGGCTTC TTTGATAATG ACCGTAGGGT CGGCAGCCAG
201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCGA
251 CGGCAGGAAT TTTGCTGAAC GGACGGGTGC GCAGCGCAGT CCACAAACCG
301 GATTGGATCA GGTTGCGGCG CACTTCTTCG CCGCTTAAGT TTGCCAGCGC
351 TTCAGGTGCG TAG

This corresponds to the amino acid sequence <SEQ ID 2018; ORF 628>:

m628.pep
1 MCVPLKPAGC GPPNSCVSML AAFSDGTSAP AALQWILRS VKRLNTNRP
51 LKSSAASLIM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP
101 DWIRLRRTSS PLKFASASGA *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m528/g628 93.3% identity in 119 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAPAAALQWILRSVKRLNTNRP	RLKSSAASLIM			
g628	MCVPLKPAGCGPPNSCVSILAAFS	DGTSAPAAALHTWILRSVRRNTNRP	RLKSSAASLMM			
	10	20	30	40	50	60
	70	80	90	100	110	120
m628.pep	TVGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVHKPDWIRLRRTSSPLKFASASGA				
g628	TVGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVHKPDWIRLRRTSSPLKFASASGT				
	70	80	90	100	110	120
m628.pep	X					
g628	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2019>:

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```

a628.seq
1  ATGTGCGTGC  CACTCAAACC  GGCCGGATGC  GGGCCGCCGA  ATTCATGTGT
51  TTCGATGTTG  GCAGCATTTT  CAGACGGCAC  GTCTGCGCCA  GCTGCCTTAC
101 ACACATGGAT  TTTACGCTCG  GTCAAACGGC  TCAATACCAG  CAAACCTCGT
151 CTGAAATCCT  CGGCGGCTTC  TTTGATCACA  ACCACAGGGT  CTGCCGCCAG
201 CGGATTGGTG  TCCATCGCAT  TGACGAAGAT  GCGGAACGGC  TCGGCATCGA
251 CGGCAGGGAT  TTTGCTGAAC  GGACGGGTAC  GCAGCGCAGT  CCACAAACCG
301 GATTGGATCA  GATTGCGGCG  CACTTCTTCG  CCGCTTAAGT  TTGCCAACGC
351 TTCGGGCGCG  TAG

```

This corresponds to the amino acid sequence <SEQ ID 2020; ORF 628.a>:

```

a628.pep
1  MCVPLKPAGC  GPPNSCVSML  AAFSDGTSAP  AALHTWILRS  VKRLNTSKPR
51  LKSSAASLIT  TTGSAASGLV  SIALTKMANG  SASTAGILLN  GRVRSVHKP
101 DWIRLRRTSS  PLKFANASGA  *

```

m628/a628 95.0% identity in 120 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS DGT SAPAALQTWILRSVKRLNTNRPRLKSSAASLIM					
a628	MCVPLKPAGCGPPNSCVSMLAAFS DGT SAPAALHTWILRSVKRLNTSKPRLKSSAASLIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m628.pep	TVGSAASGLVSIALTKMANGSASTAGILLNGRVRSVHKPDWIRLRRTSSPLKFASASGA					
	:					
a628	TTGSAASGLVSIALTKMANGSASTAGILLNGRVRSVHKPDWIRLRRTSSPLKFANASGA					
	70	80	90	100	110	120

```

m628.pep      X
               |
a628           X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2021>:

```

g629.seq
1  ATGACTGCca  aacCTTTTTC  CCTCAACCTG  GCcaaCCTCC  TGCTGCCggc
51  ggtattGTTT  GCCGTCAGcc  tGtcggTCGG  cattgccgaT  TTCCGCTGGT
101 CGGATGTGTT  TTCGCTGTCC  GACAGCCAGC  AAGTGATGTT  CATCAGCCGC
151 CTGCCGCGCA  CGTTTGcgaT  TGTGTTGACG  GGCgcgtcga  tagcgGtggc
201 gGGGatgatt  atgcagATTC  TGATGCGCAA  CcgtTTGTGC  GAGCCTtcta
251 tggcgGGTGC  GGGCCAAAGt  gcgGCTTTGG  GTttgcttct  gAtgtccctg
301 ctgctgcctg  CgcGcccgt  gccgtcaAA  ATGTCGGtag  Cgcgccgtgc
351 CGCGCTGATC  GGGATGTTGG  -ctTtatgct  gctaataccgC  Cgcctgccac
401 cgacggcgca  gctgatgGTg  ccgCTGGTGG  Gg.ttATTTT  CGGCGGCGTG
451 GttgaGGCGG  TGGCAGCGTT  TGTGCGGTAT  GAGTTTGAGA  TGCTGCAAAT
501 GTTGGGCGTG  TGGCAGCAGG  GCGACTTTTC  AAGCGTGCTG  CTGGGGCGGT
551 ACGAGCTGCT  TTGGATTACG  GCGGTTTGG  CGGTGTTTGC  CTACCTGATT
601 GCGGACCGGC  TGACGATTTT  GGGGCTGGGC  GAGACGGTGA  GCGTGAATTT
651 GGGTTTGAAc  CGGACGGCGG  TGTGTGGTGC  GGGTTTGATT  ATTGTGGCAC
701 TGATTACATC  GCTGGTCATT  GTAACGGTCG  GCAATATTCC  GTTTATCGGG
751 CTGGTCGTGC  CGAATAACGT  CAGCCGCCTG  ATGGGCGACA  GGCTGCGCCA
801 AAGCCTGCCT  GCGGTCGCCC  TCTTGGGCGC  GTCTTTGGTT  TTATTGTGCG
851 ACATTATCGG  ACGCATGATT  GTGTTTCCGT  TTGAAATTCC  GGTCTCCACG
901 GTTTTGGTG  TGTGGGTAC  GGCTTTGTTT  TTGTGGCTTT  TGTTGAGGAA
951 ACCCGCTAT  GCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2022; ORF 629.ng>:

```

g629.pep
1  MTAKPFSLNL  ANLLPAVLf  AVLSVGIAD  FRWSDVFSLS  DSQQVMFISR
51  LPRTEAIVLT  GASIAVAGMI  MOILMRNRFV  EPSMAGAGQS  AALGLLLMSL
101 LLPAAPLPVK  MSVAAVAALI  GMLVFMLLIR  RLPPTAQLMV  PLVGXIFGGV

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151 VEAVATFVAY EFEMLOMLGV WQOGDFSSVL LGRYELLWIT GGLAVFAYLI
 201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG
 251 LVVPNIIVSRL MGDRLRQSLP AVALLGASLV LLCDIIGRMI VFPFPIPVST
 301 VEGVLTALF LWLLLRKPAY AV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2023>:

m629.seq
 1 ATGACTGCCA AACCTTTTTC CCTCAACCTG ACCAACCTGC TGCTGCTGGC
 51 GGTGTTGTTT GCGTCAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT
 101 CTGATGTGTT TTCACGTGCC GACAGCCAGC AGGTCATGTT CATCAGCCGC
 151 CTGCCGCGCA CGTTTGGCAT TGTGCTGACG GCGCGCTCGA TGGCGGTGGC
 201 CCGCATGATT ATGCAGATTT TGATGCGCAA CCGTTTGTGC GAACCGTCGA
 251 TGTTGGGCGC AAGCCAAAGC GCGGCTTAG GTTTGCTGCT GATGACCCTG
 301 CTGCTGCGCG CCGCGCGCT GCGGCGGAAA ATGTCGGTTG CCGCGGTTGC
 351 CCGCTGATC GGGATGTTGG TCTTTATGCT GCTGATCCGC CGCCTGCCGC
 401 CGACCGCGCA ACTGATGGTG CTTTGGTTCG GGATTATTTT CCGCGGTGTG
 451 ATTGAGGCGG TAGCCACCTT TATCGCGTAT GAAAACGAAA TGCTGCAAT
 501 GCTCGGCGTG TGSCAGCAGG GCGATTTTTC GAGCGTGCTG CTGGGCGGT
 551 ACGAGCTGCT TTGGATTACG GCGGTTTGG CCGTGTGTC CTATCTGATT
 601 GCCGACCGGC TGACGATTTT GGGGCTGGGC GAAACGGTAA GCGTGAATTT
 651 GGGTTTGAAC CGGACGCGCG GTTGTGGTC GGGTTTGATT ATTGTGGCTT
 701 GTATTACGTC GCTGGTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG
 751 CTGGTCTGTC CGAACATCAT CAGCCGCTG ATGGGCGACA GGTGCGCCA
 801 AAGCCTGCCT GCSGTGGCCT TGCTGGGCGC ATCTTTGGTG TTGCTGTGCG
 851 ACATTATCGG ACGCGTGATT GTGTTCCGT TTGAAATCC GGTCTCTACG
 901 GTTTTGGTG TATTGGGTAC GGCTTGTTT TTGTGGCTTT TGTTGAGGAA
 951 ACCCGCTAT GCCGTCTGA

This corresponds to the amino acid sequence <SEQ ID 2024; ORF 629>:

m629.pep
 1 MTAKPFSLNL TNLLLLAVLF AVSLSVGVAD FRWSDVFSLS DSQQVMFISR
 51 LPRTFAIVLT GASMAVAGMI MQILMRNRFV EPSMV GASQS AALGLLMLTL
 101 LLPAAPLPAK MSVAAVAALI GMLVFMLLIR RLPPTAQLMV PLVGIFGGV
 151 IEAVATFIAY ENEMLOMLGV WQOGDFSSVL LGRYELLWIT GGLAVFAYLI
 201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG
 251 LVVPNIISRL MGDRLRQSLP AVALLGASLV LLCDIIGRVI VFPFPIPVST
 301 VEGVLTALF LWLLLRKPAY AV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m629/g629 95.7% identity in 322 aa overlap

	10	20	30	40	50	60
m629.pep	MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISR					
	: : : : : : : :					
g629	MTAKPFSLNLANLLPAVLFAVSLSVGIADFRWSDVFSLSDSQQVMFISR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m629.pep	GASMAVAGMIMQILMRNRFVEPSMV GASQS AALGLLMLTL LPAAPLPAKMSVAAVAALI					
	: : : : : : : :					
g629	GASIAVAGMIMQILMRNRFVEPSMAGAGQS AALGLLMSLL LPAAPLPVKMSVAAVAALI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m629.pep	GMLVFMLLIRRLPPTAQLMVPLVGIIFGGVIEAVATFIAYENEMLOMLGVWQOGDFSSVL					
	: : : : : : :					
g629	GMLVFMLLIRRLPPTAQLMVPLVGXIFGGVIEAVATFVAYEFEMLOMLGVWQOGDFSSVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m629.pep	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLI IVALITSLVI					
	: : : : : : :					

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```

g629      LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           190      200      210      220      230      240

           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVFNIIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g629      VTVGNIPFIGLVVFNIVSRLMGDRLRQSLPAVALLGASLVLLCDIIGRMIVFPFEIPVST
           250      260      270      280      290      300

           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g629      VFGVLGTALFLWLLLRKPAYAVX
           310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2025>:

```

a629.seq
1  ATGACTGCCA AACCTTTTTC CCTCAACCTG ACTAACCTCC TGCTGCTGGC
51  GGTGTTGTTT GCCGTGAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT
101 CGGATGTGTT TTCGCTGTCG GACAGCCAGC AGGTTATGTT CATCAGCCGC
151 CTGCCGCGCA CGTTTGCGAT TGTGTTGACG GGCGCGTCGA TGGCGGTGGC
201 GGGGATGATT ATGCAGATTG TGATGCGTAA CCGTTTGTC GAGCCTTCTA
251 TGGCGGGCGC GGGTCAGAGT GCGGCTTTGG GTTTGCTTCT GATGTCCTG
301 CTGCTGCCTG CCGCGCCGCT GCCGGTCAAA ATGTCGGTTG CCGCCGTTGC
351 CGCGTTAATC GGGATGTTGG TGTATTATGAT GCTTATCCGC CGCCTGCCGC
401 CGACGGCGCA ACTGATGGTG CCTTTGGTCG GGATTATTTT CGGCGGCGTG
451 GTTGAGGCGG TGGCCACCTT TATTGCGTAT GAAAACGAAA TGCTGCAAA
501 GCTGGGCGTG TGGCAACAGG GCGATTTTTC CGGCGTGTG CTCGGACGGT
551 ATGAACGTG GTGGGCAACG GGGATTTTGG CTTTGTGTC CTATTGATT
601 GCCGACCAGC TGACGATTTT GGGTTTGGGC GAAACGGTAA GCGTGAACCT
651 GGGGCTGAAC CGGACGGCGA TTCTGTGTC GGGGCTGATT ATTGTGGCTT
701 TGATTACGTC GCTGGTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG
751 CTGGTCGTGC CGAACATCAT CAGCCGCTG ATAGGCGACA GGCTGCGCCA
801 AAGCCTGCCT GCGGTGGCTT TGCTGGGTGC GTCTTTGGTT TTATTGTGCG
851 ACATTATCGG ACGAGTGATT GTGTTCCGT TTGAAATTCC GGTATCGACC
901 GTCTTCGGCG TATTGGGTAC GGCCTTGTTT TTATGGCTTT TGTAAAGGAA
951 ACCTGCTCAT GCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2026; ORF 629.a>:

```

a629.pep
1  MTAKPFSNLN TNLLLLAVLF AVSLSVGVAD FRWSDVFSLS DSQQVMFISR
51  LPRTFAIVLT GASMAVAGMI MQILMRNRFV EPSMAGAGQS AALGLLMSL
101 LLPAAPLPVK MSVAAVAALI GMLVFMLIR RLPPTAQLMV PLVGIIFGGV
151 VEAVATFIAY ENEMQLMLGV WQQGDFSGVL LGRYELLWAT GILALFAYLI
201 ADQLTILGLG ETVSVNLGLN RTAILWSGLI IVALITSLVI VTVGNIPFIG
251 LVVFNIIISRL IGDRLRQSLP AVALLGASLV LLCIDIIGRVI VFPFEIPVST
301 VFGVLGTALF LWLLLRKPAH AV*

```

m629/a629 95.7% identity in 322 aa overlap

```

           10      20      30      40      50      60
m629.pep  MTAKPFSNLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      MTAKPFSNLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT
           10      20      30      40      50      60

           70      80      90      100     110     120
m629.pep  GASMAVAGMIMQILMRNRFVEPSMV GASQAALGLLMTLLLPAAPLPKMSVAAVAALI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      GASMAVAGMIMQILMRNRFVEPSMAGAGQAALGLLMSLLLPAAPLPVKMSVAAVAALI
           70      80      90      100     110     120

           130     140     150     160     170     180
m629.pep  GMLVFMLLIRRLPPTAQLMVPLVGIIFGGVIEAVATFIAYENEMQLMLGVWQQGDFSSVL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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```

a629      GMLVFMMILIRRLPPTAQLMVLVGIIFGGVVEAVATFIAYENEMLQMLGVWQQGDFSGVL
           130      140      150      160      170      180

           190      200      210      220      230      240
m629.pep  LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           ||||| || ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      LGRYELLWATGILALFAYLIADQLTILGLGETVSVNLGLNRTAILWSGLIIVALITSLVI
           190      200      210      220      230      240

           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFVIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      VTVGNIPFIGLVVPNIISRLIGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFVIPVST
           250      260      270      280      290      300

           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||
a629      VFGVLGTALFLWLLLRKPAHAVX
           310      320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2027>:

```

g630.seq (partial)
1  aTgatGATTT TGGTGTGGCT ggctttgttt ccccccatgt tttacggcat
51  gtacaacgctc GGCACACAGG CATTCGGTGC CTTAACGCCC GAtttgctgc
101 aacaaagcat cgcccacgac ggcaattacg ccctcgccaa cgctttgggc
151 atcaatatgt ccccgaaGc ggcggtgtTg ggcaaaatgc tgttcgGCGC
201 GATttacttc ctgccgattt acgcgaccgt aTTTATCTCTG GCGggttct
251 ggGaagtCTT GTTCGCATCc gtACGCAAAc ACGAAATCAA CGAAGGTTTC
301 TTCGTTACTT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGCAGGCGG GCTTTGGGTA TTTCTTTTCG CGTTGTGTTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAa AACTTCATGA ACCCTGCGCT GGCAGGCCCG
451 GCCTTCCTGT TCTTCGCCTA CCCCGCCAAC TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCACAAC CGCGCTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAAAcGCGG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTTATCGG CAAACTGCCG GGCTCCATCG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTC GCCCGCATCG
701 CTtcttgGCG CATTATTGCC ggCGTGATGA TCGGTatGat tGcgatgTCT
751 tcgctgatta acttcatCGg ttctgacacc aaagctatgt ttgctatgca
801 cttgggtacat ggcacttggT GGAaagatGa ttAtcactca ctgtacatta
851 aa.....

```

This corresponds to the amino acid sequence <SEQ ID 2028; ORF 630.ng>:

```

g630.pep
1  MMILVWLALF PPMFYGMYNV GAQAFGALTP DLLQOSIAHD GNYALANALG
51  INMSPEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFAV VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLEFFAYFAN LSGDAVWTAV DGYSGATALA QWAHAGADGL KNAVGTQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVE ARIASWRIIA GVMIGMIAMS
251 SLINFIGSDT KAMFAMHLVH GTWWKDDYHS LYIK....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2029>:

```

m630.seq
1  AIGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
51  GIACAACGTC GGCACACAGG CATTCGGTGC GTTAACGCCCT GATTGCTGTC
101 AACAAAACAT CGCCAACGAC TGGCATTACG CCTTTGCCAA CGCTTTGGGC
151 AICAAATATGT CGTCTGAAGC GGGCGTGTCT GACAAAATGC TGTTTGGCGC
201 GATTTACTTC CTGCCGATTT ACGCGACTGT ATTTGTGTGT GCGGGTTTCT
251 GGGAAAGTTT GTTCGCCACC GTGCGCAAAc ACGAAATCAA CGAAGGTTTC
301 TTCGTTACTT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGCAGGCGG GCTTTGGGTA TTTCTTTTCG CGTTGTGTTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAa AACTTCATGA ACCCTGCGCT GGCAGGCCCG
451 GCTTTCCTGT TCTTCGCCTA CCCCGCCAAC TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCACAAC CGCACTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAAAcGCGG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTTATCGG CAAACTGCCG GGCTCCATG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTC GCCCGCATCG
701 CTTCTTGGCG CATTATTGCC GCGGTGATGA TCGGTATGAT TGCGATGTCT
751 TCGCTGTGTA ACTTCATCGG TTCGGACACC AACCGTATGT TTGCTATGCC

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801 TTGGTACTGG CACTTGGTGG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCCTGTTTCC GCTTCCTTTA CCAATGTCCG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTGCC AACCTGTTTG
1001 CCCCAGATTT CGACTATTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
1051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2030; ORF 630>:

```

m630.pep
  1 MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQONIAND WHYAFANALG
 51 INMSSEAGVS DKMLFGAIYF LPIYATVFVV GGFWEVLFAT VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA OWAHAGADGL KNAVGTQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVPAYP EGMMLAILFA NLFAPIDYF VAQANIKRRK
351 ARSNG*

```

m630/g630 93.5% identity in 275 aa overlap

	10	20	30	40	50	60
m630.pep	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQONIANDWHYAFANALGINMSSEAGVS					
g630	MMILVWLALFPMPFYGMYNVGAQAFGALTPDLLQQSIAHDGNYALANALGINMSPEAGVL					
	10	20	30	40	50	60
m630.pep	DKMLFGAIYFLPIYATVFVVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA					
g630	GKMLFGAIYFLPIYATVFIVVGGFWEVLFASVRKHEINEGFFVTSILFALIVPPTLPLWQA					
	70	80	90	100	110	120
m630.pep	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA					
g630	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA					
	130	140	150	160	170	180
m630.pep	QWAHAGADGLKNAVGTQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
g630	QWAHAGADGLKNAVGTQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
	190	200	210	220	230	240
m630.pep	GVMIGMIAMSSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIGMLFMATDPVSASFTNVGKWW					
g630	CVMIGMIAMSSLINFIGSDTKAMFAM----HLVHCTWKKDDYHSLYIK.					
	250	260	270	280	290	300
m630.pep	YGALIGVMCVLIRVVPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX					
g630						
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2031>:

```

a630.seq
  1 ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
 51 GTACAACGTC GCGGCACAGG CATTCCGTGC GTTAACGCCC GATTGCTGTC
101 AACAAAGCAT CGCCAACGAC TGGCATTACG CCCTTGCCAA CGCTTTGGGC
151 ATCAATATGT CGTCTGAAGC GGGCGTGTG GGCAAAATGC TGTTCCGCGC
201 GATTTACTTC CTGCCGATTT ACGCGACCGT ATTTATGTGC GCGGTTTCT
251 GGGAAGTTT GTTCGCCACC GTGCGCAAAC ATGAAATCAA CGAAGTTTC
301 TTTGTTACCT CGATTCTGTT TGCCCTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCA GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAA AACTTCATGA ACCCTGCGCT GGCAGGCCGT
451 GCCTTCCTGT TCTTCGCCTA CCCTGCCAAC TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCACAAC CGCGCTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCTG AAAAAACGCCA TAACCGGTCA AACCATCACT
601 TGGATGGATG CGTTTATCGG CAAACTGCCG GGCTCCATCG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTC GCCCGCATCG

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701 CTTCTTGGCG CATTATTGCC GCGGTGATGA TCGGTATGAT TGCCATGTCT
751 TCGCTGTTCA ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC
801 TTGGTACTGG CATTGGGTCG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCCCCTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGGCGCAT TCTGTTTGCC AACCTGTTTG
1001 CCCCATTTC CGACTATTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
1051 GCGCGCAGCA ATGGCTAA

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This corresponds to the amino acid sequence <SEQ ID 2032; ORF 630.a>:

```

a630.pep
1  MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQOSIAND WHYALANALG
51  INMSSEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFAT VRKHEINEGF
101 FVTSILEALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAITGQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVE ARIASWRIIA GVMIGMIAMS
251 SLNFIGSDT NAMFAMPWYW HLVVGGFAIG MLEMATDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIDYF VAQANIKRRK
351 ARSNG*

m630/a630 98.3% identity in 355 aa overlap

          10      20      30      40      50      60
m630.pep  MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQONIANDWHYAFANALGINMSSEAGVS
          |||||||
a630      MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQOSIANDWHYALANALGINMSSEAGVL
          10      20      30      40      50      60

          70      80      90      100     110     120
m630.pep  DKMLFGAIYFLPIYATVFVVGGEVLVATVRKHEINEGFFVTSILFALIVPPTLPLWQA
          |||||||
a630      GKMLFGAIYFLPIYATVFIVVGGEVLVATVRKHEINEGFFVTSILFALIVPPTLPLWQA
          70      80      90      100     110     120

          130     140     150     160     170     180
m630.pep  ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA
          |||||||
a630      ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA
          130     140     150     160     170     180

          190     200     210     220     230     240
m630.pep  QWAAHGADGLKNAVGTGQITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA
          |||||||
a630      QWAAHGADGLKNAITGQITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA
          190     200     210     220     230     240

          250     260     270     280     290     300
m630.pep  GVMIGMIAMSSLENFIGSDTNAMFAMPWYWHLVVGGFAIGMLEMATDPVSASFTNVGKWW
          |||||||
a630      GVMIGMIAMSSLENFIGSDTNAMFAMPWYWHLVVGGFAIGMLEMATDPVSASFTNVGKWW
          250     260     270     280     290     300

          310     320     330     340     350
m630.pep  YGALIGVMCVLIRVVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX
          |||||||
a630      YGALIGVMCVLIRVVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX
          310     320     330     340     350

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2033>:

```

g635.seq
1  ATGACCCGGC GACGGGTCGG CAAGCAAAAC CGTATTGCCA TCCACTCCGC
51  GCAATACCGA AAAATGGTCG TCTTTGCGGT ATTTCAGATA CACGATGACG
101 GGGATTTTCA ACTGCGCGAG CTGTTTGAAA GACAGGCCAT AGCCTTTCGC
151 CTCAAAACCC AAATCGGGCA TAATGCGCCG CATATCCTCA AACGACGCGC
201 GCATCTGTTT CTTACCCAGT TTTTCAACA CTCTCTCTTC CGTCAGCTTT
251 TGCCCGTAAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGGAGA

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301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCCCGCCGC GCTTTCCAAC
 351 TCTGCAATTT GATTTTCCG TAAACAACAG GATTATCGTT AAACATCGGT
 401 GCAGCATTC AAGGATAAGA CAAGGCTCTG TACCAGATTA G

This corresponds to the amino acid sequence <SEQ ID 2034; ORF 635.ng>:

g635.pep

1 MTRRRVGKQN RIAIHSQYR KMVVFVFCI HDDGDFQLRE LFERQGIAGR
 51 LKTQIGHNAP HILKRRHLF LTOFFQHFFF RQLLPVKIVQ KRRHRSRPAG
 101 KIQILLYNIE IPPRFPTLQF DFSVNNRIIV KHRCSIQTIR QGSVPD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2035>:

m635.seq

1 ATGACCCAGC GACGGGTCCG CAAGCAAAAC CGTATTGCCG TCTATACCGC
 51 GCAATACCGA GAAATGATCA TCCTTGCGGT ATTCAGATA CACGATGACG
 101 GGGATTTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTCGC
 151 TTCAAACCC AAATCAGGCA TAATGCGCCG CATATCCTCA AACGACGCGG
 201 GCATCTGCTC CTTATCCAGT TTTTCAACA CGTCCTCTTC CGTCAGCTTT
 251 TGCCCGTGAA AATTGTTCAA AAGCGTCACC ACCGAAGCCG CCCCAGGGA
 301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC
 351 TCTGCACCTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA

This corresponds to the amino acid sequence <SEQ ID 2036; ORF 635>:

m635.pep

1 MTQRRVGKQN RIAVYTAQYR EMILAVFQI HDDGDLQLCK LLERQGIAGR
 51 FKTQIRHNAP HILKRRGHLI LIQFF*HVLV RQLLPVKIVQ KRRHRSRPAG
 101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D*

m635/g635 80.0% identity in 130 aa overlap

	10	20	30	40	50	60
m635.pep	MTQRRVGKQNRIAVYTAQYREMI	ILAVFQIHDDGDLQLCKLLERQGI	AFR	FKTQIRHNAP		
g635	MTRRRVGKQNRIAIHSQYRKM	VVFVFCIHDDGDFQLREL	FERQGI	AFRLKTQIGHNAP		
	10	20	30	40	50	60
	70	80	90	100	110	120
m635.pep	HILKRRGHLI	LIQFFXHVLF	RQLLPVKIVQ	KRRHRSRPAG	KIQILLYNIE	IAPFFPTLHF
g635	HILKRRHLELT	QFFQHF	FRQLLPVKIVQ	KRRHRSRPAG	KIQILLYNIE	IPPRFPTLQF
	70	80	90	100	110	120
	130					
m635.pep	DFSISNRIIVDX					
g635	DFSVNNRIIVK	HRC	SIQTIR	QGSVPDX		
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2037>:

a635.seq

1 ATGACCCAGC GACGGGTCCG CAAGCAAAAC CGTATTGCCG TCTATACCGC
 51 GCAATACCGA GAAATGATCA TCCTTGCGGT ATTCAGATA CACGATGACG
 101 GGGATTTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTCGC
 151 CTCAAAACCC AAATCAGGCA TGATGCGCCG CATATCCTCA AACGACGCGC
 201 GCATCTGCTC CTTATCCAGC TTTTCAACA CGTCCTCTTC CGTCAGCTTT
 251 TGCCCGTGAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGGGA
 301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC
 351 TCTGCACCTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA

This corresponds to the amino acid sequence <SEQ ID 2038; ORF 635.a>:

a635.pep

1 MTQRRVGKQN RIAVYTAQYR EMILAVFQI HDDGDLQLCK LLERQGIAGR
 51 LKTQIRHDAP HILKRRHLI LIQLFQHVLF RQLLPVKIVQ KRRHRSRPAG
 101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D*

m635/a635 95.4% identity in 131 aa overlap

10	20	30	40	50	60
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m635.pep	MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIARFKTQIRHNAP
a635	MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIARFLKTQIRHDAP
	10 20 30 40 50 60
	70 80 90 100 110 120
m635.pep	HILKRRGHLLLIQFFXHVLFQRLLPVKIVQKRHRHSRPAGKIQILLYNIEIAPFFPTLHF
a635	HILKRRRAHLLLIQLFQHVLFQRLLPVKIVQKRHRHSRPAGKIQILLYNIEIAPFFPTLHF
	70 80 90 100 110 120
	130
m635.pep	DFSISNRIIVDX
a635	DFSISNRIIVDX
	130

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g638.seq
1  ATGATTGGCG  GACAGTTTAT  cGTAGtTgGc  atGTAGGCA  AAAACGCAT
51  TGCCCGCTTT  TTGTGATATA  ttgtcGTGAA  TAtcGAAAT  GTTGACATAG
101  TTGAGCATGA  TGCCCTAATC  GCGGCTGCCG  ACGGCGATAT  TGTcGAACAC
151  TTTGAGCGCT  TCGGAAACA  TCAGACATA  GCCCATATTG  TtgcCCACG
201  AAATATGCTT  GCGTgacttc  ctgtcgTTGG  TGTACATATA  GTTGACGGCG
251  APACGCAGGT  CGCTGAAGCG  GTTGTTTTAA  TAGGTGTTGT  GCGTGCTGGT
301  ATTTGGAAAG  ATCGCGCTCG  GCCCTTTGGA  AATGTcGT7G  cGcAGCAGCT
351  GCGCGcgggg  CgcgtTCCAA  CGCGTAACGC  CATTGCCGGC  CTCATTACG
401  CGCAAGGTcg  catcgCCGAC  GATTTTATTC  TCGCGCACCA  TCGCATCGGC
451  AGAACCATGA  AGGTATACGC  CGAACGAATT  ATCAAAAAAT  TTGT7TGTGT
501  CAACCAAGGG  GCGCGGGGCG  GCTTTTTCGA  GATAAATACC  GGCATTCATT
551  GCTGGCAGGC  TCATACCGGA  ACGGGTAACG  GTCAGGTTGC  GGAGCGTTAC
601  GTCCGGCGCG  TGTAACGCTA  TGTGATCGCC  GCTCT7GTCT  CCTCTCGATG
651  TTGCGGAAGC  GTCGCGAGCA  CCTTCAATCG  TAATCGGTTT  TGTGATATAA
701  AGTTTGTTT  GATATACGCC  GGAAGCCAGT  TTGATCGTAT  CGCCCGCCCG
751  GCGCGCGGCA  AAAATTTTGA  CAAAGTTGTC  TTGCGGGGAA  ACGTGAGACGA
801  CGGTCTCGGA  TGCGGTCTCG  AAAATGCTGC  CGCGGCGAAG  TATACAGCA
851  GCCTTCAGCC  ATATACGGAG  CGCGGATGTG  TGCATAGTGT  CCCTCTGTTT
901  CGTTCTGGTAT  GGCCGAACAA  AATAAGACAT  CATTTCAAAT  TGCGT7TTTT
951  TATAGCGAAA  CCGCTGTAAA  CGGTACCGCA  AGCGGTTTGG  CTATAA

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g538 .pep

1	MIGGQFIIVG	IVGNALARF	VDNIIVNIGI	VDIVEHDALI	AAADGDIVEH
51	FEPFGKHQHI	AHIVAHGNIA	ADFVAVGVHI	VDGETQVAEV	VVIFGVVRAG
101	IGKNVAAPPFG	NVAVDDLRA	RVNGNIAIAA	LIHAQGRID	DFILAAHRRIG
151	RTMKVYAERL	IKNIIVENQG	ARGGFFEINT	GIHCWQAHT	TGNQQAVER
201	VRRVYGYGTP	ALVPFDGCGT	VGRPNRNRF	VDIKFGLIYA	GQSFDRIAR
251	GAGNFGKVG	LRGNVDGCR	CLRNKAAGGK	YQHGLQPYTE	RGCVHSVPLF
301	RSVVPNKIKH	HSNVPEVIAI	PPETVROAVN	L*	

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m538.seq
1  ATGATTGGCG  AAAAGTTTAT  CGTAGTTGGC  ATTATAGGCA  AATACGCAC
51  TGCCTGCTT  GTTGATAATG  TTGTCGTGAA  TATCGGAATA  GTTGACATAG
101  TTAGCATAA  TGCCCTGATC  GCGGCTGCCG  ACGGCGATAT  TGTCAATAC
151  TTTGAGCCGC  TCGGAAARAC  TCAGCACATA  GCCCATATTT  TTGCCACGG
201  AAATATGCT  GCGTGATTTC  CTGTGCTTGG  TGTACATATG  GTGGACGGC
251  AAACGCAAT  CGCTGAAGCG  GTTGTTTTGG  TAGTGTGTGT  GCGTGCTGG
301  ATTGGA AAA  ATGCCGTCCC  GCCCTTTTGA  AATGTCGTTG  CCGCAGCACT
351  CGCGACGGG  TGCCTTCCAA  ACGGTAAACG  CGTTGCCGGC  CTCGTTACG
401  CGCAAATCG  CGTCGCCGAC  GATTTTATTC  TCGCGCACA  TCGCATCGGC
451  AGAAATATG  AGATATACGC  CGACCGAATT  ATCCAAAAAT  TTGTTGTGTT
501  CAATCAGGC  GCGCGGGGCA  GTTTCTTCGA  GATAAATACC  GCGATCCATT
551  CGGGGACGG  TCATACCGGA  ACGGGTAACG  GTCAGGTTCG  GGAGCGTTAC
601  GTCGCGGCG  TGTAACGGTA  TGTAAGCCGC  GCTCTGTCTG  CTTCTGATG
651  TIGCGGAAC  GTCGGCAGGC  CCTTCAATCG  TAATCGGTTT  GTCATGTGA
701  ACTTTGGTT  TATATACGCC  GGAAGCCAGT  TTGAGCGTAT  CGCCCGCCGC
751  GCGCGGCGCA  AATCGGGGAT  ACCGATCAGC  ATAATCGGTT  CGTGA

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This corresponds to the amino acid sequence <SEQ ID 2042; ORF 638>:

m638.pep
 1 MIGEKFIVVG IIGKYALACL VDNVVVNIGI VDIVHNALI AAADGDIVEY
 51 FEPLGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFGVVRAG
 101 IGKNAVPPFG NVVADDLRTG CVPNGNAVAA LVHAQSRVAD DFILAHHRIG
 151 RTMQIYADRI IQNIVFVNOG ARGSFFEINT GIHCGQAHTG TGNGQVAERY
 201 VRRVYGYGTP APVAFDGGCT VGRPFNNRNF VNVKFGFIYA GSQFERIARP
 251 GAGKCGIPIS IIGS*

m638/g638 88.2% identity in 254 aa overlap

m638.pep	10	20	30	40	50	60
	MIGEKFIVVG	IIGRYALACL	VDNVVVNIGI	VDIVEHNALI	AAADGDIVEY	FEPLGKHQHI
g638	MIGGQFIVVG	IVGKNALARF	VDNVVVNIGI	VDIVEHDALV	AAADGDIVEH	FEFFPGKHQHI
	10	20	30	40	50	60
m638.pep	70	80	90	100	110	120
	AHIVAHGNIA	ADFAVVGVHI	VDGETQIAEA	VVFGVVRAG	IGKNAVPPFG	NVVADDLRTG
g638	AHIVAHGNIA	ADFAVVGVHI	VDGETQVAAE	VVFGVVRAG	IGKNAVPPFG	NVVADDLRAG
	70	80	90	100	110	120
m638.pep	130	140	150	160	170	180
	CVPNGNAVAA	LVHAQSRVAD	DFILAHHRIG	RTMQIYADRI	IQNIVFVNOG	ARGSFFEINT
g638	RVPNGNAIAA	LIHAQGRVAD	DFILAHHRIG	RTMKVYAE	RIKQIVFVNOG	ARGGFFEINT
	130	140	150	160	170	180
m638.pep	190	200	210	220	230	240
	GIHCGQAHTG	TGNGQVAERY	VRRVYGYGTP	APVAFDGGCT	VGRPFNNRNF	VNVKFGFIYA
g638	GIHCWQAHTG	TGNGQVAERY	VRRVYGYGTP	ALVFPDGGCT	VGRPFNNRNF	VDIKFGLIYA
	190	200	210	220	230	240
m638.pep	250	260				
	GSQFERIARP	GAGKCGIPIS	IIGSX			
g638	GSQFDRIARP	GAGKNFGKVV	LRGNVDDG	RCRLKNAAG	GKYQHGLQPY	TERGCVHSVPLF
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2043>:

a638.seq
 1 ATGATTGGCG GACAGTTTAT CGTAGTTGGC ATTGTAGGCA AAAACGCACT
 51 TGCCCGCTTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
 101 TTGAGCATGA TGCCTTGGTC GCGGCTGCCG ACGGCGATAT TGTCAAACAC
 151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACGG
 201 AAATATTGCC GCTGATTTCG CTGTCGTTGG TGTACATATA GTGGACGGCG
 251 AAACGCAAT CGCTGAAGCG GTTGTTTTGA TAGGTGTTGT GCGTGCTGGT
 301 ATTGGAATA ATGCCGTCCC GCCCTTTGGA AATATCGTTG CCGACGACCT
 351 GCGCGCCGGG CGCGTTCCAA ACGGTAACGC CATGCGCGCG CTCGTTACAG
 401 CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCCCGCACCA TCGCATCGGC
 451 AGAACCATGC AGATAGACGC CGACCGAATT ATCCAAAATA TTATTGTGTT
 501 CAATCAGGGC GCGCGGGGCA GTTCTTTCGA GATAAATACC GGCATCCATT
 551 GCGGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAACGTTAC
 601 GTCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCCTGTCT CCTTCGATGG
 651 TTGCAGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCGATGTGA
 701 AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCC
 751 GCGCGGGGCA AATGCGGGAT ACCGATCAGC ATAATCGACT CATGGTGA

This corresponds to the amino acid sequence <SEQ ID 2044; ORF 638.a>:

a638.pep
 1 MIGGQFIVVG IVGKNALARF VDNVVVNIGI VDIVHDALV AAADGDIVKH
 51 FEPLGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFIGVVRAG
 101 IGKNAVPPFG NIVADDLRAG RVPNGNAIAA LVHAQSRVAD DFILPHHRIG
 151 RTMQIDADRI IQNIVFVNOG ARGSFFEINT GIHCGQAHTG TGNGQVAERY
 201 VRRVYGYGTP APVSFDGCRT VGRPFNNRNF VDVKEGLIYA GSQFERIARP

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251 GAGKCGIPIS IIDSW*

m638/a638 91.3% identity in 264 aa overlap

	10	20	30	40	50	60
m638.pep	MIGEKFIVVGIIGKYALACLV	DNVVVNIGIVDIVEH	NALIAAADGDIVEY	FEPLGKHQHI		
a638	MIGGQFIVVGIIGKALARFV	DNVVVNIGIVDIVEH	DALVAAADGDIVKH	FEPLGKHQHI		
	10	20	30	40	50	60
m638.pep	70	80	90	100	110	120
a638	70	80	90	100	110	120
	130	140	150	160	170	180
m638.pep	130	140	150	160	170	180
a638	130	140	150	160	170	180
	190	200	210	220	230	240
m638.pep	190	200	210	220	230	240
a638	190	200	210	220	230	240
	250	260				
m638.pep	250	260				
a638	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2045>:

g639-1.seq

```

1  ATGAGCCTGC CAGCAATGGA TGCCGCTATT TATCTCGAAA AAGCCGCCCC
51  GCGCGCCCTG GTTGAACACA ACAATATTTT TGATAATTCG TTCGGCGTAT
101 ACCTTCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GATGCGACCT TGCGCGTGAA TGAGCGCGGC AATGGCGTTA CCGTTTGGA
201 CGCGCCCGGC GCGCAGGTCC TCGGCAACGA CATTTCCTAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAAAC CCTATAAAAA CAACCGCTTC
301 AGCGACCTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAGT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAACGGCT CAAAGTGTTC GACAATATCG CCGTCGGCAG CCGCGATTAG
451 GGCATCATGC TCAACTATGT CAACTATTCG GATATTCACG ACAATATTAT
501 CAACAAAGCG GGCAAGTCCG TTTTGCCTA CAATGCCAAC TACGATAAAC
551 TGTCGCGCAA TCATTTTGAA AACTGCCAAA TCGGCATGCA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGGAAG
651 CCAGGTCAAA TATGTCAGTA CGCGCTTTCT CGACTGGAGC GAGGCGGGAC
701 ACGGCAACTA CTGGAGCGAC AACAGCCCGT TCGATTGAA CCGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCGACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAATATGGC GCAGGCGCAG TTTCCCGCCG TTCTGCCCGG CGGCGTGGTG
901 GACAGCAACG CGCTGATGAA GCCTTATGCC CCCAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGT TGCTCAAAGA AGCCGAAACG CGGCAGTCGG
1001 AACGGGCGAC GCGGAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2046; ORF 639-1.ng>:

g639-1.pep

```

1  MSLPAMDAGI YLEKAAPRAL VEHNIFDMS FGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNPAG AQVVGNDISK GRDGIFNTS THNTYKNNRF
101 SDLRFVHYM YTNDSEVSGN ISVGNNMGYV LMFSERLKVF DNIAVGSRD*
151 GIMLNYVNS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGMHFTA
201 AIEGTSLHDN SFINNGSQVK YVSTRFLDWS EGGHGNYSW NSPFDLNGDG
251 FGDSAYRPDG IIDQIIWRAP VSRLMNSPA ISIVKWAQAO FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLKEAET ROSERGRAEN GSLN*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2047>:

1014

m639-1.seq

```

1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAAGTGGCCC
51  GCGCGCCCTG ATTGAACACA ACAATATTTT GGATAATTCG GTCGGCGTAT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AACGGCGTTA CCGTTTGGAA
201 CGCACCCCGT GCGCAGGTGC TCGGCAACGA CATTTCCTAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAAAC CCTACAAAAA CAACCGCTTC
301 AGCGATTTCG GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCCAGCCGCT CAAACTATTC GACAATATCG CCGTCGGCAG CCGCGATCAG
451 GGCATTATGC TCAACTATGT CAACTATTCC GATATTACAG ACAACATTAT
501 CAACAAGGCA GGCAGTGC TATTGCCTA TAATGCCAAC TACGATAAAC
551 TTTTCGCCAA TCATTTTGAA AACTGTCAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCTT GCATGACAAT TCCTTTATCA ACAACGAAAG
651 CCAGGTCAA TACGTACGCA CGCGCTTCT CGATTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTGAA CCGGCGCGGC
751 TTCGGAGACA GCGCGTACCG CCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TTTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAATGGGCG GCAGGCGCAG TTTCCCGCGC TTCTGCCTGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGC TACTCAAAGA AGTCGAAACG CCGCAGTCGG
1001 AATGGGGCAG GCGGAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2048; ORF 639-1>:

m639-1.pep

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFSNIS THNTYKNNRF
101 SDLRFVHYM YTNDEISGN ISVGNMGYV LMFSERLKVF DNIAVGSRDQ
151 GIMLNYVNY DIHDNIINKA GKCVFAYNAN YDKLFANHFE NCQIGIHFTA
201 AIEGTSLHDN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRPNG IIDQIWRAP VSRLLMNSPA ISIVKWAQQAQ FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLKEVET RQSEWGRAEN GSLN*

```

g639-1/m639-1 95.9% identity in 344 aa overlap

	10	20	30	40	50	60
g639-1.pep	MSLPAMDAGIYLEKAAPRALVEHNNIFD	NSFGVYLHGSADAMVRENKIVGDATLRVNERG				
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNS	VGVLHGSADAMVRENKIVGDATLRVNERG				
	10	20	30	40	50	60
g639-1.pep	NGVTVWNAPGAQVVGNDISKGRDGIFSNIS	THNTYKNNRFSDLRFVHYMYTNDSEVSGN				
m639-1	NGVTVWNAPGAQVVGNDISKGRDGIFSNIS	THNTYKNNRFSDLRFVHYMYTNDSEISGN				
	70	80	90	100	110	120
g639-1.pep	ISVGNMGYVLMFSERLKVF	DNIAVGSRDQXGIMLNYVNYSDIHDNIINKAGKCVFAYNAN				
m639-1	ISVGNMGYVLMFSERLKVF	DNIAVGSRDQXGIMLNYVNYSDIHDNIINKAGKCVFAYNAN				
	130	140	150	160	170	180
g639-1.pep	YDKLSANHFENCQIGMHFTA	AIEGTSLHDNSFINNGSQVKYVSTRFLDWS				
m639-1	YDKLFANHFENCQIGIHFTA	AIEGTSLHDNSFINNESQVKYVSTRFLDWS				
	190	200	210	220	230	240
g639-1.pep	NSPFDLNGDGF	FGDSAYRPNGIIDQIWRAPVSRLLMNSPAISIVKWAQQAQFPAVLPGGVV				
m639-1	NSAFDLNGDGF	FGDSAYRPNGIIDQIWRAPVSRLLMNSPAISIVKWAQQAQFPAVLPGGVV				
	250	260	270	280	290	300
g639-1.pep	DSKPLMKPYAPKIQTRYQAM	KDELLKEAETRQSERGRAENGSLNX				
m639-1	DSKPLMKPYAPKIQTRYQAM	KDELLKEVETRQSEWGRAENGSLNX				
	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2049>:

a639-1.seq

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```

1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAAGTGCCTC
51  GCGCGCCCTG ATTGAACACA ATAATATTTT GGATAATTCG GTCGGCGTCT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GGGAGAAATA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AATGGCGTTA CCGTTTGGA
201 CCGCGCCGCG GCGCAGGTGC TCGGCAACGA TATTTCCAAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAAAC CCTATAAAAC CAACCGCTTC
301 AGCGATTTCG GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAGCGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGACCAA
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTCACG ACAACATTAT
501 CAACAAAGCG GCAAGTGC TTTTGCCTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGAAAG
651 CCAGGTCAAA TACGTAGCA CGCGCTTCT CGACTGGAGC GAGGCGGAC
701 ACGGCAACTA TTGGAGGAC AACAGCGCGT TCGATTGAA CCGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCACCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAATGGGC GCAGCGCAA TTTCCCGCCG TTTGCCTGG CCGCGTGGTG
901 GACAGCAAAAC CGCTGATGAA GCCTTATGCC CCAAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGGGC TGCTCAAAA AGTCGAAACG CGGCAGTTGG
1001 AATGGGGCAG GCGGAAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2050; ORF 639-1.a>:

a639-1.pep

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNPAG AQVVGNDISK GRDGFISNTS THNTYKNNRF
101 SDLRFVAVHYM YTNDSEISGN ISVGNMNGYV LMFSERLKVF DNIAGVSRDQ
151 GIMLNVNYS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGIHFTA
201 AIEGTSLEHNS FINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRPNQ IIDQIIWRAP VSRLMNSPA ISIVKWAQAF PAVLPQGGV
301 DSKPLMKPYA PKIQTRYQAM KDGLLKKVET RQLEWGRAEN GSLN*

```

a639-1/m639-1 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
a639-1.pep	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
	70	80	90	100	110	120
a639-1.pep	NGVTVWNPAGAQVVGNDISKGRDGFISNTSTHNTYKNNRFSDLRFVAVHYMYTNDSEISGN					
m639-1	NGVTVWNPAGAQVVGNDISKGRDGFISNTSTHNTYKNNRFSDLRFVAVHYMYTNDSEISGN					
	70	80	90	100	110	120
	130	140	150	160	170	180
a639-1.pep	ISVGNMNGYVLMFSERLKVFVFNIAVGSRDQGIMLNVNYSIDIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMNGYVLMFSERLKVFVFNIAVGSRDQGIMLNVNYSIDIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
	190	200	210	220	230	240
a639-1.pep	YDKLSANHFENCQIGIHFTAAIEGTSLEHNSFINNESQVKYVSTRFLDWSDEGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTAAIEGTSLEHNSFINNESQVKYVSTRFLDWSDEGGHGNYSW					
	190	200	210	220	230	240
	250	260	270	280	290	300
a639-1.pep	NSAFDLNGDGFSGDSAYRPNQIIDQIIWRAPVSRLMNSPAISIVKWAQAFPAVLPQGGV					
m639-1	NSAFDLNGDGFSGDSAYRPNQIIDQIIWRAPVSRLMNSPAISIVKWAQAFPAVLPQGGV					
	250	260	270	280	290	300
	310	320	330	340		
a639-1.pep	DSKPLMKPYAPKIQTRYQAMKDGLLKKVETRQLEWGRAENGSLN					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLKEVETRQSEWGRAENGSLN					
	310	320	330	340		

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The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2051>:

```

g640.seq
1  ATGATTCATA TAATATCAAT ATTAAGAGT ATCGGTATAT CGGGGATAGC
51  TATGTCCTGT TTTTCAATCC GCGGTATGTC TCGGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TACCGCCTTT GTCTTTTGA CGGcggcACT GCCCGCTTAT
151 GcggAgcgTc tgcctGATT TCTGgcgAAA ATacAgcctT CGGAAATTTT
201 TCCGGGTGCG GATCGTTACG GCAAGCCGGA aggcAAGCCT AtggtTGCCC
251 GCgtttACAA AGgcgATGAG CAGCTCGGTT TGGTTTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATCGATA CGCTGATGGC
351 TTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GATCATCACG
401 AACCGATTAT GCTGATCGGT ATCCCGCAAT CGCGTGCGA TAAGTTCATC
451 GACAAATATA TCGGTCTGAA TTTTATTAAA AATCCGCCGA CCCCAGCGT
501 GCGCGCGGGC GACATCATCA GcggTGCGAC TgttaCACTG ATGGTGGTTA
551 ACGACAGCAT CCAGCGTTCG TACAAGGTCA TGGCAAACCA ATACCGTCTG
601 GGTTCGGACA AGGCCCTTCA GACGGCATCC GCTTCCGATG TTCGGGAAGC
651 CGCGCCTGCG TCAGAAACCC GTCCGCGCCG TATGGCAAAT CCGGACAGC
701 AGGATATTTT GTCTTGGGAC GAACTTTTGA AACAAAGGC CGTCCGCCAT
751 CTGCATATCA GCCTCGATCA AATCAACAAA CTGTTTGAGA AAGGCGCAA
801 GGCCGGCGTG GCGGATCAG CCGAACAGGG CGATCCTGAC GATACCTTTA
851 TTGATTTGTA TGTTCCTTG GTGAGCCAGC CTCCATCGG TAAAGCCTG
901 CTGGGTGAGG ACGGCTGGGC GCATCTGCAA AAACGGCTGA AACCCGGGCA
951 GCAGGCGGTT TTGGTTGCCG GAGAGGGCCG TTATTCTTGG AAAGETTGG
1001 GCTATGTGCG CGCGGCTATT TTCGACCGTA TCGAGATGAT TCAGGGGAG
1051 AACAGCTTCC GTTTTACCGA TGCCCAACAC GAACGCTCG TCGAGCTGTC
1101 TGCCGCCGAT GCGCCGCGTT TTAAGAAGT TTCTTGTTT ACCATCCCTG
1151 AAGCGTAGC GTTTGACGGT GCGGAGCCGT GCGGCTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2052; ORF 640.ng>:

```

g640.pep
1  MIHIISILKS IGISGIAMSC FSIRMSAFR ARITAFFTAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAN DGTIAGAKLV DHHEPIMLIG IPQSRVDKFI
151 DKYIGLNFIL NPPTPSVAPG DIISGATVTL MUVNDSIQRS YKVIANQYRL
201 GSDKALQTAS ASDVREAAFA SETRPRRMAN PDKQDILSWD ELLKQKAVGH
251 LHITLDQINK LFEKGGKAGV ADHAEQGDPD DTFIDLYVAL VSQPSIGKSL
301 LGEDGWAHLQ KRLKPGQQAV LVAGEGRYSW KSGYVRGGI FDRIEMIQGE
351 NSFRETDAQH ERVELSAAD APRFEKVSF TIPEGVAFDG AEPWRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2053>:

```

m640.seq (partial)
1  ATGATTCATA TAATATCAAT ATTAAGAGT ATCGGTATAT CGGGGATAGT
51  CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCTGATT TCTGGCGAAA ATACAGCCTT CGGAAATTTT
201 TCCGGGTGCG GACCGTTACG GCAAGCCGGA AGGTAAGCCT ATGTTTGCCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGT
351 GTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GACCATCACG
401 AACCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2054; ORF 640>:

```

m640.pep (partial)
1  MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMVLAN DGTIAGAKLV DHHEPIMLIG IPH...

```

m640/g640 96.5% identity in 143 aa overlap

	10	20	30	40	50	60
m640.pep	MIHIISILKS	IGISGIVMSC	FSIKRMSAFR	ARITAFFAAF	VFLTAALPAY	AERLPDFLAK
g640	MIHIISILKS	IGISGIAMSC	FSIRMSAFR	ARITAFFTAF	VFLTAALPAY	AERLPDFLAK
	10	20	30	40	50	60
	70	80	90	100	110	120

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```

m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMVLAN
               |||||||
g640          IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMALAN
               70      80      90      100     110     120

               130      140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
               |||||||
g640          DGTIAGAKLVDHHEPIMLIGIFQSRVDKFIDKYIQLNFIKNPPTPSVAFGDIISGATVTL
               130      140      150      160     170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2055>:

```

a640.seq (partial)
1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATA  CGGGGATAGT
51 CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCAC  GCCCGCTTAT
151 GCGGAGCGTC TGCCGTGATT TCTGGCGAAA ATACAGCCT  CGGAAATTGT
201 TCCGGGTGCG GACCGTTACA GCAAGCCGGA AGGTAAGCCT ATGTTTGCCT
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATA  CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAA CCGATTGATA CGCTGATGGC
351 GTTGGCTAAA GACGGTACGA TAGCCGAGC GAAATTGGT  GATCACCATG
401 AGTCGATTAT SCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2056; ORF 640.a>:

```

a640.pep (partial) Length: 143
1  MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
51  AERLPDFLAK IQPSEIVPGA DRYSKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAK DGTIAGAKLV DHESIMLIG IPH...

```

m640/a640 96.5% identity in 143 aa overlap

```

               10      20      30      40      50      60
m640.pep      MIHIISILKSIGISGIVMSCFSIKRMSAFRRARITAFFAAFVFLTAALPAYAERLPDFLAK
               |||||||
a640          MIHIISILKSIGISGIVMSCFSIKRMSAFRRARITAFFAAFVFLTAALPAYAERLPDFLAK
               10      20      30      40      50      60

               70      80      90      100     110     120
m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMVLAN
               |||||
a640          IQPSEIVPGA DRYSKPEGKP MVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMALAK
               70      80      90      100     110     120

               130      140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
               |||||||
a640          DGTIAGAKLVDHHEPIMLIGIPH
               130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2057>:

```

g642.seq
1  ATGCGGTATC CGCCGCAATC GCGGTTTTG CAGAATGCCG CGCGTTGCCT
51  TTTGCGCCGC CCGAAATCTG CCTGCCGCCG TATTGCCCCG CTATCCGCAA
101 TATCGGCAGT CCAATATATC TTTGCGGATG TCGTTCAGCA GGAAGGCTGT
151 GGTGTCTTCG TGTTCCTCCT GTACGAAGAC AAAAAGTCGG GCGATGATT
201 TGCCGATGAA GACTTTTTGC AGGCGCAGG CGTCGGTCAG GGTGTGTTC
251 TGCAGGAAGC TGCGGATGTC TTCGGGCAA GCGTAgTcgc gGGCAACGGC
301 GGcaaaagcg ACatcggtT GcacggcgTc gagCAGGgtt tggTTTTTGT
351 CCAACTTAAT GCCTGCTTCT TTTCTTCGG CGGTGGCGCG GACGAAGTGG
401 TCGTAAATTT CGGCATAAAG CATATCGTTC GGCCTTCAA AAATCGTGAA
451 GGGGCGGATA TCGATGGCGA TATTGCCGGC TGGGTGTCCG CGTTCAAAAC
501 CCTTCGCGCC CAAGAGTTTT TGCAACATT GCGCGCGGc qTAAGTGTAT
551 TCCGTGGCGa ggTTTTGAc gatgTTCGCC TCCATCAATT GATGGGCGAc
601 ggGCGgacg ggCGAAACGG AATGGCAGAC GTAGCGGTAA AGGATTTCCG
651 AAACCTGATG GCGGCGTTGG ATTCGCGGC GTTCGTAATC GACGAATCTG

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701 ATATCGTTGC GGACATATCG GTTCAGGTTG TCAACGATGT ATTCCATAAT
751 GCCGTCCGTC ATGCCGATCA GTTGCAGGCG GCTGCGGATA AAGATGTTTT
801 GGAACGCGCG CAAACCGGCA GCGTCGCCCC GGGAGAGTTT CATCACGGCG
851 GTTGCAGGCA TTTCGGCATC GATGCGGTTG ACGGCGTAAC GGACGGCGCG
901 CAGGCCTTCG GATGCGAGGG TTTCGACGCG GATGTATGTT TTGGGGACGA
951 GCAGCAGGTC GATGactttg gcgagtttgC Cgtttttgcg ctctttggcg
1001 gcaacgaggA GGAAGTCGCT TTGCGAATTG CCCTGCCAGT ATTTCGCGGC
1051 GttgACGTAA ATGGTTtgtt cgtcggataa ttcgtagcag gactgcaTTT
1101 CGCGTGCAAT cgCcgcgccg gaggtTtcgg gttcggtaAc gcccacacgg
1151 cggctttcgc cttTGAAAAT CATGTCCAAA CCTTGTGCGA CTTCGcttcc
1201 gccgcccgaac tCTTGACAGG GCTGCAACAC CAGCGCGCCT TCGATGCCGG
1251 TACGCAGCGT AACGGGCACG CCGTAATGCC CCGCAATCCT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2058; ORF 642.ng>:

```

g642.pep
1 MRYPPQSAVL QNAARCLLRE PKSACRRICP LSAISAVQYI FADVQQEUGC
51 GVVFVLLYED KKSDDDFADE DFLQGAGVGQ GVFLQEAADV FGQSVVAGNG
101 GKADIGLHGV EQGLVFVQLN ACFFFFGGGA DELVVNFGIK HIVRAFKNRE
151 GADIDGDIAG WVSFAFKTLRA QEFLQHLRGG VSVFRGEGFD DVLRLHQLMGD
201 GRDGRNGMAD VAVKDFGNLM AALDFAAFVI DESDIVADIS VQVVKDVFHN
251 AVRHADQLQA AADKDVLERA QTGSVAPGEF HHGGCRHFGI DAVDGVTDGA
301 QAFGCEGFAA DVCFGDEQQV DDFGEFAVFA LFGGNEEEVA LRALPVRFG
351 VDVNGLFVGE FVAGLHFACN RRAGGFGFGN AQTAFAFEN HVQTLCDLRF
401 AAELLQRLQH QRAFDAGTQR NGHAVMPRNP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2059>:

```

m642.seq (partial)
1 GCCTGCCGCC GTATTGCCCC GCTACCCGCA ATATCGGCAG TCCAATATAT
51 CTTTGGCGAT GTCGTTACAG AGGAAGGCTG CCGTGTCTTC GTGTTTCGCC
101 TGTACGAAGA CAAAGAGTCG GCGGATGATT TTGCCGATAA AGACTTTTGT
151 CAGGGCGCAG GCATC3GTCA GGGTGTGTTC CTGCAGGAAG CTGCGGATGT
201 CTTACGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAACCTCA TGCCTGCTTC
301 TTTTCTTCG CGCGTGGCGC GGACAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCCG CCGTGTGTCC GCGTTCAAAA CCCTTCGCAC CCAAGAGTTT
451 TTGCAACATT TGCGCGGCGG CGTAAGTGTA TTCCGTGGCG AGGGTTTTGA
501 CGATGTTCGC CTCCATCAGC TGATGGGCGA CGGGGGCAAC AGCGGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GCGGCGCGCG
601 GATTCGCGG CGTTCGTAAT CGACGAATTT GATGTCGTTG CGGACGTATC
651 GTTCCAGATT TTCAAGGATG TATTCCATAA TGCCGTGCGT CATGCCGATC
701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTCAGGC ATTTCGGCAT
801 CGATGCGGTT GACGCGTAA CGGACGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTCGCGG CGTTGACGTA AATGGTTTGT
1001 CCGTCGATAT ATTCGTAGTA GGACTGCATT TCGCGTGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGTTAA CACCCAAACC GCGGCCCTCG CCTTTGAAAA
1101 TCATCTCCAA ACCTTGCAGC ACTTGCCTT CATCGCGGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCGG GTACGCAGCG TAACGGGCAC
1201 CCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2060; ORF 642>:

```

m642.pep (partial)
1 ACRRICPLPA ISAVQYIFAC VVQEGCGVF VFRLYEDKES GDDFADKDFL
51 QGAGIGQGVF LQEAADVFRQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VSDIAGGVS AFKTLRTQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGGN RRNGMADVAV KNLGNLMAAP
201 DFAAFVIDEF DVVADVFSQI FKDVFNHNAV HADQLQAAAD KDVLERAQTG
251 SVALGEFHFG GCRHFGIDAV DGVTDGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFAVFALFG GNEEEVALRV ALPVFRGVDV NGLSVDIFV GLHFACNRRA
351 GGFGFGNTQT AALAFENHLQ TLRDLRFIAE LLQWLQHORA FDAGTQRNGH
401 AVMPRNP

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m642/g642 90.4% identity in 407 aa overlap

m642.pep		10	20	30	
		ACRRICPLPAISAVQYIFADVQQEGCGVFVRLYED			
g642	MRYPPQSAVLQNAARCLLRPKSACRRICPLSAISAVQYIFADVQQEGCGVFVLLYED	10	20	30	40
		50	60	70	80
m642.pep	KESGDDFADKDFLQGAGIGQGVFLQEAADVFRQSVVAGDGGKAGIGLQAVEQGLVVFVQLF	40	50	60	70
g642	KKSGDDFADEDFLQGAGVGQGVFLQEAADVFGQSVVAGNGGKADIGLHGVEQGLVVFVQLN	70	80	90	100
		110	120		
m642.pep	ACFFFFGGGADKLNVNFGIKHIVRAFKNREGADVDSIAGGVSAFKTLRTQEFLOHLRGG	100	110	120	130
g642	ACFFFFGGGADELNVNFGIKHIVRAFKNREGADIDGDIAGWVSAFKTLRAQEFLOHLRGG	130	140	150	160
		170	180		
m642.pep	VSVFRGEGFDDVRLHQLMGDGNRRNGMADVAVKNLGNLMAAPDFAAFVIDEFDVVADVS	160	170	180	190
g642	VSVFRGEGFDDVRLHQLMGDGRDGRNGMADVAVKDFGNLMAALDFAAFVIDESDIVADIS	190	200	210	220
		230	240		
m642.pep	FQIFKDVFNHVRHADQLQAAADKDVLERAQTSVALGEFHHGGCRHFGIDAVDGVTDGA	220	230	240	250
g642	VQVVKDVFNHVRHADQLQAAADKDVLERAQTSVAPGEFHHGGCRHFGIDAVDGVTDGA	250	260	270	280
		290	300		
m642.pep	QAFGCEGFAADVCFGDEQQVDDFGEFAVFALFGGNEEEVALRVALPVFRGVDVNGLSVDI	280	290	300	310
g642	QAFGCEGFAADVCFGDEQQVDDFGEFAVFALFGGNEEEVALRIALPVFRGVDVNGLFVGI	310	320	330	340
		350	360		
m642.pep	FVVGHLHFACNRRAGGFGFGNTQTAALAFENHLQTLRDLRFIAELLQWLQHQRAFDAGTQR	340	350	360	370
g642	FVAGLHFACNRRAGGFGFGNAQTAALAFENHVQTLCDLRFIAELLQRLQHQRAFDAGTQR	370	380	390	400
		410	420		
m642.pep	NGHAVMPRNP	400			
g642	NGHAVMPRNPX				
		430			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2061>:

a642.seq (partial)

```

1   GCCTGCCGCC GTATTTGCCG GCTATCCGCA ATATCGGCAG TCCAATATGT
51  CTTTGCCGAT GTCGTTCCAG AGGAAGGCTG CGGTGTCTTC GTGTTCCGCC
101 TGTACGAAGA CAAAGAGTCG GCGGATGATT TTGCCGATAA AGACTTTTGT
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTTC CTGCAGGAAG CTGCGGATGT
201 CTTGCGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAACCTCA TGCCTGCTTC
301 TTTTCTTCG GCGGTGGCGC GGACAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CGGTGTGTCC GCGTTCAAAA CCCTTCGCGC CCAAGAGTTT
451 TTGCAACATT TGCAGGCGG CGTAAGTGTA TTCCGTGGCG AGGGTTTTGA
501 CGATGTTCCG CTCCATCAGT TGATGGGCGA CGGGTGCAC GGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GGCGGCGCCG
601 GATTTCGCGG CGTTCGTAAT CGACGAATCT GATGTCGTTG CGGACGTATC
651 GTTCCAGGTT TTCAAGGGTG TATTCATAA TGCCGTGCGT CATGCCGATC

```

1020

```
701 AGTTGCAGGC GGCTGCCGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTCGAGGC ATTTCCGGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTCCGGC CGTTGACGTA AATGGTTTGT
1001 CCGTCGGTAT ATTCGTAGTA AGACTGCATT TCTCGGGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CGCCTAAACC GCCGCCCTCG CCTTTGAAAA
1101 CCATGTCCAA ACCCTGTGCG ATTTGCGCTT CATCGCCGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G
```

This corresponds to the amino acid sequence <SEQ ID 2062; ORF 642.a>:

```
a642.pep Length: 407
1 ACRRICPLSA ISAVQYVFAD VVQEGCGVF VFRLYEDKES GDDFADKDFL
51 QGAGIGQGVF LQEAADVFGQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VSDIAGGVS AFKTLRAQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGCN GRNGMADVAV KNLGNLMAAP
201 DFAAFVIDES DVVADVSFQV FKGVFHNAVR HADQLQAAAD KDVLERAQTG
251 SVALGEFHHG GCRHFGIDAV DGVTDGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFVAVFALFG GNEEEVALRV ALPVFRGVDV NGLSVGIFVV RLHFSGNRRR
351 GGFGFGNA*T AALAFENHVQ TLCDLRFIAE LLOWLQHORA FDAGTQRNGH
401 AVMPRNP
```

m642/a642 95.8% identity in 407 aa overlap

```
m642.pep      10      20      30      40      50      60
ACRRICPLSAISAVQYIFADVQVQEGCGVFVFRLYEDKESGDDFADKDFLQAGIGQGVF
|||||  |||||:|||||
a642          10      20      30      40      50      60
ACRRICPLSAISAVQYVFADVQVQEGCGVFVFRLYEDKESGDDFADKDFLQAGIGQGVF

m642.pep      70      80      90     100     110     120
LQEAADVFRQSVVAGDGGKAGIGLQAVEQGLVVFVQLHACFFFFGGGADKLVVNFGIKHIV
|||||  |||||:|||||
a642          70      80      90     100     110     120
LQEAADVFGQSVVAGDGGKAGIGLQAVEQGLVVFVQLHACFFFFGGGADKLVVNFGIKHIV

m642.pep     130     140     150     160     170     180
RAFKNREGADVDSIAGGVSAFKTLRTQEFLOHLRGGVSVFRGEGFDDVRLHQLMGDGGN
|||||  |||||:|||||
a642         130     140     150     160     170     180
RAFKNREGADVDSIAGGVSAFKTLRAQEFLOHLRGGVSVFRGEGFDDVRLHQLMGDGCN

m642.pep     190     200     210     220     230     240
RRNGMADVAVKNLGNLMAAPDFAAFVIDEFDVVADVVSFQIFKDVFNHNAVRHADQLQAAAD
|||||  |||||:|||||
a642         190     200     210     220     230     240
GRNGMADVAVKNLGNLMAAPDFAAFVIDESDVVADVVSFQVFKGVFNHNAVRHADQLQAAAD

m642.pep     250     260     270     280     290     300
KDVLERAQTG SVALGEFHHGGCRHFGIDAVDGVTDGAQAFGCEGFAADVCFGDEQQVDDF
|||||  |||||:|||||
a642         250     260     270     280     290     300
KDVLERAQTG SVALGEFHHGGCRHFGIDAVDGVTDGAQAFGCEGFAADVCFGDEQQVDDF

m642.pep     310     320     330     340     350     360
GEFAVFALFGGNEEEVALRVALPVFRGVDVNGLSVDIFVVGHLHFACNRRAGGFGFGNTQT
|||||  |||||:|||||
a642         310     320     330     340     350     360
GEFAVFALFGGNEEEVALRVALPVFRGVDVNGLSVGIFVVRHLHFSGNRRAGGFGFGNAXT

m642.pep     370     380     390     400
AALAFENHLQTLRDLRFIAELLQWLQHQRADFAGTQRNGHAVMPRNP
|||||  |||||:|||||
a642         370     380     390     400
AALAFENHVQTLCDLRFIAELLQWLQHQRADFAGTQRNGHAVMPRNP
```

1021

370 380 390 400

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2063>:

```
g643.seq
  1 ATGGTGTTC CTTGATGTT GTTGGCGACA ATCAGgTcgg CTACGCTGAc
  51 gttgtancGt TTGGcaATGt tGaaCAgggt gtcgccTTCT ACAACGCGGT
 101 GGATGCTGGC ATGGagcGGG GAGGTTTCGG CTTCGCCGTC GGCAGCTTTG
 151 GCTACGCGCG TTTCCAAACG TGCCCGCGT TtgCCGTCGG CGGCAACGGT
 201 ATGTTGCGGA GATGAGGAAA TGTGTGTTC GGCAACTGTG TCAGGCGTGC
 251 CGATGACGGC GGagaTGGTT TCTTCAGCCT GCCGGCGCag gTTGTTTCGG
 301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTGGGGGGAt
 351 GACCTGCGCg aGTGtTCCGG TTTGGGTTTC agacgGCATG GCACTCTGTT
 401 TTTcggTTTG a
```

This corresponds to the amino acid sequence <SEQ ID 2064; ORF 643>:

```
g643.pep
  1 MVLPLMLLAT IRSATLTLXR LAMLN RVSPS TTRWMLAWSG EVSASPSAAL
  51 ATRVSKRRRR LPSAA TVCCG DEEMLC SATV SGVPM TAEMV SSACRRRLFR
 101 ATSCMSSSAA CMSFGGMTCA SVAVW VSDGM AVCFSV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2065>:

```
m643.seq
  1 ATGGTGTTC CTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
  51 GTTG TAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
 101 GGATGCTGGC ATGGAGCGGG GAGATTTCGG CTTCGCCGTC GGCAGCTTTG
 151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAGCGGT
 201 ATGTTGCGGA GATGCGGAAA TTTGTGTTC GGCAACTGTG TCAGGCGTGC
 251 CGATGACGGC GGAGATGGTT TCTTCAGCCT GTCGGCGCAG GTTGTTCGG
 301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAT
 351 GATCTGCGCG AGTGTTCGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
 401 TTTCGGTTTG A
```

This corresponds to the amino acid sequence <SEQ ID 2066; ORF 643>:

```
m643.pep
  1 MVLPLMLLAT IRSATLTL*R LAMLN RVSPS TTRWMLAWSG EISASPSAAL
  51 ATRVSKRRRR LPSAA AVCCG DAEILC SATV SGVPM TAEMV SSACRRRLFR
 101 ATSCMSSSAA CMSFWGMICA SVAVW VSDGM AVCFSV*
```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 643 shows 94.9% identity over a 136 aa overlap with a predicted ORF (ORF643.a) from *N. gonorrhoeae*:

m643/g643

	10	20	30	40	50	60
m643.pep	MVLPLMLLAT	IRSATLTLXRL	LAMLN RVSPS	TTRWMLAWSG	EISASPSAAL	ATRVSKRRR
g643	MVLPLMLLAT	IRSATLTLXRL	LAMLN RVSPS	TTRWMLAWSG	EVSA SPSAAL	ATRVSKRRR
	10	20	30	40	50	60
	70	80	90	100	110	120
m643.pep	LPSAAAVCCG	DAEILCSATV	SGVPM TAEMV	SSACRRRLFR	ATSCMSSSAA	CMSFWGMICA
g643	LPSAA TVCCG	DEEMLC SATV	SGVPM TAEMV	SSACRRRLFR	ATSCMSSSAA	CMSFGGMTCA
	70	80	90	100	110	120
	130					
m643.pep	SVAVW VSDGM	AVCF SVX				
g643	SVAVW VSDGM	AVCF SVX				
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2067>:

1022

```

a643.seq
1   ATGGTGTTC CTTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
51  GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
101 GGATGCTGSC ATGGAGCGGG GAGATTCGG CTTGCGCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAACCGT
201 ATGTTGCGGA GATGAGGAAA TGTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC AGAGATGGTT TCTTCAGCCT GTCGGCGCAG GTTGTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAC
351 GATCTGCGCG AGTGTGCGG TTTGGGTTTC AGACGGCATG GCGTCTGTT
401 TTTGCGTTG A

```

This corresponds to the amino acid sequence <SEQ ID 2068; ORF 643.a>:

```

a643.pep
1   MVLPLMLLAT IRSATLTL*R LAMLN RVSPS TTRWMLAWSG EISASPSAAL
51  ATRVSKRTRR LPSAATVCCG DEEMLCSATV SGVPM TAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFWGTICA SVAVWVSDGM AVCFSV*

```

m643/a643 97.1% identity in 136 aa overlap

	10	20	30	40	50	60
m643.pep	MVLPLMLLATIRSATLTLXRLAMLN RVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
a643	MVLPLMLLATIRSATLTLXRLAMLN RVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m643.pep	LPSAAVCCGDAEILCSATVSGVPM TAEMVSSACRRRLFRATSCMSSSAA CMSFWGMICA					
a643	LPSAATVCCGDEEMLCSATVSGVPM TAEMVSSACRRRLFRATSCMSSSAA CMSFWGTICA					
	70	80	90	100	110	120
	130					
m643.pep	SVAVWVSDGM AVCFSVX					
a643	SVAVWVSDGM AVCFSVX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2069>:

```

g644.seq
1   ATGCCSTCTG AAAGGccgGC GGATTGTTGC CCGGTGCACT TTGTGGTAAA
51  GTTTAGAAAA TTAACCTAA ACTGTGGCAG GCGGTTTGAC CGGCCCGCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACCCGA ACCGAGCGCG
151 CAGCCGTCAG CCATGGACAC GGCTGCTTTT TTAAGcaca tgaatCCGC
201 ATTCCCCCGC ATTTTTCAG ACGGCATCGA CCTGATGCGA TACCTGCCCG
251 AAGACAAATG GCTTGCTTG AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
301 GACAAAAAAC ACGGCGGGCG CAAGGGCAGT CAGTTTGAAA TCCAAGAAGT
351 CCTAAGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
401 TCGAAGGCGC GCTGGTGTG CAGCCTCTGC AAGagttcgg cggcgaagcG
451 CAAGTCGCAC AAGGTTTGA CATGATTTTC AAaggcgaaa gccgcggtt
501 gggcgTtacc gaaccgaaAa cctccggcgc gGcgaTTGCA CGCGAAAtgc
551 agtctgcta cgaatatacc gacgaacaAA CCATTACGT caaCGCCGCG
601 AAATACTGGC AGGGCAATTC GCAAAGCGAC TTCCTcctcg ttgccgccaa
651 agagcgcaaa aacGGcaaac tcgccaagt CATCGACCTG CTGCTCGTCC
701 CCAAACATA CATCCGCTGC GAAACCTCG CATCGAAGG CCTGCGCGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
801 GATGAACTC TCCCGGGCGG ACGCTGCCGG TTTGCGCGCG TTTCAAACA
851 TCTTTATCCG CAGCCGCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACATCC TTGACAACT GAACCGATAT GTCCGCAACG ATATCAGATT
951 CGTCGATTAC GAACGCCCGG AATCCAACG CCGCCATCAG GTTTCCGAAA
1001 TCCTTTACCG CTACGCTGCG CATTCGTTT CGcccgctgc GCccgTCGCC
1051 CATCAATTGA TGGAGGCGAA catcgTCAAA AccctCGCCA CGGAATACAC
1101 TTAegcCGCC GCGCAATGT TGCAAAACT CTTGGGCGCG AAGGTTTGTG
1151 AACCGCGACA CCCAGCCGGC AATATCGCCA TCGATATCCG CCCCTTCACG
1201 ATCTTTTGAAG GCCCGAACGA TATGCTTTAT CCGCAAAATT ACGACCAATT
1251 CGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATTAAG TTGGACAAAA
1301 accaaACCCT Gctcgagccc gtgCAAcgg atGTCcgctt tgCCGCGGTT
1351 GCCcgGacT ACGCTTTGCC CGAAGACATC CGCAGTTCC TGCAGGAACA
1401 CACCCTGACC GACGCTGCG CCCTGCAAAA AGTCTTCATC GGCAAAATCA

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1023

1451 TCGCCCGACT TTTGTCTTC GTACAGGAGG AACACGAAGA CACCACAGCC
 1501 TTCTGTCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
 1551 ATAG

This corresponds to the amino acid sequence <SEQ ID 2070; ORF 644.ng>:

g644.pep
 1 MPSEPADCC PVHEVVKFRK LTLNCGRRFD RPPINGNRQR KPMIHTEPSA
 51 QPSTMDTAAF LKHIESAFPR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL
 101 DKKHGGGRKS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGEA
 151 QVAQGLDMIF KGESRRLGVT EPETSGAIA REMQSCYEY DEQTIYVNAA
 201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
 251 VRYAVNRIDA EMPATAVMKL SRGDAAGLRA FQNFIRSRL QLIGMTHGIM
 301 EYILDNLNRY VRNDIRFVDY ERREIQRHQ VSEILYRYVC HSVSPVAPVA
 351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHPAG NIAIDIRPFT
 401 IFEGPNOMLY AEIYDQFVRA TAEKEAGIK LDKNQTLLDA VQTDVRFPAV
 451 ARDYALPEDI RSFLQEHILT DACALQKVFI GKIIARLFVF VQEHEDTTA
 501 FLLNDIRKDI LDCRYCG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2071>:

m644.seq
 1 ATGCCGCTCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
 51 GTTTAGAAAA TCAACTCTAA ACTGTGGCAG CGGTTTGAC CGGCCGCCGA
 101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
 151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TTAAAGCACA TCGAATCCGC
 201 ATTCCGCGCG ATTTTTCAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
 251 AAGACAAATG GCTTGCCCTG AAGCAGCGCG GTTTGCTGTT GCCCTTCCTC
 301 GACAAAAAAT ACGGCGGGCG CAAGGGCAGC CAGTTTGAAA TCCAAGAAAT
 351 CcTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
 401 TCGAAGGCGC GCTGGTGTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
 451 CAAGTCGCGC AAGTTTGA GAATGATTTT AAAGGCGAGG GCGGCGGTTT
 501 GGGTGTACC GAACCCGAAA CCTCCGGCGC GCGGATTGCA CGCGAAATGC
 551 AGTCCTACTA CGAATATATC GACGGACAAA CCATTTACGT CAACGCCGCG
 601 AATACTGGC AGGGCAACTC GCAAAGCGAC TTCTCTCTCG TTGCGGCCAA
 651 AGAGCGCAAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
 701 CCCAAACATA CATCCGCTGC GAAACCTCG CATCCGAAGG CTGCGCGCG
 751 CTCGCTTACG CCGTCAACCG CATCGATGCC GAAATGCTG CAACCGCGCT
 801 GATGAAATCT TCCCAGAGCG ACGCTGCCCG TTGCGCGCG TTCCAAAACA
 851 TCTTTATCCG CAGCCGCGCT CAACTGATCG GCATGACGCA CGGCATTATG
 901 GAATACATCC TTGAAAATCT GGAACGATAC GTCCGCAACG ACATCAAAT
 951 GTCTCGATTAC GAACGCCGCG AAATCCGCGC CCGCATCAG GTTTCGAGA
 1001 TTCTTTACCG CTACGTCTGC CATTCCGTTT CGCCTGTTGC CCCCGTCGCC
 1051 CATCAGCTGA TGGAGGCGAA CATCGTCAA ACCCTCGCCA CGGAATACAC
 1101 TTACGCGCGC GCGCAATGT TGCAAAACT CTGGGTGCG AAGGGTTTGT
 1151 AACGCGGACA CACCGCCGCG AATATCGCTA TCGACATCCG CCCCTTCACG
 1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACAGTT
 1251 TGTCGCGCGC ACCGCGGAG AAAAAGAAG AGGCATGAAG TTGGACAAAA
 1301 ACCAAACCTT GCTCGACCGC CTGCAAACCG ATGCCCGCTT TGCCGCGCTC
 1351 GCCCGGACT ACACCTTGCC TGAAGACATC CGCAGCTTCC TGCAGGAACA
 1401 CACCTGACG GATGCTGCG CCCTGCAAAA AGTCTTTAT GGCAAAATCA
 1451 TCGCCCGACT CTTGTCTTC GTACAGGCGA AACACGAAGA CACCGCAGCC
 1501 TTCTGTCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
 1551 STAG

This corresponds to the amino acid sequence <SEQ ID 2072; ORF 644>:

m644.pep
 1 MPSEPADCC PAHEVVKFRK STLNCGRRFD RPPINGNRQR KPMIHTEPSA
 51 QPSTMDTAAF LKHIESAFRR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL
 101 DKKYGGGRKS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGEA
 151 QVAQGLEMIF KEGGGGLGVT EPETSGAIA REMQSYEYI DGOTIYVNAA
 201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
 251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNFIRSRL QLIGMTHGIM
 301 EYILENLERY VRNDIKFVDY ERREIRRHQ VSEILYRYVC HSVSPVAPVA
 351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
 401 IFEGPNOMLY AEIYDQFVRA TAEKEAGMK LDKNQTLLDR LQTDARFAAV
 451 ARDYTLPEDI RSFLQEHILT DACALQKVFI GKIIARLFVF VQAKHEDTAA
 501 FLLNDIRKDI LDCRYCG*

m644/g644 94.6% identity in 517 aa overlap

	10	20	30	40	50	60
m644.pep	MPSEPADCCPAHEVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQFSTMDTAAF					
g644	MPSEPADCCPVHEVVKFRKLTNCGRRFDRPPINGNRQRKPMIHTEPSAQFSTMDTAAF					

1024

	10	20	30	40	50	60
m644 . pep	70	80	90	100	110	120
	LKHIESAFRRIFSDGIDLRYLPEDKWLALKQAGLLPFLDKKYGGKSGQFEIQEVLRI					
g644	LKHIESAFRRIFSDGIDLRYLPEDKWLALKQAGLLPFLDKKHGGKSGQFEIQEVLRI					
	70	80	90	100	110	120
m644 . pep	130	140	150	160	170	180
	AGHYGVPTLRTGIEGALVLQPLQEFGEAQAQGLEMIKFGEGGGLGVTEPETSGAAIA					
g644	AGHYGVPTLRTGIEGALVLQPLQEFGEAQAQGLDMIFKGESRRLGVTEPETSGAAIA					
	130	140	150	160	170	180
m644 . pep	190	200	210	220	230	240
	REMQSYEYIDGQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
g644	REMQSCYEYTDGQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
	190	200	210	220	230	240
m644 . pep	250	260	270	280	290	300
	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI F I R S R L Q L I G M T H G I M					
g644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSRGDAAGLRAFQNI F I R S R L Q L I G M T H G I M					
	250	260	270	280	290	300
m644 . pep	310	320	330	340	350	360
	EYILENLERYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLM E A N I V K					
g644	EYILDNLNRYVRNDIRFVDYERREIQRRHQVSEILYRYVCHSVSPVAPVAHQLM E A N I V K					
	310	320	330	340	350	360
m644 . pep	370	380	390	400	410	420
	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
g644	TLATEYTYAAAQMLQKLLGAKGFERGHPAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
m644 . pep	430	440	450	460	470	480
	TAEKEAGMKLDKNQTL DRLQTDARFAAVARDYTL PEDIRSFLQEH T L T D A C A L Q K V F I					
g644	TAEKEAGIKLDKNQTL DAVQTDVRF A A V A R D Y A L P E D I R S F L Q E H T L T D A C A L Q K V F I					
	430	440	450	460	470	480
m644 . pep	490	500	510			
	GKIIARLFVVFQAKHEDTAAFLNDIRK D I L D C R Y C G X					
g644	GKIIARLFVVFQEEHEDTAAFLNDIRK D I L D C R Y C G X					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2073>:

```

a644 . seq
1  ATGCCGTC TG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
51  GTTTAGAAAA TCAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TTAAAGCACA TCGAATCCGC
201 ATTCCGCCGC ATTTTTCGAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
251 AAGACAAATG GCTTGCCCTTG AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
301 GACAAAAAAT ACGGCCGGCG CAAGGCAGC CAGTTTGAAA TTCAGGAAGT
351 CTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTANNNNN NNNNNNNNNN
401 NNGAAGGCGC GCTGGTGTTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
451 CAAATCGCAC AGGGTTTGGA CATGGTTTTC AAAGGCGAGG GCGGCGGTTT
501 AGCGGTTACC GAACCCGAAA CCTCCGCGC GCGGATGCCC CGAGAAATGC
551 AGTCTTACTA CGAATATACC GACGGACAAA CCATTACGT CAACGCCGCG
601 AAATACTGGC AGGGCAATC GCAAAGCGAC TTCCTCTCG TTGCCGCCAA
651 AGAGCGCAAA AACGGCAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCTCG CATCCGAAGG CTTGCGGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
801 GATGAACTC TCCAGAGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA

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1025

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851 TCTTTATCCG CAGCCGCCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACACCC TTGAAAACCT GGAACGATAC GTCCGCAACG ACATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCGCGC CGGCCATCAG GTTCCGAGA
1001 TTCTTTACCG CTACGTCTGC CATTCGGTTT CGCCCGTTGC ACCCGTCGCC
1051 CATCAACTGA TGGAGGCGAA CATCGTCAAA ACCCTCGCCA CGGAATACAC
1101 TTACGCCGCC GCGCAAATGT TGCAAAACT CTGGGCGCG AAGGGTTTGT
1151 AACGCCGACA CACCGCCGGC AATATCGCTA TCGACATCCG CCCCTTCACG
1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATT ACGACCACTT
1251 TGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
1301 ACCAAACCTT GCTCGACCGC CTGCAAACCG ATGCCCGCTT TGCCGCCGTC
1351 GCCCCGCGCT ACACCTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCTGACC GATGCCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
1451 TCGCCCGACT CTTTGTCTTC GTACAGGCGG AACACGAAGA CACCGCAGCC
1501 TTCCTGCTGA ACGACATCCG CAAAGACATA TTGGACTGCC GATATTGCGG
1551 ATAG

```

This corresponds to the amino acid sequence <SEQ ID 2074; ORF 644.a>:

```

a644.pep
1  MPSERSADCC PAHFVVKFRK STLNCGRRFDRPPINGNRQRKPMIHTEPSA
51  QPSTMDTAAF LKHIESAFRR IFADGIDLMR YLPEDKWLAL KQAGLLLPFL
101 DKKYGGKSGS QFEIQEVLRI AGHYGVPVXX XXXXEGALVL QPLQEFGEA
151 QIAQGLDMVF KEGGGLGVT EPETSGAAIA REMQSYEYTG DGTIYVNA
201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNI FIRSRL QLIGMTHGIM
301 EYTLENLERY VRNDIRFVDY ERREIRRRHQ VSEILYRYVC HSVSPVAPVA
351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHGTA NIAIDIRPFT
401 IFEGPNDMLY AEIYDQFVRA TAEKEAGMK LDKNQTLDDR LQTDARFAAV
451 ARDYTLPEDI RSFLQEHILT DACALQKVFI GKIIARLFVF VQAEHEDTAA
501 FLLNDIRKDI LDCRYCG*

```

m644/a644 97.3% identity in 517 aa overlap

	10	20	30	40	50	60
m644.pep	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
a644	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
	10	20	30	40	50	60
m644.pep	70	80	90	100	110	120
a644	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGKSGSQFEIQEVLRI					
	70	80	90	100	110	120
m644.pep	130	140	150	160	170	180
a644	AGHYGVPVTLRTGIEGALVLQPLQEFGEAQVAQGLEMIFKGEGLGVTEPETSGAAIA					
	130	140	150	160	170	180
m644.pep	190	200	210	220	230	240
a644	REMQSYEYIDGQTIYVNAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
	190	200	210	220	230	240
m644.pep	250	260	270	280	290	300
a644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM					
	250	260	270	280	290	300
m644.pep	310	320	330	340	350	360
a644	EYILENLERIVRNDIRFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK					

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	310	320	330	340	350	360
	370	380	390	400	410	420
m644 . pep	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
a644	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m644 . pep	TAEKEAGMKLDKNQTLTDLRLQTDARFAAVARDYTLPEDIRSFLEHTLTDACALQKVFI					
a644	TAEKEAGMKLDKNQTLTDLRLQTDARFAAVARDYTLPEDIRSFLEHTLTDACALQKVFI					
	430	440	450	460	470	480
	490	500	510			
m644 . pep	GKIIARLFVQAKHEDTAAFLNDIRKDILDCRYCGX					
a644	GKIIARLFVQAEHEDTAAFLNDIRKDILDCRYCGX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2075>:

```

g645 . seq
1  ATGATGATGG TGTGGCGT GGGGATGTCG ATGCCGGTT CGATGATGGT
51  GGAACAGAGC AACACATGA ATCTTTGCTG CAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCAGC AGTTSTCCG? GCGCCACGCC GATACGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTCTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAaTa cCTGTCTCC GCGTTTGAGT TCGCGCAACA
251 CCGCTTCGCG CACGCTGCCT TCGCTGAACG GTTGACAAA GGTTTCACG
301 GCGAGGCGGC GGCTCGGTGC AGTGGTAATC AGCGAGAAGT CGCGCAGACC
351 TTCGAGCGCC ATGCTGAGGG TCGCGGGAAT CGCGTGGCG GTCATGGTTA
401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTT CTGTCGCACG
451 CCGAAGCGGT GTTCTTCATC GATAATCAAT AAACCTAAGT TTTTGAATTT
501 TATGTCGTCC TGCACCAATT TGTGCGTACC GATAACGATA TCGACAGTAC
551 CSTCCGCCAT GCCTTCGAGC GTGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CCGGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAAC GGTGCGCGAA
651 GTTTTGC GCGTGTCTCGA CCAGAAGCGT GGTGCGGCG AGTACGGCGA
701 CCTGTTTGCC GCCCATCACC GCCACAAACG CGGCGCGAAG GCGGACTTCG
751 GTTTTGCCGA AACCAGATC GCCGCACACA AGTCGGTCCA TCGGCTTCGC
801 CTGCGTCAAA TCTTTAATCA CGGcgcgat ggcggcgcc TGGTCTTCGG
851 TTTCTCTGTA G

```

This corresponds to the amino acid sequence <SEQ ID 2076; ORF 645.ng>:

```

g645 . pep
1  MMMVLALGMS MPVSMMEQ S NTLNLCKKS RMTCSSRSR SCPCATPIRA
51  SGRVSSRSR IFSIVSTSLC RNTCPPLRS SRNTASRTLP SLNGLTKVFT
101 ARRLGAVVI SEKSRPSSA MLRVRGIVA VMVRMSTLAR RRLSCSFCRT
151 EKRCSSSIIN KPKFLNFMSS CTNLCVPITI STVPSAMPSS VALVALLLLK
201 RERLATFTGK SAKRSKAFCA CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT SRSIGFACVK SLITAAMAAA WSSVSS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2077>:

```

m645 . seq
1  ATGATGATGG TGTGGCGT GGGGATATCG ATACCGGTT CGATGATGGT
51  GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCAGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTTTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAATA CCGTCTCTCC GCGTTTGAGT TCGCGCAACA
251 CCGCTTCGCG CACGCTGCCT TCGCTAAAGG GTTGACAAA GGTTTGACG
301 GCGAGGCGGC GGCTGGGCGC GGTGGTAATC AGCGAGAAGT CGCGCAGTCC
351 TCCAACGCC ATACTTAAAG TACGCGGAAT CGGCGTGGCG GTCATGGTTA
401 GGATATCAAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTT CTGACGCACG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTAAGT TTTTGAATTT
501 GATGTCGTCC TGCACCAATT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCTGCCAT GCCTTCAGC GCGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAAC GGTGCGCGAA
651 GTTTTGC GCGTGTCTCGA CCAAAAGCGT GGTGCGGAGCA AGTACGGCGA
701 CCTGTTTGCC GCCCATCACC GCCACAAACG CGGCGCGCAG GCGGACTTCG
751 GTTTTGCCGA AGCCGACATC GCCGCACACA AGCGGATCCA TCGGCTTCGC
801 TTGCGTCAAA TCTTTAATCA CGGCGGCGAT GCGGCGGCC TGGTCTTCGG

```

1027

851 TTTCCTCGTA G

This corresponds to the amino acid sequence <SEQ ID 2078; ORF 645>:

m645.pep
 1 MMVLALGIS IPVSMVVEQS NTLNRCCKKS RMTCSSSRSR SCPCATPMRA
 51 SGSRVSSRSR IFSIVSTSLC RKNTCPPLRS SRNTASRTLP SLKGLTKVLT
 101 ARRLGAVVI SEKSRSPSNA ILKVRGIGVA VMVRISTLAR RRLSCSF*RT
 151 PKRCSSSIIT KPKFLNLMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
 201 RERLATFTCK SAKRSKAFCA CCSTKSVVGA STATCLPPIT ATNAARRATS
 251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

m645/g645 93.7% identity in 286 aa overlap

	10	20	30	40	50	60
m645.pep	MMVLALGISIPVSMVVEQSNTLNRCCKKS	RMTCSSSRSR	SCPCATPMRA	SGSRVSSRSR		
g645	MMVLALGMSIPVSMVVEQSNTLNRCCKKS	RMTCSSSRSR	SCPCATPMRA	SGSRVSSRSR		
	70	80	90	100	110	120
m645.pep	IFSIVSTSLCRKNTCPPLRSSRNTASRTLP	SLKGLTKVLTARRRLGAVVISEKSRSPSNA				
g645	IFSIVSTSLCRKNTCPPLRSSRNTASRTLP	SLKGLTKVLTARRRLGAVVISEKSRSPSNA				
	130	140	150	160	170	180
m645.pep	ILKVRGIGVAVMVRISTLARRRLSCSF	XRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI				
g645	MLRVRGIGVAVMVRISTLARRRLSCSF	XRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI				
	190	200	210	220	230	240
m645.pep	STVPSAMPSSAALVALLLLKRERLATFTGKS	SAKRSKAFCAACCSTKSVVGASTATCLPPIT				
g645	STVPSAMPSSAALVALLLLKRERLATFTGKS	SAKRSKAFCAACCSTKSVVGASTATCLPPIT				
	250	260	270	280		
m645.pep	ATNAARRATSVLPKPTSPHTRRSIGFACVK	SLITAAMAAWSSVSSX				
g645	ATNAARRATSVLPKPTSPHTRRSIGFACVK	SLITAAMAAWSSVSSX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2079>:

a645.seq
 1 ATGATGATGG TGTGGCGTT GGAATGTCG ATACCGGTTT CGATGATGGT
 51 GGAACAGAGC AACACGTAA ATCGTTGCTG CAAAAAGTCG CGCATGACTT
 101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
 151 TCGGGCAGCA GGGTTTCCAG CCGCTCAGC ATGTTTTCGA TGGTATCCAC
 201 TTCATTGTGC AGGAAAAATA CTGCCC GCCGTTTGAGT TCGCGCAATA
 251 CGGCTTCGCG CACGCTGCCT TCGTGAACG GTTTGACAAA GGTTTTGACG
 301 GCGAGGCGCG GGCTGGGCGC AGTGGTAATC AGCGAGAAGT CGCGCAGTCC
 351 TTCCAGCGCC ATACTTAAAG TACGCGGAAT CGGCGTAGCG GTCATGGTAA
 401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGCACG
 451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTACGT TTTTGAATTT
 501 TATGTCTGTC TGCACCAATT TGTGCGTACC GATAACAATA TCGACCGTGC
 551 CGTCCGCCAT GCCTTCCAGC GCGGCTTTGG TGGCTTTGCT GTTGTGAAA
 601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGCGCAAGC GGTGCGCAAA
 651 ATTTTGCGCG TGCTGCTCGA CCAGAAGCGT GGTGCGTGCG AGTACGGCAA
 701 CTTGTTTGCC ACCATTACC GCCACAAACG CGGCGCGCAG GCGCACTTCG
 751 GTTTTGCCGA AACCGACATC GCCGCACACG AGGCGTCCA TCGGCTTCGC
 801 CTGCGTCAA TCTTAATCA CGGCGCGGAT GCGGCTGCC TGGTCTTCGG
 851 TTCTTCGTA G

This corresponds to the amino acid sequence <SEQ ID 2080; ORF 645.a>:

a645.pep
 1 MMVLALGMS IPVSMVVEQS NTLNRCCKKS RMTCSSSRSR SCPCATPMRA

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```

51  SGRVSSRSR MFSMVSTSLC RKNTCPPLRS SRNTASRTLPL SLNGLTKVLT
101 ARRRLGAVVI SEKSRSPSSA ILKVRGIGVA VMVRMSTLAR RRLSCSF*RT
151 PKRCSSSIIT KPTFLNFMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
201 RERLATFTGK SAKRSAKFCA CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

```

m645/a645 96.9% identity in 286 aa overlap

```

m645.pep      10      20      30      40      50      60
MMMVLALGISIPVSMVVEQSNTLNRCCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645          10      20      30      40      50      60
MMMVLALGMSIPVSMVVEQSNTLNRCCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR

m645.pep      70      80      90     100     110     120
IFSIVSTSLCRKNICPPRLSSRNTASRTLPSLKGKLTAVLTARRRLGAVVISEKSRSPSNA
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a645          70      80      90     100     110     120
MFSMVSTSLCRKNICPPRLSSRNTASRTLPSLKGKLTAVLTARRRLGAVVISEKSRSPSSA

m645.pep     130     140     150     160     170     180
ILKVRGIGVAVMVRISTLARRLSCSFXRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645         130     140     150     160     170     180
ILKVRGIGVAVMVRMSTLARRLSCSFXRTPKRCSSSIITKPTFLNFMSSCTSLCVPITI

m645.pep     190     200     210     220     230     240
STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSKFCACCSTKSVVGASTATCLPPIT
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645         190     200     210     220     230     240
STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSKFCACCSTRSVVGASTATCLPPIT

m645.pep     250     260     270     280
ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645         250     260     270     280
ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2081>:

g647.seq

```

1  ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAGGTGTCGA
51  TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGACGCT
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAGTAGGCGT AGTTGATGAC ACCGATGCCG
251 AGCGAACGGC GGTCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence <SEQ ID 2082; ORF 647.ng>:

g647.pep

```

1  MQRLAADGIQ IFFVGVGQF ALRINGLVKE RARSVFFGKV CRCFEQVILY
51  GFKGTVGQTE RGTVAADTV FRQIVGVDD TDAERTAVHS RGRGFYRIS
101 LII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2083>:

m647.seq

```

1  ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAAGTGTGCA
51  TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGACGCA
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAATAAGCAT AGTTAATCAC GCCGATGCCG
251 AGCGAACGGC GGCCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence <SEQ ID 2084; ORF 647>:

m647.pep

```

1  MQRLAADGIQ IFFVSDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY

```

1029

51 GFKGTVGQTE RGTAVADTV FRQIISIVNH ADAERTAHS RGRGFYRIS
101 LII*

m647/g647 91.3% identity in 103 aa overlap

	10	20	30	40	50	60
m647.pep	MQR	LAADGIQIFFVSV	DGQFALRINGLV	KERARTVFFGK	VCRCFEQVILY	GFKGTVGQTE
g647	MQR	LAADGIQIFFVSV	DGQFALRINGLV	KERARSVFFGK	VCRCFEQVILY	GFKGTVGQTE
	10	20	30	40	50	60

	70	80	90	100	
m647.pep	RGT	VAVADTVFRQIIS	IVNHADAERTA	HSRGRGFYRIS	LIIX
g647	RGT	VAVADTVFRQIV	GVDDTAERTAV	HSRGRGFYRIS	LIIX
	70	80	90	100	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2085>:

a647.seq
1 GTGCAAAGGC TCGTTACACA CAGCGTCCAA GTCTTTTTTG TAGGTGTCGA
51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCA
101 CCGTATCTTT TGGCAAAGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAGCCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAAA TAATACGCAT AGTTGATCAC GCCGATACCG
251 AGCGAACGGC GGCCCATAGT GGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

This corresponds to the amino acid sequence <SEQ ID 2086; ORF 647.a>:

a647.pep
1 VQRLVTHSVQ VFFVGVGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY
51 GFKGTVGQTE RGAVAVADTV FRQIIRIVDH ADTERTAHS GGTRGFYRIS
101 LII*

m647/a647 87.4% identity in 103 aa overlap

	10	20	30	40	50	60
m647.pep	MQR	LAADGIQIFFVSV	DGQFALRINGLV	KERARTVFFGK	VCRCFEQVILY	GFKGTVGQTE
a647	VQR	LVTHSVQVFFV	GVGQFALRING	LVKERARTVFF	GKVCRCFEQV	ILYGFKGTVGQTE
	10	20	30	40	50	60

	70	80	90	100	
m647.pep	RGT	VAVADTVFRQIIS	IVNHADAERTA	HSRGRGFYRIS	LIIX
a647	RG	AVAVADTVFRQI	IRIVDHADTERT	AAHSGGTRGFY	RISLIIX
	70	80	90	100	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2087>:

g648.seq
1 ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51 CGACGTTTTG AATGTAGATG CGCCCGGTCC CGGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCGGCAGC CGGAATGATA CGCTTGCGTA TGTTCCGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAACCCCGAA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATTG GCACGCCATA
301 ATCAAGCTGG CGGATACGGT TGTCTCCAC GCCCCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCA ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCGCG GCACGCCACC TTGCGAACAA GATTGACCG CCGCTGAAA
451 CATCTTAAAG AAGGGAATGC AGCCGGTATG CCGGGCTTCA CCGCCCCGGA
501 TTTCGCTGTC CAGCCCGCGG ATACGTCCGG CATTGATGCC GATGCCCGCG
551 CGTTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCAT TGATGGAATC
601 CAAACTATCG TCGATTCAA TCAGCACACA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2088; ORF 648.ng>:

g648.pep

1030

```

1  MNRRNARIER AVRIAVIDVL NVDAFPGTGL LHQRGKQVGS RNDTLAYVRV
51  LLVFRIEPLK FVLVGKKRFV QPRNLVGRKQ RNVAALNQAG VQQAVIDLHAI
101 IKLADTVVFH APVVFOHQQA FGFNMPQGV E QGCRAAAHAT LRTRFDRRLK
151 HKEGNAAGM PGFTAPDFAV QPADTSGIDA DARALGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2089>:

```

m648.seq
1  ATGAACAGGC GCGACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTTG AATGTAGATG CGCCCGGTTT CCGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCCGCAGC CGAATGATG CGCTTCCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCGGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATTT GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTTCCAC ACCGCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCCGC GCACGCCGCC TTGCGAACAG GATTGACCG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGCGCTTCG CCGCCCGGA
501 TTTCGCTGTC CAAACCGCGG ATACGTCCGG CATTGATGCC GATGCCCGCA
551 CGCTGGGAAA CGTATTTAC AATCGCGCTG GTAGTGGCAT TGATGGAATC
601 CAAACTATCG TCGATTCAA TCAGCACACA GCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2090; ORF 648>:

```

m648.pep
1  MNRRDARIER AVRIAVIDVL NVDAFPGSGL LHQRGKQVGS RNDALADIRV
51  LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVIDLHAV
101 IKLDTTVVFH TAVVFOHQQA FGFDMPOGVE QGCRAAAHAA LRTRFDRRLK
151 HFKEGNAAGM PRFAAPDFAV QTADTSGIDA DARTLGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

m648/g648 91.5% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDAFPGSGLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
g648	MNRRNARIERAVRIAVIDVLNVDAFPGTLLHQRGKQVGSRNDTLAYVRVLLVFRIEPLK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVIDLHAVIKLDTTVVFHTAVVFOHQQA					
g648	FVLVGKKRFVQPRNLVGRKQRNVAALNQAGVQQAVIDLHAIKLDADTVVFHAPVVFOHQQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m648.pep	FGFDMPOGVEQGCRAAAHAAALRTGFDRLKHKEGNAAGMPRFAAPDFAVQTADTSGIDA					
g648	FGFNMPQGVQGCRAAAHATLRTRFDRRLKHLKEGNAAGMPGFTAPDFAVQPADTSGIDA					
	130	140	150	160	170	180
	190	200	210			
m648.pep	DARTLGNVFHNRAAGSGIDGIQTIVAFNQHTAX					
g648	DARALGNVFHNRAAGSGIDGIQTIVAFNQHTAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2091>:

```

a648.seq
1  ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTTG AATGTAGATG CGCCCGGTTT CCGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCCGCAGC CGAATGATG CGCTTCCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCGGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATTT GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTTCCAC GCCCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCCGC GCACGCCACC TTGCGAACAG GATTTGACTG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGTGTCTTCG CCGCCCGGA

```

1031

```

501 TTTCGCTGTC CAGTCCGCGG ATACGTCCGG CATTGATGCC GATGCCCGCA
551 CGCTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCGT TGATGGAATC
601 CAGGCTGTCG TCGCATTCTGA TCAATACGCA GCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2092; ORF 648.a>:

```

a648.pep
1  MNRRNARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
51  LLVFRIEPLK FVLVGKKRFV QSRNLVGRKO RNVAALNQAG VQQAVIDLHAV
101 IKLTDTVVFH APVVFQHQQA FGFDMPQGV EGCRAAAHAT LRTGDCRLK
151 HFKEGNAAGM PCFAAPDFAV QSADTSGIDA DARTLGNVFH NRAGSGVDGI
201 QAVVAFDQYA A*

```

m648/a648 93.8% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGS	RNDALADIRVLLVFRIEPLK				
a648	:					
	10	20	30	40	50	60
m648.pep	FVLVGKKRFVQSRNLVGRKQNRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHTAVVFQHQQA					
a648	:	FVLVGKKRFVQSRNLVGRKQNRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHAPVVFQHQQA				
	70	80	90	100	110	120
m648.pep	FGFDMPQGVQGCRAAAHAALRTGCDRLKHFKEGNAAGMPRFAAPDFAVQTADTSGIDA					
a648	:	FGFDMPQGVQGCRAAAHATLRTGDCRLKHFKEGNAAGMPRFAAPDFAVQSADTSGIDA				
	130	140	150	160	170	180
m648.pep	DARTLGNVFHNRAAGSGIDGIQTIVAFNQHTAX					
a648	: : :	DARTLGNVFHNRAAGSGVDGIQAVVAFDQYAA				
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2093>:

```

g649.seq
1  ATGCTTGCCA TACTGTTGTC TGCAATACTG GGACTGGTAT CAACAACGTC
51  CGCTGCCGGT ACGTCAGAAC CCGCCCACCG ACATACCAAA CATATCAGCA
101 AGGCAAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTGGAACGC
151 CGTGCCCGCT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC CGCGAAAA
201 CAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATGCG GAACAGAAAA
251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGCGCGCAGG
301 TTCCGCCGTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2094; ORF 649.ng>:

```

g649.pep
1  MLAILLSAIL GLVSTTAAAG TSEPAHRHTK HISKANKQML HPECRKYLER
51  RAAWYRSQGN VQELRENKKA RKAFTLPYA EQKIQCRAY EAFDDFDGGR
101 FRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2095>:

```

m649.seq
1  ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACGTC
51  CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAAA CATATCCGCA
101 AGGCAAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTGGAACGC
151 CGTGCCCGCT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC CGCGAAAA
201 CAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATGCG GAACAGAAAA
251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGCGCGCAGT
301 TTCCGCCGTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2096; ORF 649>:

m649.pep

1032

```

1  MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
51 RAAWYRSQGN VQELRENKKA RKAFRSLPYA EQTIQCRAAY EAFDDFDGGS
101 FRR*

```

m649/g649 96.1% identity in 103 aa overlap

```

              10      20      30      40      50      60
m649.pep      MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              |||||
g649           MLAILLSAILGLVSTTAAAGTSEPAHRHTKHISKANKQMLHPECRKYLERAAWYRSQGN
              10      20      30      40      50      60

              70      80      90      100
m649.pep      VQELRENKKA RKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX
              |||||
g649           VQELRENKKA RKAFTLPYAEQKIQCRAAYEAFDDFDGGRFRRX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2097>:

```

a649.seq
1  ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACTGC
51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAAA CATATCCGCA
101 AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTGGAACGC
151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC GCGAAAA
201 CAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATAAG GAACAGAAAA
251 CCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCAGCAGG
301 TTCCGCCGTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2098; ORF 649.a>:

```

a649.pep
1  MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
51 RAAWYRSQGN VQELRENKKA RKAFRSLPYK EQTQCRAAY EAFDDFDGSR
101 FRR*

```

m649/a649 96.1% identity in 103 aa overlap

```

              10      20      30      40      50      60
m649.pep      MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              |||||
a649           MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              10      20      30      40      50      60

              70      80      90      100
m649.pep      VQELRENKKA RKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX
              |||||
a649           VQELRENKKA RKAFTLPYKEQKIQCRAAYEAFDDFDGSRFRRX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2099>:

```

g650.seq
1  ATGTCCAAAC TCAAAACCAT CGCCCTGACC GCATCAGGTC TGTCCGTTTG
51 TCCGGGTTTC CTATATGCCC AAAACACCTC ATCACACCAA GTCGGTTTAG
101 CGATTATGCG GTTAAACTCT TCAATACTCG ACCTGCCACC GACAAACAA
151 TATTTCGAAT CCGGCAGCCT GTGGGACGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAGGCCGCGC CTATTTCGAC AGGGTCGTCA ACCGGAGCCG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCCGC
351 CCGCTTCCC TTATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGCTACCGG CAGGCATTAC
451 CGCTTGGAAA AAACaccgGT TTACGacggc aggcacGacg TTtacqcaGc
501 taccgatgcc gcacTCAACT AtctGcAATA TCTCTatgga CTGTTCCGCG
551 ACTGGCCGCT CGCCTTGGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCCTCA ACCGCGCCCG CGACCAAGGG CTCGAACCGA CCTACGAAAA
651 CCGCGTATG CCCAACGAAA CGCGCAACTA TGTCCCAAG CTGCTCGCCG
701 TCGCAACAT TATTGCCACC CCCCAATCTT TCGGCATGAA TATCAGCGAC

```

1033

```

751 ATAGACAACA AACCCATTTT TCAGGCAGTC GAACCGGGCC GTCCGCTCGA
801 caacGAagcC ATCGCCCCGC TTGCCGGCAT CACGCAAAAGC GAGCTGCTCG
851 CCTCGAATCC TGCATTCAAC GTCCCGCGt tcatCCCCAA AAACaaacgc
901 aaactGCTGC TTCCTGTGCG GTCCGTCCAA ACCTTccaaa gcaACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAAC GCCTCAACAA CCTGAACGGC AACCTTGTCa ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAGAC CCTTCATACG GCATCGGAaT
1151 ccGTCGTTTC CATCGACATC GACAATACGC CcgacacCTa ccgttccaaT
1201 ATGcCggcag gcaCGGTGAA CGTCAGCATt gccCgaatcc aacCCgccgc
1251 cgcaCAGACA gcggaatta ccgtcgacc tttgccgcaa gaaaccgtcc
1301 gtacgggaac ccgatccctt tgtccgcaTt accgaaccgc ccttTGGGAC
1351 AGCCGACAGC CaacctCAAA ccgAAAAACA GACTGCCATG CcgtctGA

```

This corresponds to the amino acid sequence <SEQ ID 2100; ORF 650.ng>:

```

g650 .pep
1  MSKLKTIALT ASGLSVCPGF LYAQTSSHQ VGLAIMRLNS SILOLPPTKQ
51  YFQSGSLWGE LRQGRMGEV NPFLVRRHES KFIASRSYFD RVVNRSRPYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWEGNVG
201 RAVNFARDQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPFYQAV EPGRPLDNEA IARLAGITQS ELLALNPAPN VPAFIPKNKR
301 KLLLPPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DTKRLNNLNG NLVNAGRSIL VAKNGKTLHT ASESVVSDI DNTPTYRSN
401 MPAGTVNVSI ARIQPAAAOQ ADITVAPLPQ ETVRTGTRSP CPHYRTRPCD
451 SRSATSNRKT DCHAV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2101>:

```

m650 .seq
1  ATGTCCAAC TCAAACCAT CGCTCTGACC GCATCAGTTC TGTCCGTTTG
51  TCCGGGTTTC CTATACGCCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGCG CTAAACTCT TCAATACTCG ACCTGCCCCC GACAAAACAA
151 TATTTCATC CCGGACGCT GTGGGGCGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTCAAC AGGGTCATCA ACCGGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCGCG
351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC AGGATTATGG CAGTTTATGC CCGTACCGG CAGGCATTAC
451 GGCCTGGAAA AAACACCGGT TTACGACGGC AGGCACGACG TTTACGCCGC
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCCGCG
551 ACTGGCGCGT TGCTTTGCG GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAA
651 CTGCGCTATG CCAACGAAA CGCGCAACTA TGTCGCCAAG CTAGCTCGCG
701 TCGGCAACAT TATTGCCACT CCCAATCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCCATTTT TCAGGCAGTC GAACCGGATC GTCCGCTCGA
801 CAACGGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAAG GAGCTGCTCG
851 CCTAAACCC CGCATTCAAC GTCCCGCGGT TTATCCCAA AAGCAAACGC
901 AAACCTGCTG TTCCTGTGCG GTCCGTACAA ACCTTCCAAA GCACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAAC GCCTCAACAA CCTGAACGGC AACCTTGTCa ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCGACACCTA CCGTTCGAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG .AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGGCAG
1351 AGCCGACAGC CAACCTCAAA CCGAAAAACA GACCGCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2102; ORF 650>:

```

m650 .pep
1  MSKLKTIALT ASGLSVCPGF LYAQTSSHQ IGLAIMRLNS SILOLPPTKQ
51  YFQSGSLWGE LRQGRMGEV NPFLVRRHES KFIASHSYFN RVINRSRPYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWEGNVG
201 RAENRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPFYQAV EPDRPLDNEA IARLAGITOS ELLALNPAPN VPAFIPKSKR
301 KLLLPPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSDI DNTPTYRSN
401 MPAGTVNVGI ARIRPAAAOQ ADITVAPLPQ KTVRTXTRSP CPYCRTCPD
451 SRSATSNRKT DRHAV*

```

m650/g650 96.1% identity in 465 aa overlap

1034

m650.pep	10	20	30	40	50	60
	MSKLTIALTASGLSVCPGLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
g650	MSKLTIALTASGLSVCPGLYAQNTSSHQVGLAIMRLNSSILDLPPTKQYFQSGSLWDE					
	10	20	30	40	50	60
m650.pep	70	80	90	100	110	120
	LRQGFMRGEVNPPELVRRHESKFIAHSYFNVRVNRSPYMYHIANEVKKRNMPAEALLP					
g650	LRQGFMRGEVNPPELVRRHESKFIAHSYFDRVNRSPYMYHIANEVKKRNMPAEALLP					
	70	80	90	100	110	120
m650.pep	130	140	150	160	170	180
	FIESAFVTKAKSHVGSGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
g650	FIESAFVTKAKSHVGSGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
	130	140	150	160	170	180
m650.pep	190	200	210	220	230	240
	LFGDWPLAFAAYNWGEVGRVNRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIAT					
g650	LFGDWPLAFAAYNWGEVGRVNRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIAT					
	190	200	210	220	230	240
m650.pep	250	260	270	280	290	300
	PQSFQGMNISDIDNKPYPQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKSKR					
g650	PQSFQGMNISDIDNKPYPQAVEPGRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKNKR					
	250	260	270	280	290	300
m650.pep	310	320	330	340	350	360
	KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
g650	KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
	310	320	330	340	350	360
m650.pep	370	380	390	400	410	420
	NLVNAGRSILVAKNGKTLQTASESVVSDIDNTPDYRSNMPAGTVNVGIARIRPAAAQT					
g650	NLVNAGRSILVAKNGKTLHTASESVVSDIDNTPDYRSNMPAGTVNVSIARIQAAAQT					
	370	380	390	400	410	420
m650.pep	430	440	450	460		
	ADITVAPLPQKTVRTXTRSPCYCRTCPDSRSATSNRKTDHRAVX					
g650	ADITVAPLPQETVRTGTRSPCYHYRTRPCDSRSATSNRKTDCHAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2103>:

a650.seq

1	ATGTCCAAAC	TCAAAACCAI	CGCCCTGACC	GCGTCAGGTC	TGTCCGTTTG
51	TCCGGGTTTC	CTATACGCC	AAAACACCTC	ATCACACCAA	ATCGGTTTGG
101	CGATTATGCG	CTTAACTCT	TCAATACTCG	ACCTGCCACC	GACAAAACAA
151	TATTTCCAAT	CCGCAGCCT	GTGGAGCGAG	CTCGCCAAG	GCTTCCGGAT
201	GGGCGAAGTC	AATCCGAAC	TGGTACGCCG	CCACGAAAGC	AAATTCATCG
251	CAAGCCACAG	CTATTCAAC	AGGGTCATCA	ACGGAGTAG	ACCCTATATG
301	TACCATATCG	CCAACGAAGT	CAAAAACGC	AATATGCCCG	CCGAAGCCGC
351	CCTGCTTCCC	TTCATCGAAA	GCGCTTCGT	CACCAAAGCC	AAATCACACG
401	TCGGCGCATC	GGGCTGTGG	CAGTTCATGC	CCGCTACCGG	CAGGCATTAC
451	GGCCTGGAAA	AAACACCGGT	TTACGACGGC	AGGCACGACA	TTTACGCCGC
501	CACCGATGCC	GCACTCAACT	ATCTGCAATA	CCTCTATGGA	CTGTTCCGGC
551	ACTGGCCGCT	CGCCTTGCC	GCCTACAAC	GGGTGAAGG	CAACGTCGGA
601	CGCGCCATCA	ACCGCGCCG	CGCCAAGGG	CTCGAACCGA	CCTACGAAAA
651	CCTGCGTATG	CCCAACGAAA	CGCGCAACTA	TGTTCCCAAG	CTGCTCGCCG
701	TGCGCAACAT	CATTGCCCGC	CCCAATCTT	TCGGCATGAA	TATCAGCGAC
751	ATAGACAACA	AACCGTATT	TCAGGCAGTC	GAACCGGACC	GTCCGCTCGA
801	CAACGAAGCC	ATCGCCCGG	TTGCCGGCAT	CACGCAAAGC	GAGCTGCTCG
851	CCCTAAACCC	CGCATTCAAC	GTCCCCGCGT	TCATCCCCAA	AAGCAAACGC

1035

```

901  AAACTGCTGC TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951  CAACGCCGCA CCCGACAGCC TGTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CTTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCAACACCTA CCGTTCCAAT
1201 ATGCCGCGAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCGAC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2104; ORF 650.a>:

```

a650.pep
  1  MSKLKTIALT ASGLSVCPGF LYAQTSSHQ IGLAIMRLNS SILDLPPTKQ
 51  YFQSGSLWSE LRQGFMRGEV NPELVRHES KFIASHSYFN RVINRSRPMY
101  YHIANEVKKR NMPAEALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151  GLEKTPVYDG RHDYIYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201  RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAA PQSFGMNISD
251  IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301  KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351  DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPTYRSN
401  MPAGTVNVGI ARIRPAAAQT ADITVAPLPQ KTVRTXTRSP CPYCRTCPCD
451  SRSATSNRKT DRHAV*

m650/a650  99.1% identity in 465 aa overlap

      10      20      30      40      50      60
m650.pep  MSKLKTIALTASGLSVCPGFLYAQTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE
          |||
a650      MSKLKTIALTASGLSVCPGFLYAQTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWSE
          10      20      30      40      50      60

      70      80      90      100     110     120
m650.pep  LRQGFMRGEVNPELVRHESKFIASHSYFNRVINRSRPMYHIANEVKKRNMPAEALLP
          |||
a650      LRQGFMRGEVNPELVRHESKFIASHSYFNRVINRSRPMYHIANEVKKRNMPAEALLP
          70      80      90      100     110     120

      130     140     150     160     170     180
m650.pep  FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG
          |||
a650      FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDYIYAATDAALNYLQYLYG
          130     140     150     160     170     180

      190     200     210     220     230     240
m650.pep  LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT
          |||
a650      LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAA
          190     200     210     220     230     240

      250     260     270     280     290     300
m650.pep  PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR
          |||
a650      PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR
          250     260     270     280     290     300

      310     320     330     340     350     360
m650.pep  KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
          |||
a650      KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
          310     320     330     340     350     360

      370     380     390     400     410     420
m650.pep  NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPDYRSNMPAGTVNVGIARIRPAAAQT
          |||
a650      NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTNYRSNMPAGTVNVGIARIRPAAAQT

```

1036

	370	380	390	400	410	420
	430	440	450	460		
m650.pep	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTDRAVX					
a650	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTDRAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2105>:

g652.seq

```

1 ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGG GTGCGAATCC
51 GACTTTGGCG GTCTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGTCGGAT GTCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTGAA AAAACTGTGC
301 GACAGTAAAG GCTTCCCGAC CACAGTCGGC GACGAAGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAAGCGGCCG
401 AAGCCGCCGG CTACAAGGCG GCGAAGACG TATTATTCGC ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGGCCGA ATACTTGGAA GGCTTGGTTA
551 ACGAATTCCT GATTATTTCC ATTGAAGACG GGATGGACGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAATTG GGCAAAAAAG TTCAATTGGT
651 CGGCGACGAC TTGTTTCGTAA CCAATCCGAA AATTCTTGCC GAAGGCATCG
701 AAAAAGCGCT AGCAAAACGCA TTGCTGGTCA AAGTCAACCA AATCGGTACT
751 TTAAGCGAAA CCTGAAAGC cgtcgatctg gCAAAATGCA accgctacGc
801 cagCGTGATG AGCCACcgct ccggCGAAAC CGAAGACAGT Accattgccc
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TTAACAacgG TTCTTTGAGC
901 cgtTCCGACC GCATGGCGAA ATACAACCAa ctGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GcgcctACT ACCCGGGCAA AGCCGCATTC TACCAACTGG
1001 GCAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2106; ORF 652.ng>:

g652.pep

```

1 MIELDGTENK GN LGANATLA VSM AVARAAA EDSGLPLYRY LGGAGPMSLP
51 VPMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 ESKGFPTTVG DEGGFAPNLN SHKEALQLMV EAAEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFPIS IEDGMDENDW
201 EGWKKLLTEK GKVKQLVGDD LFTVNPKILA EGIKGVANA LLVKVNQIGT
251 LSETLKAVDL AKCNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAYNQ LLRIEELAE AAYYPGKAAF YQLGK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2107>:

m652.seq

```

1 ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGG GTGCGAATGC
51 GACTTTGGCG GTTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGCGCG CAGGCCCGAT GTCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTGAA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCCGG CTACAAGGCG GCGAAGACG TATTATTCGC ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGGCCGA ATATCTGGAA GGCCTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GCATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAACTG GCGGCTAGAG TTCAATTGGT
651 TGGCGACGAC TTGTTTCGTAA CCAATCCAAA AATCTTGGCC GAAGGCATCG
701 AAAAAGCGT AGCAAAACGCA TTGCTGGTCA AAGTCAATCA AATCGGTACT
751 TTGAGCGAGA CCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGCGGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
901 CGTTCGACC GCATGGCGAA ATACAACCAa CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCCCGCGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
1001 GCAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2108; ORF 652>:

m652.pep

```

1 MIELDGTENK GN LGANATLA VSM AVARAAA EDSGLPLYRY LGGAGPMSLP
51 VPMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
```

1037

101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC
 151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFPIIS IEDGMDENDW
 201 EGWKLLETKL GGRVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
 251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
 301 RSDRMAYNQ LLRIEELAE AADYPSKAAF YQLGK*

m652/g652 98.2% identity in 335 aa overlap

	10	20	30	40	50	60
m652.pep	MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
g652	MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m652.pep	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN					
g652	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m652.pep	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
g652	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m652.pep	GLVNEFPIISIEDGMDENDWEGWKLLEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA					
g652	GLVNEFPIISIEDGMDENDWEGWKLLEKLGKVKQLVGDDLFVTNPKILAEGIEKGVANA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m652.pep	LLVKVNQIGTLSETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS					
g652	LLVKVNQIGTLSETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS					
	250	260	270	280	290	300
	310	320	330			
m652.pep	RSDRMAYNQLLRIEELAEAAADYPSKAAFYQLGKX					
g652	RSDRMAYNQLLRIEELAEAAAYPGKAAFYQLGKX					
	310	320	330			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2109>:

a652.seq
 1 ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGG GTGCGAATGC
 51 GACTTTGGCG GTTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
 101 GCCTGCCGCT TTACCGCTAC TTGGGCGGCG CAGGCCCGAT GTCCCTGCC
 151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
 201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCCTTCCGCG
 251 AAGCGTTCCG CTGCGGTGCG GAAATTTTCC ACGCCTTGA AAAACTGTGC
 301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
 351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
 401 AAGCCGCCGG CTACAAAGCG GGCGAAGACG TATTATTGCG ATTGGACTGC
 451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCCTTGG AAGCCGAAGG
 501 CCGCTCTTAC ACCAACGCGG AATTGCGCA ATATCTGGAA GGCCTGGTCA
 551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GGATGGATGA AAACGACTGG
 601 GAAGGCTGGA AACTGCTGAC CGAAAACTG GCGCGCAAG TCCAACTCGT
 651 TGGCGACGAC CTCTTCGTTA CCAACCCGAA AATCCTTGCC GAAGGCATTG
 701 AAAAAGCGT GGCAACGCA CTATTGGTCA AAGTCAACCA AATCGGTACT
 751 TTGAGTGAAA CCCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
 801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCGG
 851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
 901 CGTTCCGACC GCATGGCGAA ATACAACCAA CTGCTGCGTA TCGAGGAAGA
 951 ATTGGCGGAA GCGCCGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
 1001 GCAATAA

This corresponds to the amino acid sequence <SEQ ID 2110; ORF 652.a>:

a652.pep
 1 MIELDGTENK GNLANATLA VSMVARARA EDSGLPLYRY LGGAGPMSLP
 51 VPMNVINGG EHANNSLNIQ EFMIMPVGRK SFREALRCGA EIFHALKKLC
 101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC

1038

```

151 ASSEFYKD GK YHLEAEGRSY TNAEFAEYLE GLVNEFP IIS IEDGMDENDW
201 EGWKLLETKL GGVQLVGDD LFVTNPKILA EGIKGVANA LLVKVNQIGT
251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAYNQ LLRIEELAE AADYPSKAAF YQLGK*

m652/a652 99.7% identity in 335 aa overlap

      10      20      30      40      50      60
m652.pep MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a652      MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
      10      20      30      40      50      60

      70      80      90     100     110     120
m652.pep EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a652      EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN
      70      80      90     100     110     120

      130     140     150     160     170     180
m652.pep SHKEALQIMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a652      SHKEALQIMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
      130     140     150     160     170     180

      190     200     210     220     230     240
m652.pep GLVNEFP IIS IEDGMDENDWEGWKLLEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a652      GLVNEFP IIS IEDGMDENDWEGWKLLEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA
      190     200     210     220     230     240

      250     260     270     280     290     300
m652.pep LLVKVNQIGT LSETLKAVDLAKRNRYASVM SHRSGETEDSTIADLAVATN CMQIKTGSLS
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a652      LLVKVNQIGT LSETLKAVDLAKRNRYASVM SHRSGETEDSTIADLAVATN CMQIKTGSLS
      250     260     270     280     290     300

      310     320     330
m652.pep RSDRMAYNQ LLRIEELAE AADYPSKAAF YQLGKX
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a652      RSDRMAYNQ LLRIEELAE AADYPSKAAF YQLGKX
      310     320     330

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2111>:

g652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTGCCCCG GAAATTTTGG ACTCAGCGCG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GTGCGGCCGT ACCGAGCGGC GCATCCACCG GTCAGAAAGA AGCTTTGGAA
151 CTTGCGGACG GCGACAAATC CCGCTATTCC GGCAAAGGCG TATTGAAGGC
201 CGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATC GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAAACAAAG GCAATTTGGG TCGGAATGCG ACTTTGGCGG TCTCTATGGC
351 GGTTCACGCG GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGGGGCGC AGGTCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GGCACAAAAT CTTTCCGCGA AGCGTTGCGC TCGCGTGCGG
551 AAATTTTCCA CGCCTTGAAA AACTGTGCG ACAGTAAAGG CTTCCTGACC
601 ACAGTCGGCG ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAGA
651 AGCCCTGCAA CTGATGTCG AAGCGGCCGA AGCCGCCGCG TACAAGGCGG
701 GCGAAGACGT ATTATTGCGA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAAAT ACCACTTGG AAGCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TACTTGGAAG GCTTGGTTAA CGAATTCCTG ATTATTTCGA
851 TTGAAGACGG GATGGACGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAATTGG GCAAAAAAGT TCAATTGGT GCGCAGCACT TGTTCGTAAC
951 CAATCCGAAA ATTCTTGCCG AAGGCATCGA AAAAGGCGTA GCAAAACGAT
1001 TGCTGGTCAA AGTCAACCAA ATCGGTACTT TAAGCGAAAC CCTGAAAGCC
1051 GTCGATCTGG CAAAATGCAA CCGCTACGCG AGCGTGATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGTA CCATTGCCSA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT TAAAACCGGT TCTTTGAGCG GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCTACTA
1251 CCCCAGCAAA GCCGATTCTT ACCAATGCG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2112; ORF 652-1.ng>:

1039

g652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDVLES G VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRY S GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGA NA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNV I
151 NGGEHANNS L NIOEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEAEEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEF AE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKQVLV GDDLFTVNP K ILAEGIEKGV ANALLVKVNO IGTLSSETLKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAAAYPGK AAFYQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2113>:

m652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTGCCCCG GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTGCGGACG GCGACAAATC CCGTTATTCG GCGAAGGCGG TATTGAAGGC
201 GGTGCAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTGGG TCGCAATGCG ACTTGGCGG TTTCTATGGC
351 GGTTCACGCG GCCGCTGCGG AAGACTCAGG CTTGCCGCTT TACCGCTACT
401 TGGGCGGCGC AGGCCGATG TCCCTGCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCCAAAAT CTTTCCGCGA AGCGTTGCGC TCGGGTGGCG
551 AAATTTTCCA CGCCTTGAAA AAAGTGTCG ACAGCAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTGCCCCC AACCTGAACA GCCACAAGA
651 AGCCCTGCAA CTGATGGTCG AGCGACCGCA AGCCGCCGCG TACAAAAGCG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CCTCCAGCGA GTTCTACAAA
751 GACGGCAAAAT ACCACTTGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG CATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAACTGG GCGGTAGAGT TCAATTGGTT GCGGACGACT TGTTCGTAAC
951 CAATCCAAA ATCTTGGCGG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGGTCAA AGTCAATCAA ATCGGTACTT TGAGCGAGAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTAGGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCCAGCAA GCCGCAATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2114; ORF 652-1>:

m652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDVLES G VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRY S GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGA NA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNV I
151 NGGEHANNS L NIOEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEF AE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKQVLV GDDLFTVNP K ILAEGIEKGV ANALLVKVNO IGTLSSETLKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAAAYPSK AAFYQLGK*

```

m652-1/g652-1 98.6% identity in 428 aa overlap

	10	20	30	40	50	60
m652-1	MSAIVDIFAREILDSRGNPTVECDVLES GVMGRAAVPSGASTGQKEALELRDGDKSRY S					
g652-1	MSAIVDIFAREILDSRGNPTVECDVLES CVMGRAAVPSGASTGQKEALELRDGDKSRY S					
	10	20	30	40	50	60
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGA NATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGA NATLAVSMAVAR					
	70	80	90	100	110	120
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGA NATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGA NATLAVSMAVAR					
	70	80	90	100	110	120
m652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIOEFMIMPVGAKSFREALR					
g652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIOEFMIMPVGAKSFREALR					
	130	140	150	160	170	180
m652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIOEFMIMPVGAKSFREALR					
g652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIOEFMIMPVGAKSFREALR					
	130	140	150	160	170	180

1040

	190	200	210	220	230	240
m652-1	CGAEIFHALKKLCD	SKGFPTTVGDEGGF	APNLNSHKEALQ	LMVEATEAAGYK	AGEDVLFA	
g652-1	CGAEIFHALKKLCD	SKGFPTTVGDEGGF	APNLNSHKEALQ	LMVEATEAAGYK	AGEDVLFA	
	190	200	210	220	230	240
	250	260	270	280	290	300
m652-1	LDCASSEFYKDG	KYHLEAEGRSY	TNAEFAEYLEGL	VNEFPIISIEDG	MDENDWEGW	KLLT
g652-1	LDCASSEFYKDG	KYHLEAEGRSY	TNAEFAEYLEGL	VNEFPIISIEDG	MDENDWEGW	KLLT
	250	260	270	280	290	300
	310	320	330	340	350	360
m652-1	EKLGGRRVQLV	GDDLFTVNP	KILAEGIEKGV	ANALLVKVNQ	IGTLSETLKA	VDLAKRNRYA
g652-1	EKLGGRRVQLV	GDDLFTVNP	KILAEGIEKGV	ANALLVKVNQ	IGTLSETLKA	VDLAKRNRYA
	310	320	330	340	350	360
	370	380	390	400	410	420
m652-1	SVMSHRSGETED	STIADLAVAT	NCMQIKTGSLS	RSRDRMAKYN	QLLRIEEEEA	ADYPSK
g652-1	SVMSHRSGETED	STIADLAVAT	NCMQIKTGSLS	RSRDRMAKYN	QLLRIEEEEA	ADYPSK
	370	380	390	400	410	420
	429					
m652-1	AAFYQLGKX					
g652-1	AAFYQLGKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2115>:

a652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCGCCCGC GAAATTTTGG ACTCAGCGGG
51  CAACCCACACA GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTCGCGACG GCGACAAATC CCGTTATTCT GGCAAGGGCG TATTGAAGGC
201 GGTGGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAACAAAGG GCAATTGGG TGCGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTTCGACCG GCGCTGCCG AAGACTCAGG CCGTCCGCTT TACCGTACT
401 TGGGCGGCGC AGGCCCGATG TCCCTGCCG TACCGATGAT GAACGTCATC
451 AACGCGCGCG AACACGCCA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCCGC GCGCAAAAT CTTCCGCGA AGCGTTGCGC TCGGTTGCGG
551 AAATTTTCCA CGCCTGAAA AAACGTGCGC ACAGCAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTCGCCCGC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGCTCG AGGCGACCGA AGCCGCGCGC TACAAAGCGG
701 GCGAAGACGT ATTATTGCGA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAAAT ACCACTTGGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG GATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAACTGG GCGGCAAAAT CCAACTCGTT GCGCAGGACC TCTTCGTTAC
951 CAACCCGAAA ATCCTTGCCG AAGGCATTGA AAAAGGCGTG GCAACGCGC
1001 TATTGGTCAA AGTCAACCAA ATCGGTACTT TGAGTGAAAC CCTGAAAGCC
1051 GTCGACTTAG CCAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGCGAARAC GAAGACAGCA CCATTGCCGA CTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCCAGCAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2116; ORF 652-1.a>:

a652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECVLLLESG VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRY S GKV LKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGA NA TLAVSMAVAR AAEDSGLP YRYLGAGP M SLVPVPMNVI
151 NGGEHANNS L NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMD E NDWEGWLLT
301 EKLGGKVLQ V GDDLFTVNP K ILAEGIEKGV ANALLVKVNQ IGTLSLTLKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEADYPSK AAFYQLGK*

```

m652-1/a652-1 99.8% identity in 428 aa overlap

10 20 30 40 50 60

1041

```

m652-1      MSAIVDIFAREILDSRGNPTVECDVLESVMGRAAVPSGASTGQKEALELRDGDKSRY
a652-1      MSAIVDIFAREILDSRGNPTVECDVLESVMGRAAVPSGASTGQKEALELRDGDKSRY
              10      20      30      40      50      60

m652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
a652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
              70      80      90      100     110     120

m652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNLSLNIQEFMIMPVGAKSFREALR
a652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNLSLNIQEFMIMPVGAKSFREALR
              130     140     150     160     170     180

m652-1      CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
a652-1      CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
              190     200     210     220     230     240

m652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPIISIEDGMDENDWEGWKLLT
a652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPIISIEDGMDENDWEGWKLLT
              250     260     270     280     290     300

m652-1      EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
a652-1      EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
              310     320     330     340     350     360

m652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEELAEAAADYPSK
a652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEELAEAAADYPSK
              370     380     390     400     410     420

m652-1      AAFYQLGKX
a652-1      AAFYQLGKX
              429

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2117>:

```

g653.seq
1  ATGGCGGcgg aaccgatgcg gAtgccggag gtaAcgtaCG GTTTTCCGG
51  ATCGTTCGGG ATGGCGTTTT TGTtgacggt GATGTGCGCt ttgcccAAG
101 CGGCTtcggc ggctttgcCg gtgaTTTTCa TCGGTTGCAG GtcgacgaGG
151 AAaacgTGGC TTTCGGTGCG GCCGGAaacy atgcgCaaac cgCGTttaac
201 caactcttcc gccATGACGG CAGCATTGAT TTTCACTTGT TTTGCGTATT
251 GTTTGAactC GGGTTGcaac gcttctTTAA acgctACGGC TttgCGCGCG
301 ATAACGTgca tcaACGGacc gCCTTGcAGG CTTGGGAAGA TGGAAGAGTT
351 CAGCGCTTTT TCGTGGGTAT TGTCACGGCA CAAATCACA CCGCCGCGAG
401 GCGCGCGTAG GGTTTTGTGG GTGGTAGTGg ttACgaaGtc GCAGaAtggc
451 ACGGGgttag gatattcgcc gccGCCAACC AgtccgGCAT Ag

```

This corresponds to the amino acid sequence <SEQ ID 2118; ORF 653.ng>:

```

g653.pep
1  MAAEPMRMPE VTYGFSGSFG MAFLLTMCA LPKAASAALP VIFIGCRSTR
51  RTWLSVRPET MRKPRLTNSS AMTAAALIFC FAYCLNSGCN ASLNATALAA
101 ITCINGPPCR LGKMEEFSAF SWVLSRHKIT PPRGPRRVLW VVVVTKSQNG
151 TGLGYSPPAT SPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2119>:

```

m653.seq
1  ATGGCAGCGG AGCCGATGCG GATGCCGGAG GTAACGAAGG GTTTTCCGG
51  ATCGTTCGGA ATGGCGTTTT TGTTGACGGT GATGTGCGCT TTGCCCAAG
101 CGGCTTCGGC GGCTTTCGCC GTAATTTTCA TCGGTTGCAG GTCAACGAGG

```

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```

151 AAAACGTGGC TTTCGGTGCG GCCGGAACG ATGCGCAAAC CGCGTTTAAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCATTGT TTTGCGTATT
251 GTTTGAACCT GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGACC GCCTTGCAAG CTTGGGAAGA TGGAAAGAGT
351 CAACGCTTTT TCGTGGGTAT TGTGCGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GCTTTTGTGC CTGCTGGTGG TCACCAACTC GCAGAACGGC
451 ACCGGGTTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2120; ORF 653>:

```

m653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRRLW VVVVTKSONG
151 TGLGYSPPAT RPA*

```

m653/g653 96.9% identity in 163 aa overlap

	10	20	30	40	50	60
m653.pep	MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET					
g653	MAAEPMRMPEVTYGFSCSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m653.pep	MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF					
g653	MRKPRLTNSSAMTAALIFTCFAYCLNSGCNASLNATALAAITCINGPPCRLGKMEEFSAF					
	70	80	90	100	110	120
	130	140	150	160		
m653.pep	SWVLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATRPAX					
g653	SWVLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATSPAX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2121>:

```

a653.seq
1  ATGCGCGCGG AACCGATGCG GATGCCGGAG GTAACGAAGS GTTTTCCCG
51  ATCATTCCGG ATGGCGTTT TGTGACAGT GATGTGCGCT TTGCCCAAAG
101 CAGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTGCAG GTCACGAGG
151 AAAACGTGGC TTTCGGTGCG GCCGGAACG ATGCGCAAAC CGCGTTTAAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCATTGT TTTGCGTATT
251 GTTTGAACCT GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGACC ACCTTGCAAG CTTGGGAAGA TGGAAAGAGT
351 CAACGCTTTT TCGTGGGTAT TGTGCGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GCTTTTGTGG GTGCTGGTGG TAACGAAGTC GCAGAACGGC
451 ACGGATTGGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2122; ORF 653.a>:

```

a653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRRLW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/a653 100.0% identity in 163 aa overlap

	10	20	30	40	50	60
m653.pep	MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET					
a653	MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m653.pep	MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF					
a653	MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF					
	70	80	90	100	110	120
	130	140	150	160		
m653.pep	SWVLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATRPAX					
a653	SWVLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATRPAX					

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130 140 150 160

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2123>:

```
g656.seq
1  ATGCCGCGTT TCTCCGGTTC GATTTCCTCG ATGATTTCCTCA TCGCGCGGAC
51  TTTTggcGCG CCGGAGAGTG TGCcggcagg gAAGGTGGCG GCGAGGATGT
101 CCATATTGGT AACGCCCTCT TTCAAACAGc ctTCGACGTT GGAAACGATG
151 TGCATCACAT GGGAGTATTT TTCAATCACC ATTTTGTCTGG TGACTTTGAC
201 TTCGCCTGTT TTGCTGATGC GTCCGACATC GTTGCGCCCC AAATCGATAA
251 GCATAACGTG TTCGGCGgatt TCTTTGGCGT CGCTTAACAA ATCTTGTTCG
301 TTGGCAAGGT CTTCGGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATGACGTcat CGCGTTCGCG GCGGACGAGG ATTTCCGGCG
401 AGGAACCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2124; ORF 656.ng>:

```
g656.pep
1  MPRFSGSISS MISIARTFGA PESVPAGKVA ARMSILVTPS FKQPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSIISITCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRRTR ISGEEPTMWK SPKS*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2125>:

```
m656.seq
1  ATGCCGCGTT TGCTCGGTTC GACTTCTTCG ATGATTTCCTCA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTCGACGTT GGAAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTCTGG TAACTTTGAC
201 TTCGCCGGTT TTAAGTATGC GGCCGACGTC GTTGCCTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTCG
301 TTGGCAAGGT CTTCGGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATAACGTCGT TCGTTCGCG TCGGACGAGG ATTTCCGGCG
401 AGGAGCCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2126; ORF 656>:

```
m656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT ITSLSRRTR ISGEEPTMWK SPKS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m656/g656 91.0% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRPSTLETMCITWEYFSIT					
	: : : : : : :					
g656	MPRFSGSISSMISIARTFGAPESVPAGKVAARMSILVTPSFKQPSTLETMCITWEYFSIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m656.pep	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
	: : : : : : : :					
g656	ILSVTLTSPVLLMRPTSLRPKSISITCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
	70	80	90	100	110	120
	130	140				
m656.pep	ITSLSRRTRISGEEPTMWKSPKSX					
	:					
g656	MTSSRSRRTRISGEEPTMWKSPKSX					
	130	140				

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2127>:

```
a656.seq
1  ATGCCGCGTT TGCTCGGTTT GACTTCTTCG ATGATTTCCA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTCCGACGT GGAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTGGG TAACTTTGAC
201 TTCGCCGGTT TTAAGTATGC GGCCGACGTC GTTGGCTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTCC
301 TTGGCAAGGT CTTCCGCGGG GGTTTTGGCG CGCAGGCGCG TGCCGGCGAT
351 GGGCGGACG ATGACATCGT CGCGTTCCGG GCGGACGAGG ATTTCGGGCG
401 AGGAGCCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2128; ORF 656.a>:

```
a656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRRTR ISGEEPTMWK SPKS*

m656/a656 98.6% identity in 144 aa overlap

      10      20      30      40      50      60
m656.pep MPRLLGSTSSMISMARTLGAPEsVPAGKVAARMSMLVMPsFRRPSTLETMCITWEYFSIT
a656.     MPRLLGSTSSMISMARTLGAPEsVPAGKVAARMSMLVMPsFRRPSTLETMCITWEYFSIT
      10      20      30      40      50      60

      70      80      90     100     110     120
m656.pep ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT
a656     ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT
      70      80      90     100     110     120

      130     140
m656.pep ITSLSRSRRTRISGEEPTMWKSPKSX
a656     MTSSRSRRTRISGEEPTMWKSPKSX
      130     140
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2129>:

```
g657.seq
1  ATGAACACAC CCCCCATCCT TCCTCCCGCC ATGCTCGGCA TCCTCGGCGG
51  CGGACAATTa ggcagAATGT TTGCCGTTGC CGCTAAAACC ATGGGCTACA
101 AAGTAACCGT TCTCGATCCC GACCCGAATG CGCCGGCGGC GGAATTTGCC
151 GACCGCCATT TGTGCGCGCC GTTTGACGAC CGGGCCGCGT TGGACGAATT
201 GGC AAAATGC GCGGCGGTTa cgACCGAATT TGAAAacgtc aaTGCCGACG
251 CGATGCGCTC TCTGGCAAAG CATAACCAACG TTTCCCCCAG CGGCGACTGC
301 GTGTCCATTG CACAAAACCG CATTACAGGA AAAGCGTGGA TACGCAAAGC
351 AGGCTTGCAA ACCGCGCCGT ATCAGGCGGT TTGCAAGGCC GAAGACATTA
401 CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
451 GGCTACGACG GCAAAGGTCA AATCCGCGTC AAAACGTTGG ACGAACTCAA
501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTTG GAAAAAATGG
551 TGGACTTGCG CGGCGAGATT TCCGTGATCG TATGCCGTCT GAACGATGAA
601 AACGTGCAAA CCTTCGACCC CGCCGAAAAC ATCCACGAAA ACGGCATCTT
651 GGCTTatteC ATCGTCcccg CGCGGCTGAG TGCCGACGTG CAGCAACAGG
701 CGCGGCAGAC GCGCAACgc tTGGCGGACG AATTGGATTA TGTGCGCgta
751 TTGGCGGTAG AAATGTTTGT TGTGCGGCAC ACACATGAAT TGCTCGTCAA
801 TGAACCGGCC CCGCGCACGC ACAATTCGGG CCACCATACG ATAGATGCCT
851 GCGCCGCAGA CCAGTTCCAA CAGCAGGTAC GCATTATGTG CAACctGCCG
901 cccGccgACA CCAAATTATT aTCCCcttgC TGTATGGCGA ATATTTTGGg
951 CGACGTTTGG CAGGAAGATG GCGGCGAACC GGATTGGCTG CCGTGCAGAA
1001 GCCGGCCGAA TGCACACCTG CACCTATACG GAAAAAAAC CGCACAGAAA
1051 GGTCTGGAAA TGGGCACTT TaccgTTTTG ACCACCGATT CGGACaccgC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2130; ORF 657.ng>:

1045

g657.pap

1	MNTPPILPPA	MLGILGGGQL	GRMFAVAAKT	MGYKVIVLDP	DPNAPAAEFA
51	DRHLCAPFDD	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC
101	VSIAQNRIQE	KAWIRKAGLQ	TAPYQAVCKA	EDITEASAQF	LPGILKTATL
151	GYDGKGQIRV	CTLDELKAAF	AEHGGVDCVL	EKMVDLRGEI	SVIVCRLNDE
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADV	QQQARQTAQR	LADEL DYVGV

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251 LAVEMFVVD THELVNETH PRTHNSGHHT IDACAADQFQ QQVRIMCNLP
 301 PADTKLLSPC CMANILGDVW QEDGGEFDWL PLQSRPNAHL HLYGKKTAQK
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQSL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2131>:

m657.seq
 1 ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTTGCCA TCCTCGGCGG
 51 CGGACAATTA GGCAGAATGT TTACCGTTGC CGCCAAAACC ATGGGCTACA
 101 AAGTAACCGT TCTCGACCCC GATCCGGACG CGCCGGCAGC AGAATTGACC
 151 GACCGCCATT TGTGCGCGCC GTTTAACGAC CAAGCTGCTT TGGACGAATT
 201 GGCAAAATGC GCGCGGTGA CCACTGAATT TGAAAACGTC AATGCCGATG
 251 CGATGCGCTT TTTGGCAAAA CATACCAATG TTTCCCTAG CGGCGATTGT
 301 AGGCGGATTG CACAAAACCG CATTGAGGAA AAGGCATGAC TACGCAAGC
 351 GGGATTGCAA ACCGCGCCGT ATCAAGTGGT TTGTAAGGCT GAAGACATCA
 401 CTGAAGCAAG CGCGCAATTT TTGCCCGCA TCCTGAAAAC GGCTACGTTG
 451 GGTACGACG GCAAAGGTCA AATCCGCGTA AAAACATTGG ATGAACCTCAA
 501 AGCGCGTATT GCCGAACACG GCGCGGTGGA TTGCGTTTGG GAAAAAATGG
 551 TGATTTCGCG CAGTGAAAT TCCGTAATCG TATGCCGTTT GAACAATGAC
 601 AACGTGCAAA CTTTCGACCC TGCCGAAAAC ATCCACGAAA ACGGCATCTT
 651 GGTATTATCC ATCGTCCCGG CGCGACTGAG TGCCGACGTG CAGCAACAGG
 701 CGCGGCAGAT GCGCAACGC TTGGCGGACG AATTGGATTA TGTCCGCGTA
 751 TTGGCGGTAG AAATGTTTGT TGTGCGTGAC ACGCATGAAT TGGTCGTCOA
 801 CGAAATCGCC CCGCGCCCGC ACAATTCCGG ACACCATACG ATAGATGCCT
 851 GCGCAGCAGA CCAGTTCCAG CAGCAGGTAC GCATTATGTG CAACCTGCCG
 901 CCTGCCGATA CCAAATTACT GAGTTCCTGC TGTATGGCAA ATATTTTGGG
 951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGCTG CCCTTGCAAA
 1001 GCCATCCGAA TGCACACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA
 1051 GGGCGGAAAA TGGGACACTT TACCGTTTAA ACCACCGATT CGGACACCGC
 1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

This corresponds to the amino acid sequence <SEQ ID 2132; ORF 657>:

m657.pep
 1 MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGKVTVLDP DPDAAPAEFA
 51 DRHLCAPFND QALDELAKC AAVTTEFENV NADAMRFLAK HTNVSPSGDC
 101 VAIAQNRIQE KAWIRKAGLQ TAPYQVCKA EDITEASQF LFGILKTATL
 151 GYDGKGQIRV KTLDELKAAF AEHGGVDCVL EKMVDLRSEI SVIVCRLLND
 201 NVQTFDPAEN IHENGILAYS IVPARLSADV QOARQMAQR LADELQYVGV
 251 LAVEMFVVD THELVVNEIA PRPHNSGHHT IDACAADQFQ QQVRIMCNLP
 301 PADTKLLSSC CMANILGDVW QEDGGEFDWL PLQSRPNAHL HLYGKKTAHK
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQSL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m657/g657 93.9% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPA	MLGILGGGQL	GRMFTVAAKT	MGYKVTVLDP	DPDAAPAEFA	DRHLCAPFND
g657	MNTPLPILPP	AMLGILGGGQL	GRMFAVAAKT	MGYKVTVLDP	DPNAPAEFA	DRHLCAPFND
	70	80	90	100	110	120
m657.pep	QALDELAKCA	AAVTTEFENV	NADAMRFLAK	HTNVSPSGDC	VAIAQNRIQE	KAWIRKAGLQ
g657	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC	VSIAQNRIQE	KAWIRKAGLQ
	130	140	150	160	170	180
m657.pep	TAPYQVCKA	EDITEASQFL	PGILKTATL	GYDGKGQIRV	KTLDELKAAF	AEHGGVDCVL
g657	TAPYQAVCKA	EDITEASQFL	PGILKTATL	GYDGKGQIRV	KTLDELKAAF	AEHGGVDCVL
	130	140	150	160	170	180

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	190	200	210	220	230	240
m657.pep	EKMVDLRSEISVIVCRLNNDENVQTFDPAENIHENGILAYSIVPARLSADVQQQARQMAQR					
g657	EKMVDLRGEISVIVCRLNDENVQTFDPAENIHENGILAYSIVPARLSADVQQQARQTAQR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m657.pep	LADEL DYVGV LAVEMFVVGDTHEL VVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP					
g657	LADEL DYVGV LAVEMFVVGDTHELLVNETAPRTHNSGHHTIDACAADQFQQQVRIMCNLP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m657.pep	PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSHPNALHLYGKKTAHKGRKMGHFTVL					
g657	PADTKLLSPCCMANILGDVWQEDGGEPDWLPLQSRPNALHLYGKKTAQKGRKMGHFTVL					
	310	320	330	340	350	360
	370	379				
m657.pep	TTDSDTAFQEAKKLHQSXLX					
g657	TTDSDTAFQEAKKLHQSXLX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2133>:

```

a657.seq
1  ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTCGGCA TTCTTGCGCG
51  CGGACAATTA GGCAGAAATG TTAAGTGTGC TGCCAAAACC ATGGGGCTACA
101 AAGTAACCGT ACTCGATCCC AACCCGAATG CGCCGGCAGC GGAATTTGCC
151 GACCGCCATT TGTGTGCGCC GTTTGACAAC CAAACCGCTT TGGAAGAATT
201 GGCAAAATGT GCGGCTGTTA CGACCGAGTT CGAAAACGTC AATGCCGATG
251 CGATGCGTTT TCTCGCCAAA CATACCAATG TTTCCCCCAG CGGCGACTGC
301 GTTGCCATCG CGCAAAACCG CATTCAAGAA AAGGCATGGA TACGCAAAAG
351 AGGCCTGCAA ACCGCGCCGT ATCAAGCAAT TTGCAAGCC GAAGACATCA
401 CTGAAGAAAG CATACAATTT CTGCCCGGCA TCCTGAAAAC CGCTACATTG
451 GGCTATGACG GCAAAGGCCA AATCCGCGTC AAAACGGTGG ATGAACTCAA
501 AGCCGCGTTT GCCGAACACC GCGGCGTGGA TTGCGTTTTG GAAAAAATGG
551 TGGACTTGCG CGGCGAAATT TCCGTTATCG TATGCCGTCT GAACAATGAC
601 AACGTGCAAA CTTCGATCC TGCCGAAAAC ATTCACGAAA ACGGTATCCT
651 CGCTACTCC ATCGTCCAG CCCGACTGAG TGCCGACATT CAGCAACAGG
701 CGCGACAAAT GGCGCAGCGT TTGGCCGATG AATTGAACTA CGTCGCGGTA
751 TTGGCGGTAG AAATGTTTGT TGTCCGCGAC ACGCATGAAT TGGTCGTCAA
801 CGAAATCGCG CCGCGTCCGC ACAATTCCGG CCACCATACC GTCGACGCCT
851 GCGCGGCAGA CCAATTCAG CAACAGGTCC GCCTGATGTG CAACCTGCCA
901 CCTGCTGACA CCAAATTGCT GAGTTCTTGC TGTATGCGCA ATATTTTGGG
951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGTTT CCCCTGCAAA
1001 GCCGCGCCGA CGCGCACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA
1051 GGGCGGAAAA TGGGACACTT TACCATTTTA AGCACCGATT CGGACACCGC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2134; ORF 657.a>:

```

a657.pep
1  MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP NPNAPAAEFA
51  DRHLCAPFDN QTALEELAKC AAVTTEFENV NADAMRFLAK HTNVSPSGDC
101 VAIAQNRIQE KAWIRKAGLQ TAPYQAICKA EDITEESIQL LPGILKTATL
151 GYDGKGQIRV KTVDELKAAF AEHRGVDCVL EKMVDLRGEI SVIVCRLNND
201 NVQTFDPAEN IHENGILAYS IVPARLSADI QQQARQMAQR LADELNYVGV
251 LAVEMFVVGDT HELVVNEIA PRPHNSGHHT VDACAADQFQ QQVRLMCNLP
301 PADTKLLSSC CMANILGDVW QEDGGEPDWF PLQSRPDAHL HLYGKKTAHK
351 GRKMGHFTIL STDSDTAFQE AKKLHQSXL*

```

m657/a657 94.2% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP DPDAPEAEFADRHLCAPFDN					

a657	MKNISLSPPAMLGILGGGQLGRMFTVAAKTMGYKVTVLDPNPNAPAAEFADRHLCAPFDN	10	20	30	40	50	60
m657.pep	QAALDELA KCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ	70	80	90	100	110	120
a657	QTALEELAKCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ	70	80	90	100	110	120
m657.pep	TAPYQVVCKAEDITEASQFLPGILKTATLGYDGKGQIRVKTLDLKAFAEHGGVDCVL	130	140	150	160	170	180
a657	TAPYQAICKAEDITEESIQLPGILKTATLGYDGKGQIRVKTVDLKAFAEHRGVDCVL	130	140	150	160	170	180
m657.pep	EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQARQMAQR	190	200	210	220	230	240
a657	EKMVDLRGEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADIQQARQMAQR	190	200	210	220	230	240
m657.pep	LADEL DYVGVLAVEMFVVGDTHEL VVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP	250	260	270	280	290	300
a657	LADEL NYVGVLAVEMFVVGDTHEL VVNEIAPRPHNSGHHTVDACAADQFQQQVRLMCNLP	250	260	270	280	290	300
m657.pep	PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSHPNALHLHYGKKTAAHKGRKMGHFTVL	310	320	330	340	350	360
a657	PADTKLLSSCCMANILGDVWQEDGGEPDWFLQSRPDAHLHLHYGKKTAAHKGRKMGHFTIL	310	320	330	340	350	360
m657.pep	TTSDS TAFQEAKKLHQS LX	370	379				
a657	STDS S TAFQEAKKLHQS LX	370					

g658.seq

This corresponds to the amino acid sequence <SEQ ID 2136; ORF 658.ng>:

q658.pcp

1 MVAGIVRARG GFIDEQFMCV ADNKHFYRQY ADIIQFVRQA LRRLPRLLLH
51 VGTQPRGDDG ISQDAVFVDV FGGVEGLHVF IVQTAYDHGN LAAOVHHFFO

1049

```

101 NAIHAAVFGK RGFEFVQRFQ ADLTFVAVQA RSRFQDAGQK LRACFSNVFG
151 LANRLIRRLG QACFAYPRFF LNAVLCNGHA VAAGGNVGM LQRAHRVGLD
201 VFKFGRNRRR FCQFVQRPV VKRRAQMAVG KFRRRRIRVG IENGYFVAHG
251 FSGNGKHSAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2137>:

```

m658.seq
1  ATGGTGTCCG GAATTGTGCG GCGCGGGGCG GATTTCTGTTG ACGACCAATT
51  CATGCGTGTC ACCGACAACA AACATTTCTA CCGCCAATAC GCCGACATAA
101 TCCAATTCGT CCGCCAAGCG TTGCGCCATC TGCCGCGCCT GTTGCTGCAC
151 GTCGGCACTC AGTCGCGCGG GGACGATGGA ATAAGCCAAG ATGCCGTTT
201 CGTGGATGTT TTCGGCAGGG TCGAAAGTTT GCACGTTGTC ATTGTTCAAA
251 CGGCATACGA TTACGGAAAT TTCACTGCGC AAATCCACCA TTTTTCCAA
301 AACGCAATCC ACGCCGCCGT GTTCGGCAAA CGCGGCTTTG AGTTCATCCA
351 ATGTTTATTAC GCGGATTTGA CCTTGCCGT CGTAGCCAA CGTAGCGTT
401 TTCAGGATGC CGGGCAAAAA TTGCGCGCTT GCTTCAGTGA TGTCTTCAGC
451 CTTACAAACC ACTTGATACG GCGCGTTTG CAATCCCGCT TTGCGTATCC
501 ATGCTTTTTC CTGAATGCGG TTTTGTGCAA TCGCCACACA ATCGCCGCTA
551 GGGGAAACAT TGGTATGTTT TGCCAAAAG CGCATCGCAT CGGCATTGAC
601 GTTTTCAAAT TCAGTGGTCA CCGCCGCGCA TTTTGCCAA TCGTCCAAAG
651 CAGCTTGCTC GTTAAACGGC GCGCACAAAT GCGGTCGCGC AAATTCTGCT
701 GCCGCGCGCT CCGGATCGGG GTCGAGAACG GTTACTTTGT AGCCCATGGT
751 TTTGCGGCA ACGGTAAACA TTCTGCCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2138; ORF 658>:

```

m658.pep
1  MVSGIVRARG DFVDDQFMRV TDNKHFYRQY ADIIQFVRQA LRHLPRLLLH
51  VGTQSRGDDG ISQDAVFVDV FGRVESLHV IVQTAYDYG NFTAQIHFFQ
101 NAIHAAVFGK RGFEFIQCFY ADLTFVAVQA RSRFQDAGQK LRACFSNVFS
151 LTNHLIRRLG QSRFAYPCLF LNAVLCNRHT IAARGNIGMF CQKAHRIGID
201 VFKFSGHRRR FCQFVQSSLV VKRRAQMAVG KFCCRRVRIG VENG YFVAHG
251 FGGNGKHSAX

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m658/g658 82.2% identity in 259 aa overlap

	10	20	30	40	50	60
m658.pep	MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLLHVGTQSRGDDG					
g658	MVAGIVRARGGFIDEQFMCVADNKHFYRQYADIIQFVRQALRRLPRLLLHVGTQPRGDDG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m658.pep	ISQDAVFVDVFGRVESLHVIVQTAYDYGNTAQIHFFQNAIHAAVFGKRGFEFIQCFY					
g658	ISQDAVFVDVFGGVEGLHVFIVQTAYDHGNLAAQVHHFFQNAIHAAVFGKRGFEFVQRFQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m658.pep	ADLTFVAVQAQRSRFQDAGQKLACFSDFSLTNHLIRRLGQSRFAYPCLFLNAVLCNRHT					
g658	ADLTFVAVQAQRSRFQDAGQKLACFSNVFGLANRLIRRLGQACFAYPRFFLNAVLCNGHA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m658.pep	IAARGNIGMFCQKAHRIGIDVFKFSGHRRRAFCQFVQSSLVVKRRAQMAVGKFCCRRVRIG					
g658	VAAGGNVGM LQRAHRVGLD VFKFGRNRRRAFCQFVQRPVVKRRAQMAVGKFRRRRIRVG					
	190	200	210	220	230	240
	250	260				
m658.pep	VENGYFVAHGFSGNGKHSAX					

1050

```

          :|||||:|||||
g658      IENGYFVAHGFGNGKHSAX
          250      260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2139>:

```

a658.seq
1  ATGGTGGCCG GAATTGTGCG GACGCGGCGC GATTCGTTG ACGACCAATT
51  CATCGGTGTC GCCGACAACA AACATTCTA CCGCCAATAC GCCGACGTAG
101 TTCAATTCAT CGGCCAAACG CTGCGCCATT TGTCGCGCCT GTTGCTGAAT
151 GTCGGCACTC AGTCGGGCTG GGACGATGGA GTAGGCGAGG ATACCGTTTT
201 CGTGAATGTT TTCGGCAGGA TCGAAAGTTT GCACGTTGTC ATTGTTCAGA
251 CGGCATACGA TAACGGAAAT TTCGCGCGCG AAGTCCACCA TTTTTCCTAA
301 AACGCAATCC ACGCCGCGGT GTTCGGCAAA CGCGGCTTTG AGTTCATCCA
351 CCGTTTGTAC GCGGATTTGG CCTTTGCCGT CATAGCCCAA TGTCGCGGTT
401 TTCAGGATGC CGGGCAGAAA TTGTATGCTT TCTTCAGTGA TGTCTTCGGC
451 TTTGCAAATT GCTTGATACG GCGCGGTTTG CAGGCCTGCT TTGCGTATCC
501 ATGCCTTTTC CTGAATGCGG TTTTGCCTGA TGGCAACGCA GTCGCCGCTG
551 GGGGAAACAT TGGTATGTTT GGCGAGAAAA CGCATCGCAT CGGCATTGAC
601 GTTTTCGAAC TCGGTCGTAA CAGCCGCACA TTTTGCCAAT TCTTCCAAAG
651 CGGTTTGGTT GTCAAACGGC GCACACAAAT GCGGTCGGC AAATTCGCT
701 GCCGCGCAT TCGGTTGGG ATCGAGTACG GTTACTTTGT AGCCCATGGT
751 TTTGCGAGCA ACAGTAAACA TTCTGCCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2140; ORF 658.a>:

```

a658.pep
1  MVAGIVRTRR DFVDDQFMRV ADNKHFYRQY ADVVQFIGQT LRHLSRLLLN
51  VGTQSGWDDG VGEDTVEFNV FGRIESLHV IVQTAYDNGN FAAQVHHFFQ
101 NAIHAAVFGK RGFEFIHRFD ADLAFAVIAQ CSGFQDAGQK LYAFFSDVFG
151 FANCLIRRLG QACFAYPCLF LNAVLRDNGA VAAGGNIGMF GEKTHRIGID
201 VFELGRNSRT FCQFFQSGLV VKRRTQMAVG KFCRRIRVG IEYGYFVAHG
251 FGSNSKHSAS*

m658/a658 75.3% identity in 259 aa overlap

          10      20      30      40      50      60
m658.pep  MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLRLLHVGTSRGGDDG
a658      MVAGIVRTRRDFVDDQFMRVADNKHFYRQYADVQFIGQTLRHLRLLNVGTQSGWDDG
          10      20      30      40      50      60

          70      80      90      100     110     120
m658.pep  ISQDAVFVDVFGRVESLHVIVQTAYDYGNTAQIHFFQNAIHAAVFGKRGFEFIQCFY
a658      VGEDTVEFNVFGRIESLHVIVQTAYDNGNFAAQVHHFFQNAIHAAVFGKRGFEFIHRFD
          70      80      90      100     110     120

          130     140     150     160     170     180
m658.pep  ADLTFVAVQSRFQDAGQKLACFSDFSLTNHLIRRLQSRFAYPCLFLNAVLCNRHT
a658      ADLAFAVIAQCSGFQDAGQKLYAFFSDVFGFANCLIRRLQACFAYPCLFLNAVLRDNGA
          130     140     150     160     170     180

          190     200     210     220     230     240
m658.pep  IAARGNIGMFQKAHRIGIDVFKFSGHRRAFCQFVQSSLVVKRRAQMAVGKFCRRVRIG
a658      VAAGGNIGMFGEKTHRIGIDVFELGRNSRTFCQFFQSGLVVKRRTQMAVGKFCRRIRVG
          190     200     210     220     230     240

          250     260
m658.pep  VENGYFVAHGFGNGKHSAX
a658      IEYGYFVAHGFGSNGKHSAX
          250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2141>:

1051

```

g661.seq
1  ATGCACATCG GCGGTATTAT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GCGGGGCATT GCCGACAAAC CCTTCCGCCG CCTCTGTCGG GCGTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGGCCA GCGATCCGAC GCTCAGGAAT
151 ACCGGA AAAA CCtgcaccg cagtgaTTTt gccgatgaag gCGGCATCGT
201 TGCCGTGCAG ATTGCCGGCA GCGACCccga acaGATGGCG Gatgcggcgc
251 gttacAACGT CCGACTCGGG GCGCAGGTCA TCGACATcaa TATGGGCTGC
301 cccgccaaGA AAGTGTGCAA CGTCCAAGCC GGTAGCGCGc tGATGCAGGA
351 CGAGccgctg gttgcCgcca tTTtggaggc ggtggtcAAG GCGGCGGcg
401 TACCCGTTAC cctCAAAACc cgtTtgggtt ggcacgacga cgatcaaaac
451 ctgcCcgccg tcgccaaaat cgcgaagat tgcggcattg ccgccCttgc
501 cgttccacgg gcgCGcgcgC ACGCAAATGT ACAAAGGCCG GCGcGTTAC
551 Gaactcatcg CCGAGACCAA AAGccgTCTG AACATCCCGG cctGggtCAA
601 CCGCGACATC actTCgcgcg AAAAAGCCGC CGccgTCCTC AAACAAACCG
651 CCGCCGACGG CATCATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTT
701 TTCCGCGATT TGAAGCATTG TGCCGAACAC GCGGTTTTAC CGCCTGCCTT
751 GAGTTTGGCA GAATGCAGAG CCGCCATTTT GAACACATC CGCGCCATGC
801 ACGCGTTTTA TGGTGAGACC GTCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGCGGAAAT GCCCGACGCG GAACAGGCGC GCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2142; ORF 661.ng>:

```

g661.pep
1  MHIGGYFIDN PIALAPMAGI ADKPFRRLCR AFGAGWAVCE MLASDPTLRN
51  TGKTLHRSDF ADEGGIVAVQ IAGSDPEQMA DAARYNVGLG AQVIDINMGC
101 PAKKVCNVQA GSALMQDEPL VAAILEAVVK AAGVPVTLKT RLGWHDHDDQN
151 LPVAKIAED CGIAALAVPR ARAHANVQRR GALRTHRRDQ KPSEHPGLGQ
201 RRHHFAAKSR RRPQTNRRRR HHDRRARRAQ AVVFPRFEAL CRTRRFTACL
251 EFGRMQSRHE EPHPRHARVL WXDRRCAHRT QTHRLVHRRN ARRTTGAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2143>:

```

m661.seq
1  ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GCGGGGCATT ACCGACAAAC CGTTCGCCCG ACTTTGCCGA GATTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTTGCACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTCTGCAA GTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCCGCTG GTTGCCGCCA TTTTGAAGC CGTCGTCCGT GCGGCAGGCG
401 TACCCGTTAC CCTCAAAACc CGTTTGGGTT GGCACGACGA CCATCAAAAC
451 CTGCCCCTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATCG CCGCCCTTGC
501 CGTCC.AC GG ACGCACGCGT ACGCAAATGT ACAAAGGCCG A3CGCGTTAC
551 GAACTCATCG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601 CGCGGACATT ACTTCGCCCG AAAAAAGCCA AGCCGTCCTC AAACAAACCG
651 CCGCCGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTC
701 TTCCGCGATT TGAACATTA TGCCGAACAC GGTGTTTTGC CGCCTGCCTT
751 GAGTTTGGCA GAATGCGCGC CCGCTATTTT GAACACATC CGCGCCATAC
801 ACGCGTTTTA CGGCGACACC GCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCCCGACGCG GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2144; ORF 661>:

```

m661.pep
1  MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVR AAGVPVTLKT RLGWHDHQN
151 LPVIAKIAED CGIAALAVXR THAYANVQRR SALRTHRRNQ MPSEHPGLGQ
201 RRHYFAAKSP SRPQTNRRRR HYDRARRARQ AVVLPREFEL CRTRCFAACL
251 EFGMRRRRYF EPHPRHTRVL RRHRRCAHRT QTHRLVHRRN ARRTDTS*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m661/g661 88.5% identity in 295 aa overlap

1052

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					
g661	MHIGGYFIDNPIALAPMAGIADKPFRRLLCRAFGAGWAVCEMLASDPTLRNTGKTLHRSDF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m661.pep	ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL					
g661	ADEGGIVAVQIAGSDPEQMADAARYNVGLGAQVIDINMGCPAKKVCNVQAGSALMQDEPL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m661.pep	VAAILEAVVRAAGVPVTLKTRLGWHDDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR					
g661	VAAILEAVVKAAGVPVTLKTRLGWHDDQNLPVAKIAEDCGIAALAVPRARAHANVQRR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m661.pep	SALRTHRRNOMPSEHPGLGQRRHYFAAKSPSRPQTNRNRRRHDRARRARQAVVLPREFETL					
g661	GALRTHRRDQKPSEHPGLGQRRHHFAAKSRRRPQTNRNRRRHDRARRARQAVVFPREFEAL					
	190	200	210	220	230	240
	250	260	270	280	290	299
m661.pep	CRTRCFAACLEFGRMRRRYFEPHPRHTRVLRHRRCAHRTQTHRLVHRRNARRRTDTSX					
g661	CRTRRFTACLEFGRMQSRHFEPHPRHARVLWXDRRCAHRTQTHRLVHRRNARRRTGAAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2145>:

```

a661.seq
1  ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GCGCGGCATT ACCGACAAAC CGTTCGCCCG ACTTTGCCGA GATTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTGCAACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCCGCTG GTTGCCGCCA TTTTGAGGGC GGTGGTCAA GCGGCGGGCG
401 TACCCGTTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
451 CTGCCCGTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATTG CCGCCCTTGC
501 CG.TCCACGG ACGCACGCGC ACGCAAATGT ACAAAGGCGA AGCGGCTTAC
551 GACCTGATTG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601 CCGCGACATT ACCTCGCCGC AAAAAGCCCA AGCCGTCTC AAACAAACCG
651 CCGCAGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG ACCGTGTTTC
701 TTCCGCGATT TGAACATTA CGCCGAACAC GGTGTTTAC C3CCTGCCTT
751 GAGTTTGGCA GAATGTACCG CCACTATTTT GAACCACATC CGAGCCATGC
801 ACGCGTTTTA CGCGCACACC GCCGGTGTGC GCATCGCAGC CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCCCACGGC GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2146; ORF 661.a>:

```

a661.pep
1  MHIGGYFIDN PIALAPMAGI TDKPFRRLLCR DFGAGWAVCE MLTSDPTLRN
51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQQMA DAARYNVSLG AQLIDINMG
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVK AAGVPVTLKT RLGWHDDHQN
151 LPVIAKIAED CGIAALAXPR THAHANVQRR SGLRPDCRNQ MPSEHPGLGQ
201 RRHYLAAKSP SRPQTNRNRR HYDRARRARQ TVVLPREFETL RRTRCFTACL
251 EFGMRMYRHYF EPHPSHARVL RRHRRCAHRT QTHRLVHRRN ARRRTDTS*

```

m661/a661 94.6% identity in 298 aa overlap

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					

1053

```

a661      MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF
           10      20      30      40      50      60

           70      80      90      100     110     120
m661.pep  ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           |||||
a661      ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           70      80      90      100     110     120

           130     140     150     160     170     180
m661.pep  VAAILEAVVRAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR
           |||||
a661      VAAILEAVVKAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAXPRTHAHANVQRR
           130     140     150     160     170     180

           190     200     210     220     230     240
m661.pep  SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRRRRHYDRARRARQAVVLPFRFETL
           |::|
a661      SGLRPDCRNQMPSEHPGLGQRRHYLAAKSPSRPQTNRRRRHYDRARRARQTVVLPFRFETL
           190     200     210     220     230     240

           250     260     270     280     290     299
m661.pep  CRTRCFAACLEFGRMRRRYFEPHPRHTRVLRHRHRCARHTQTHRLVHRRNARRRDTDSX
           |||||
a661      RRTRCFACLEFGRMYRHYFEPHSHARVLRHRHRCARHTQTHRLVHRRNARRRDTDSX
           250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2147>:

```

g663.seq
1  ATGTGTACCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGGCCTGATC GSTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTGGCA
151 AAATGTTTTT CCGAATGGGA CGAAGAAAAG CGTAAAACCG TGTGAAACA
201 GCATTTCAA CACATGGCAA AACTGATGCT CGAATACGGC TTATATTGGT
251 ACGCGtctGC CAAATGCCTG AAATCGCTGG TCGCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTACCC
351 GCACTTTACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATGTCC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAg gccgcaACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAagggtcg cgCGCCctcg TCAAACAGTT CCGCAAAAGC AGTGCGCCGT
551 TCCTGTATCT GCCGATCAG GATTTTCGAC GCAACAATTC GGTTTTGTG
601 GATTTTTTCG GCATtcagaC GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CCGCCTTGCA AATGCAAAAG TGATACCGC CATTCCGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAA TTCTATCCG CTTGGAATC CTTCCGAGT
751 GAAGACGCGC AAGCCGACGC GCAACGTATG AACCGCTTA TCGAAGAACG
801 CGTGCGCGAA CACCCGGAAC AATATTTCTG GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2148; ORF 663.ng>:

```

g663.pep
1  MCTEMKFIFF VLYVLQFLPF ALLHKIAGLI GSLAYLLVKP RRRIGEINLA
51  KCFPEWDEEK RKTVLKQHFH HMAKLMLEYG LYWYASAKCL KSLVRYRNKH
101 YLDDALAAGE KVILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VELIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNNSVVF
201 DFFGIQTATI TGLSRIAALA NAKVIPAI PV READNTVT LQ FYPAWSFSP
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK REKTRPEGSP DFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2149>:

```

m663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGACCTGACG GGTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTGGCA
151 AAATGTTTTT CCGAATGGAG TGAGGAAAAG CGTAAAACCG TGTGAAACA

```

```

201 GCATTTCAAA CACATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCTGC CGGACGTTTG AAATCGCTGG TGGCTACCG CAATAAGCAT
301 TATTTGACG ACACGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATATCC
401 CGCTGATCAG TATGTATTCC CATCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCCCGATCAG GATTTCGGAC GCAACGATTC GGTTTTGTG
601 GATTTTTTCG GTATTTCAGC GGCAACGATT ACCGGATTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCCGTC CGCGAGGCAG
701 ACAATACGGT TACATTGCAT TTCTACCCGT CTGGAAATC CTTCGGGGT
751 GAAGACGCGA AACCCGACGC GCAGCGCATG AACCGTTTGA TCGAAGACAG
801 GGTGCGCGAA CATCCGGAAC AATATTTTGT GCTGCACAAG CGTTTAAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2150; ORF 663>:

```

m663.pep
1  MCIEMKFIFF VLYVLQFLPF ALLHKIADLT GLLAYLLVKP RRRIGEINLA
51  KCFSEWSEK RKTVLKQHPK HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVILYPHFT AFEMAVYALN QDIPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDSVFE
201 DFFGIQTATI TGLSRIAALA NAKVIPAI PVREADNTVTLH FYPAWSFPG
251 EDAKADAQRM NRFIEDRVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m663/g663 94.9% identity in 293 aa overlap

```

m663.pep      10      20      30      40      50      60
MCIEMKFIFFVLYVLQFLPFALLHKIADLTGLLAYLLVKPRRRIGEINLAKCFSEWSEK
|||
g663          10      20      30      40      50      60
MCTEMKFIFFVLYVLQFLPFALLHKIAGLIGSLAYLLVKPRRRIGEINLAKCFPEWDEEK
|||

m663.pep      70      80      90      100     110     120
RKTVLKQHPKHKMAKLMLEYGLYWYAPAGRLKSLVRYRNKHLYDDALAAGEKVILYPHFT
|||
g663          70      80      90      100     110     120
RKTVLKQHPKHKMAKLMLEYGLYWYASAKCLKSLVRYRNKHLYDDALAAGEKVILYPHFT
|||

m663.pep     130     140     150     160     170     180
AFEMAVYALNQDIPLISMYS HQKNKILDEQILKGRNRYHN VFLIGRTEGLRALVKQFRKS
|||
g663         130     140     150     160     170     180
AFEMAVYALNQDVPLISMYS HQKNKILDEQILKGRNRYHN VFLIGRTEGLRALVKQFRKS
|||

m663.pep     190     200     210     220     230     240
SAPFLYLPDQDFGRNDSV FVDFFGIQTATITGLSRIAALANAKVIPAI PVREADNTVTLH
|||
g663         190     200     210     220     230     240
SAPFLYLPDQDFGRNNSV FVDFFGIQTATITGLSRIAALANAKVIPAI PVREADNTVTLQ
|||

m663.pep     250     260     270     280     290
FYPAWSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSPDFYX
|||
g663         250     260     270     280     290
FYPAWSFPSDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSPDFYX
|||

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2151>:

```

a663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCACTT
51  TCTGCCGTTT GCGCTGCTGC ACAAACTTGC TGATCTGACA GGCTTGCTCG
101 CCTACCTTTT GGTCAAACCC CGCCGCCGTA TCGGCGAAAT CAATTGGCA

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1055

```

151 AAATGCTTTC CCGAGTGGGA CGGAAAAAAG CGTAAACCG TGTGAAACA
201 GCATTTCAAA CATATGGCGA AACTGATGTT SGAATACGGT TTATATTGGT
251 ACGCGCCCGC CGGGCGTTTG AAATCACTGG TGGCTACCG CAACAAACAT
301 TATTTGGACG ACGCTCTGGC GGCAGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACCTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTCAAT CAGGATGTTT
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAC GTTTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCCCGATCAG GATTTCGGAC GCAACGATTC GGTTTTTGTC
601 GATTTCCTCG GTATTCGGAC GGCAACGATT ACCGGCTTGA CCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATCCCTGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAT TTCTACCTGT CTGGGAATC CTTTCCGAGT
751 GAAGATGCGC AGGCCGACGC GCAGCGCATG AACCCTTTTA TCGAGGAACG
801 CGTGCAGGAA CATCCGAGC AGTATTTTGT GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2152; ORF 663.a>:

```

a663.pep
1  MCIEMKFIFF VLYVLQFLPF ALLHKLADLT GLLAYLLVKP RRRIGEINLA
51  KCFPEWDGKK RRTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIIILYPHT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDSVFV
201 DFFGIRTTAT TGLSRIAALA NAKVIPAIPV READNTVTLH FYPAWESFBS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

m663/a663 96.2% identity in 293 aa overlap

      10      20      30      40      50      60
m663.pep MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKPRRRIGEINLAKCFSEWSEEK
a663      MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKPRRRIGEINLAKCFPEWDGKK
      10      20      30      40      50      60

      70      80      90     100     110     120
m663.pep RRTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKHYLDDALAAGEKVIILYPHT
a663      RRTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKHYLDDALAAGEKVIILYPHT
      70      80      90     100     110     120

      130     140     150     160     170     180
m663.pep AFEMAVYALNQDIPLISMYSHQKNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS
a663      AFEMAVYALNQDVPLISMYSHQKNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS
      130     140     150     160     170     180

      190     200     210     220     230     240
m663.pep SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAALANAKVIPAIPVREADNTVTLH
a663      SAPFLYLPDQDFGRNDSVFVDFFGIRTATITGLSRIAALANAKVIPAIPVREADNTVTLH
      190     200     210     220     230     240

      250     260     270     280     290
m663.pep FYPAWKSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSPDFYX
a663      FYPAWESFSEDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSPDFYX
      250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2153>:

```

g664.seq
1  ATGATACATC CGCACCACCT CCGCGCCTTT TTCATAAACG GTCATGGTGT
51  AGAAATGTGT CATCTCTCTCA TAGCTGACgg gCGCACCGG ATGGGCGGTC
101 GGGCCTGCGT CTTCCGGGGA CTGGTTCTGG CGCAGCAGGC GGATGTTCTC
151 GATCGGCGGC ACGCGCGGCG CGGCGCGGTC GCCGGAAAAC TCTTGGTCGC
201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCG
251 GTTACGCGGT TGCCCCTCCA GTTGTGGAAT TATTCGTGTC CGACCACGGA
301 TTCAATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCGAGGA
351 CGAACTTGGT GTTAAAAATG TTCAAACCTT TGTTTTCAT CCGGCCATA
401 TTGAAATCGC CTACGCGGAC GACCATGAaa atatccaagt cataTTCcaa
451 cCgaagcgc gtttcgtcCc acttcatcgC gttTTTTCaa cgaTTCCACG
501 GCAAAGCCGA CCTTGGGTTT GTCCGCTTCG GTGGTGTAaa ACTCGATTTT

```


1056

551 GA

This corresponds to the amino acid sequence <SEQ ID 2154; ORF 664.ng>:

g664.pep

```

1  MIHPHHFRAF FINGHGVEIV HLLIADGAHR MGRACVFGE LVLAQQADV
51  DAAHGAAGAV AGKLLVAEHG QPFLQRKLEP VAAGYAVARP VVEIFVSDHG
101 FNAFEIGIGG GAAVGEDELG VKNVQTLVFH RAHIEIAYGD DHENIQVIFQ
151 PEARFVPLHR VFSTIPRQSR PWVCPLRWCK TRF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2155>:

m664.seq

```

1  GTGATACATC CGCACTACTT CCGCGCCTTT TTCATAAACG GTCATGGTGT
51  AGAAATTGTT CATCTCCTCA TAGCTGGCGG GCGCACCGG ATGGGCGGTC
101 GGGCCTGCGT CTTCGGGGAA CTGGTGCTGG CGCAGCAGGC GGATGTTTTC
151 GATGCGGCGC ACGGCGCGGC TGGCGCGGTC GCCGGAAAAT TCTTGGTCCG
201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTTACGCGGT TGCCCGTCCA GTTGTGAAA TACTCGTGTC CGACCACGGA
301 TTCCGATGCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCAAGGA
351 CGAACTTGGT GTTAAAGATG TCAAAACCT TGTTTTCCAT CGCGCCATA
401 TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
451 ACCGAAGCGC GTTTCGTCCC ATTTTCATGC GTTTTTT.CAA CGATTCCACG
501 GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGTAAG ACTCGATTTT
551 GA
```

This corresponds to the amino acid sequence <SEQ ID 2156; ORF 664>:

m664.pep

```

1  VIHPHYFRAF FINGHGVEIV HLLIAGGAHR MGRACVFGE LVLAQQADV
51  DAAHGAAGAV AGKFLVAEHG QPFLQRKLEP VAAGYAVARP VVEILVSDHG
101 FDAFEIGIGG GAAVGKDELG VKDVQTLVFH RAHIEIAHGD DHENIQVVFQ
151 TEARFVFFHR VFXTIPRQSR PWACPLRWCK TRF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m664/g664 91.8% identity in 183 aa overlap

	10	20	30	40	50	60
m664.pep	VIHPHYFRAFF	FINGHGVEIV	HLLIAGGAHR	MGRACVFGE	LVLAQQADV	FDAHGAAGAV
	:					
g664	MIHPHHFRAFF	FINGHGVEIV	HLLIADGAHR	MGRACVFGE	LVLAQQADV	LDAHGAAGAV
	10	20	30	40	50	60
	70	80	90	100	110	120
m664.pep	AGKFLVAEHG	QPFLQRKLE	FVAAGYAVAR	PVVEILVSDH	GDFAFEIGIG	GGAAGKDELG
g664	AGKLLVAEHG	QPFLQRKLE	FVAAGYAVAR	PVVEIFVSDH	GFNAFEIGIG	GGAAGKDELG
	70	80	90	100	110	120
	130	140	150	160	170	180
m664.pep	VKDVQTLVFH	RAHIEIAHG	DDHENIQVVF	QTEARFVPF	HRVFXTIPR	QSRPWACPLRWCK
g664	VKNVQTLVFH	RAHIEIAYG	DDHENIQVIF	QPEARFVPL	HRVFSTIPR	QSRPWVCPLRWCK
	130	140	150	160	170	180
m664.pep	TRFX					
g664	TRFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2157>:

a664.seq

```

1  GTGATACATC CGCACCCTT CCGCGCCTTT TTCATAAACG GTCATGGTGT
51  AGAAATTGTT CATCTCCTCA TATCGGCGG GCGCACCGG ATGTGCGGTC
101 GGACCTGCGT CTTCGGGGAA CTGGTGCTGG CGCAGCAGGC GGATGTTTTC
151 GATACGGCGC ACGGCGCGGC TGGCGCGGTC GCCGGAAAAT TCTTGGTCCG
```

1057

```

201 GGAACACGGT CAACCCCTCC TTCAGCGAAA GCTGGAACCA GTCCGCGGCAG
251 GTCACGCGGT TGCCCGTCCA GTTGTGGAAA TATTCGTGTC CGACCACGGA
301 TTCGATGCTT TCAAAATCGG TATCGGTGGC GGTACGGCTG TCGGCAAGGA
351 CGAACTTGGT GTTAAAGATG TTCAAACCTT TGTTTCCAT CGCACCATA
401 TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
451 ACCGAAGCGC GTTTCGTCCC ACTTCATTGC GTTTTT.CAG CGATTCCACG
501 GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGTAAA ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence <SEQ ID 2158; ORF 664.a>:

```

a664.pep
1  VIHPHHERAF FINGHGVEIV HLLISGGAHR MGRTCVFGE LVLAQQADV
51  DTAHGAAGAV AGKFLVAEHG QPFLQRKLEP VAAGHAVARP VVEIFVSDHG
101 FDAFKIGIGG GTAVGKDELG VKDVQTLVFH RTHIEIAHGD DHENIQVVFQ
151 TEARFVPLHC VFXAIPRQSR PWACPLRWCK TRF*

```

m664/a664 92.9% identity in 183 aa overlap

```

          10      20      30      40      50      60
m664.pep  VIHPHYFRAFFINGHGVEIVHLLIAGGAHRMGRACVFGELVLAQQADVFDAAHGAAGAV
          ||||:||||:||||:||||:||||: ||:||||:||||:||||:||||:
a664       VIHPHHFRAFFINGHGVEIVHLLISGGAHRMGRTCVFGELVLAQQADVFDTAHGAAGAV
          10      20      30      40      50      60

          70      80      90      100     110     120
m664.pep  AGKFLVAEHGQPFLQRKLEPVAAGYAVARPVVEILVSDHGFDAFEIGIGGGAAGVKDELG
          ||||:||||:||||:||||:||||: ||||:||||:||||:||||:
a664       AGKFLVAEHGQPFLQRKLEPVAAGHAVARPVVEIFVSDHGFDAFKIGIGGGTAVGKDELG
          70      80      90      100     110     120

          130     140     150     160     170     180
m664.pep  VKDVQTLVFHRAHIEIAHGDHDENIQVVFQTEARFVFPFHRVEXTIPRQSRPWACPLRWCK
          ||||:||||:||||:||||:||||: ||||:||||:||||:||||:
a664       VKDVQTLVFHRTHEIAHGDHDENIQVVFQTEARFVPLHCVFXAIPRQSRPWACPLRWCK
          130     140     150     160     170     180

m664.pep  TRFX
          ||||
a664       TRFX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2159>:

```

g665.seq
1  atgaagtGgG acgaaacgcg cttcgGgttg GAAatgact tggatatttt
51  CATGGTCGTC GCCGTAGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
101 GTTTGAACAT TTTTAACACC AAGTTCGTCC TCGCCGACAG CCGCACCGCC
151 ACCGATACCG ATTTCGAAGG CATTGAATCC GTGGTCGGAC ACGAATATTT
201 CCACAACCTGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAGTT TTCCGGCGAC
301 CGCGCCGGCC GCGCCGTGCG CCGCATCGAG AACATCGGCC TGCTGCGCCA
351 GAACCACTTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCcccg
401 TCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GGCGCGGAAG TGGTGC GGAT GTATCATAACC CTGCTCGCGG AAGAGGGCTT
501 CCAAAAAGGC ATGAAGCTAT ATTTCCaacg CCACGACGGA CAGGCAGTGA
551 CCTGCGACGA TTTCCGCGCG GCGatggcgg ATGCGAACGG CATCAATCTC
601 GACCACTTCG CTTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGAAGC
651 CGAAGGCCGT CTGAAAAACA ATGTTTTCGA GTTAACCATT AAACAAACCG
701 TGCCGCCACG GCCCGATATG GCGGACAAAC AGCCGATGAT GATTCCCGTC
751 AAAGTCGGGC TTCTGAACCG CAACGCGCAA GCGGTGGCAT TCGATTATCA
801 GGGCAAACGC GCAACCGAAG CCGTGTGCT GATGACCGAA GCCGAACagg
851 CCTTCCCGCT CGAAGGTGTA ACCGAAGCCG TCGTTCCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCAGTGTA TCTGAACTAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCACG ACAGCGACGC TTTCACGTGC TGGGAAGCCG

```

```

1001 CCCAAACGCT CTACCGTCGC GCCGTCGCCG CCAACCTTGC CGCGCTTTCA
1051 GACGGCATCG GGTTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TGGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCGTC CGAAGCCGAA ctGTGGGACG GCACGGAAAA CATcgaCCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGtcCG
1251 CttcctgcCG AAATGGCACG AATTGGaccg tcagggcgcg aagCAggaaa
1301 accaaagtTA CGAATACAGC CCCGAAACCG CCGACTGGCG CACGCTGCGC
1351 AACGTTCTGCC GCGCCTtcgt cctGCGCGCC GACCCGCGCG acatcgAAAC
1401 TGTTGCCGAA Aaatacggcg AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCGCTCAAC GGCAACGAAA GCGATACGCG CAACTGCCTG
1501 CTGGCGCAGT TTGCCGcaa gTtttcAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTCGCC CTTATCGGCT CAAGcgcgcg cagCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAATTCA GTCTCGAAAA CCCCAACAAA
1651 GCCCGTTCCG TCATCGGCAG CTTAGCCCGC AACGTCCCGC ATTTTCACGC
1701 ACAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA cCCGAggtc gccGCCCGC TGGTGCAGG GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTgGTGAAC AAGAATTGCA
1851 GTGCATTCCG GCGCAGGAAG GATTGTCGAA AGacGTGSGC CAaatcgtCG
1901 GCAAGATTTT GGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2160; ORF 665.ng>:

g665.pep

```

1 MKWDETRFGL EYDLDFMVV AVGDFNMGAM ENKGLNIFNT KFLVADSRTA
51 TDTFDEGLIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RAGRAVRRIE NIRLLRQNF PEDAGPTAHP VRPVSYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAEGR LKNNVFELTI KQTVPTPDM ADKQPMIPV
251 KVGLLNRRGE AVAFDYQGR ATEAVLLMTE AEQAFPLEGV TEAVVPSLLR
301 GFSAPVYINY PYSDDDLLLL LAHDSDAFTC WEAAQTLYRR AVAANLAALS
351 DGIGLPHKEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGTENIDP
401 LRYHQAREAL LDTLAVRFLP KWHELDROAA KQENQSYEYS PETADWRTL
451 NVCR AFLRA DPAHIETVAE KYGEMAQNM HEWGILSAVN GNESDTRNCL
501 LAQFADKFSD DALVMDKYFA LIGSSRRSDT LQQVQTALQH PKFSLNPNK
551 ARSLIGFSR NVPHFHAQDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQELQCIR AQEGLSKDVG EIVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2161>:

m665.seq

```

1 ATGAAATGGG ACGAAACGCG CTTGCGTTTG GAATACGACT TSGATATTTT
51 CATGGTCGTC GCCGTGGGCG ATTTCAATAT GGGCGCGATG GAAAAACAAGG
101 GTTTGAACAT CTTTAACACC AAGTTCGTCC TTGCCGACAG CCGCACCGCC
151 ACCGATACCG ATTTCAAGG CATCGAATCC GTGGTCGGAC ACGAGTATTT
201 CCACAACCTG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAAT TTCCGGCGAC
301 CGCGCCAGCC GCGCCGTGCG CCGCATCGAA AACATCCGCC TGCTGCGCCA
351 GCACCAAGTC CCCGAAGACG CAGGCCUGAC CGCCCATCCG GTGCGCCCG
401 CCAGCTATGA GGAGATGAAC AATTCTACA CCATGACCGT TTATGAAAAA
451 GCGCGGAAG TAGTGCGGAT GTATCACACC CTGCTCGCGC AAGAGGGCTT
501 CCAGAAAGGC ATGAAGCTCT ATTTCAACG CCACGACGGA CAGGCCGTTA
551 CCTGCGACGA TTTCCGCGCG GCGATGGCGG ACGCGAAGCG CATCAATCTC
601 GACCAGTTCG CTTGTGGTA CAGCCAGCGG GGCACGCCCG TTTTGGAAGC
651 GGAAGTTCGT CTGAAAAACA ATATTTTCGA GTTGACCGTC AAACAAACCG
701 TGCCGCCAC GCGGATATG ACGGATAAAC AGCCGATGAT GATTCCCGTC
751 AAGGTCGGGC TGCTGAACCG CAACGGCGAA GCGGTGGCAT TCGACTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTGCT GCTGACCGAA GCCGAACAGA
851 CCTTCTGCT CGAAGGCGTA ACCGAAGCCG TCGTTCCTC GCTGTGCGC
901 GGGTTCAGCG CGCCGGTGCA TCTGAACTAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCATG ACAGCGACG CTTACGCGC TGGGAAGCCG
1001 CCCAAACGCT CTACCGCCGC GCCGTCGCCG CCAACCTTGC CACGCTTTCA
1051 GACGGCGTTG AGCTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TAGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCATC CGAAGCCGAG CTGTGGGACG GCGCAGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGTCCA
1251 CTTCTGCGCG AAATGGCACG AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAATACAGC CCCGAAGCCG CCGGCTGCGC CACGCTGCGC

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1059

```

1351 AACGTCTGCC GCGCCTTTGT CCTGCGCGCC GACCCCGCGC ACATCGAAAC
1401 CGTTGCCGAA AAATACGGCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTGCC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCGAACCGC CTTGCAGCAT CCGAAATTCA GCCTCGAAAA CCCCAACAAA
1651 GCGCGTTCGC TCATCGGCAG CTTAGCCGCG AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA CCCGAGGTC GCCGCCCGCT TAGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTCCG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2162; ORF 665>:

m665.pep

```

1 MKWDETRFGL EYDLDFMVV AVGDFNMGAM ENKGLNIENT KFLVADSRTA
51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPASYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFORHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAAGR LKNNIFELTV KQTPVPTPDM TDKQPMMPV
251 KVGLLNRNGE AVAFDYQGR ATEAVLLLTE AEQTFLLLEGV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLL LAHDSDAFTR WEAQAQTLYR AVAANLATLS
351 DGVELPKHEK LLAAVEKVIS DDLDNAFA LLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDTLAVHFLP KWHELNQAA KQENQSYEYS PEAAGWRTL
451 NVCRAFLRA DPAHIETVAE KYGEMAQNT HEWGILSAVN GNESDTRNRL
501 LAQFADKFS DALVMDKYFA LVGSSRRSDT LQQVRTALQH PKFSLENPNK
551 ARSLIGSFSR NVPHFHAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQIR AQEGLSKDVG EIVGKILD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m665/g665 96.1% identity in 637 aa overlap

	10	20	30	40	50	60
m665.pep	MKWDETRFGL EYDLDFMVVAVGDFNMGAMENKGLNIENTKFLVADSRTATDTDFEGIES					
g665	MKWDETRFGL EYDLDFMVVAVGDFNMGAMENKGLNIENTKFLVADSRTATDTDFEGIES					
	10	20	30	40	50	60
	70	80	90	100	110	120
m665.pep	VVGHEYFHNW TGNRVTCRDW FQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF					
g665	VVGHEYFHNW TGNRVTCRDW FQLSLKEGLTVFRDQEFSGDRAGRAVRRIENIRLLRQNF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m665.pep	PEDAGPTAHPVRPASYEEMN NFYTMTVYEK GAEVVRMYHTLLGEEGFQGMKLYFORHDG					
g665	PEDAGPTAHPVRPVSYEEMN NFYTMTVYEK GAEVVRMYHTLLGEEGFQGMKLYFORHDG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m665.pep	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTPVPTPDM					
g665	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTPVPTPDM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m665.pep	TDKQPMMPV KVGLLNRNGE AVAFDYQGRATEAVLLMTEAEQAFPLEGVTEAVVPSLLR					
g665	ADKQPMMPV KVGLLNRNGE AVAFDYQGRATEAVLLMTEAEQAFPLEGVTEAVVPSLLR					
	250	260	270	280	290	300

1060

	310	320	330	340	350	360
m665.pep	GFSAPVHLNYPYSDDDLLLLLAHDSDAFTRWEAAQTLYRRAVANLATLSDGVELPKHEK					
	: : : : :					
g665	GFSAPVYLNYPYSDDDLLLLLAHDSDAFTCWEAAQTLYRRAVANLAALSDGIGLPKHEK					
	310	320	330	340	350	360
	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNFAKALLLGVPSEAEALWDGAENIDPLRYHQAREALLDTLAVHFLP					
	: : : : :					
g665	LLAAVEKVISDDLLDNFAKALLLGVPSEAEALWDGTENIDPLRYHQAREALLDTLAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNROAAKQENQSYEYSPEAAGWRTLNRNVCRAFLVLRADPAHIETVAEKYGEMAQNMT					
	: : : : :					
g665	KWHELDROAAKQENQSYEYSPETADWRTLNRNVCRAFLVLRADPAHIETVAEKYGEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
	: : : : :					
g665	HEWGILSAVNGNESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFSRNVPHFAEDGSGYRFIADKVEIDRFNPQVAARLVQAFNL					
	: : : : :					
g665	PKFSLENPNKARSLIGSFSRNVPHFAQDGSYRFIADKVEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQIRAQEGLSKDVGEIVGKILDX					
	: : : : :					
g665	CNKLEPHRKNLVKQELQCIRAQEGLSKDVGEIVGKILGX					
	610	620	630			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2163>:

```

a665.seq
1  ATGAAGTGGG  ACGAAACGCG  CTTCGGTTTG  GAATACGACT  TGGATATTTT
51  CATGGTCGTC  GCCGTGGGCG  ATTTCAATAT  GGGTGCATG  GAAAACAAGG
101 GTTTGAACAT  CTTTAACACC  AAGTTCGTCC  TTGCCGACAG  CCGTACCGCC
151 ACCGATACCG  ATTTGAAGG  CATCGAATCC  GTGGTCGGAC  ACGAATATTT
201 CCACAACGCG  ACGGGCAACC  GCGTGACCTG  CCGCGACTGG  TTCCAGCTTT
251 CGCTGAAGGA  AGGGTTGACC  GTGTTCCGCG  ACCAAGAATT  TTCCGGCGAC
301 CGCGCCAGCC  GCGCCGTGCG  CCGTATCGAA  AACATCCGCC  TGCTGCGCCA
351 GCACCACTTC  CCCGAAGACG  CAGGTCCGAC  CGCACATCCG  GTGCGCCCCG
401 CCCGATATGA  GGAGATGAAC  AATTTCCTACA  CCATGACCGT  TTATGAAAAA
451 GCGCGCGAAG  TGGTGCGGAT  GTATCACACC  TTGCTCGGCG  AAGAGGGCTT
501 CCAAAAAGGT  ATGAAGCTCT  ATTTCCAACG  CCACGACGGA  CAGGCTGTTA
551 CCTGCGACGA  TTTCCGCGCG  GCGATGGTGG  ACGCGAACGG  CATCAACCTC
601 GACCAATTCG  CCTTGTGTA  CAGCCAAGCA  GGTACGCCGG  TTTTAGATGC
651 TCAAGGGCGT  CTGAAAAACA  ATGTGTTTGA  GTTAACCATC  AAACAAACCG
701 TGCGGCCAC  GCCGATATG  GCGGACAAAC  AGCCGATGAT  GATTCCCGTC
751 AAAATCGGGC  TGCTGAACTG  CAACGCGGAA  GCGGTGGCAT  TTGATTATCA
801 GGGCAAACGC  GCGACCGAAG  CCGTGTGTCT  GCTGACCGAA  GCCGAACAGA
851 CCTTCCAGTT  CGAAAGCGTA  ACCGAAGCCG  TCGTTCCCTC  GCTGCTSCGC
901 GGGTTCAGCG  CGCCGGTGCA  TCTGAATAT  CCGTACAGCG  ACGACGACCT
951 GCTGCTTCTG  CTCGCCCATG  ACAGCGACGC  CTTACGCGCG  TGGGAAGCCG
1001 CACAAACGCT  CTACCGCCGT  GCCGTGCGCG  CCAACCTTGC  CGCGCTTTCA
1051 GACGGCGTCG  AGTTGCCGAA  ACACGAAAAA  CTGCTTGCCG  CCGTCGAAAA
1101 AGTCATTTC  GACGACCTCT  TAGACAACGC  TTTCAAAGCC  CTGCTTTTGG
1151 GTGTGCCGTC  TGAAGCCGAG  CTGTGGGACG  GCGCGGAAAA  CATCGACCCG
1201 CTGCGCTACC  ATCAGGCGCG  CGAAGCCTTG  TTGGATATAC  TTGCCGTCGG
1251 CTTTCTGCCG  AAATGGCAGC  AATTGAACCG  TCAGGCGCGC  AAGCAGGAAA
1301 ACCAAAGCTA  CGAGTACAGC  CCCGAAGCCG  CCGGTTGCGC  CACGCTGCGC
1351 AATGTCTGCC  GCGCCTTCGT  CTTGCGCGCC  GATCCGCGCG  ACATCGAAAC

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1061

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1401 CGTTGCCGAG AAATACGCCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTCCGCC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAGTTCA GCCTCGAAAA TCCCAACAAA
1651 GCCCCGCTCGC TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTTAA CCCGCAGGTC GCCGCCCGCC TGGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCAGAGCCGA CCGCAAAAAC TTGGTGAAC AAGCATTGCA
1851 GCGCATTCCG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2164; ORF 665.a>:

```

a665.pep
  1 MKWDETRFGL EYDLDFMVV AVGDFNMGAM ENKGLNIFNT KFLVADSRTA
 51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPARYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMVDANGINL
201 DQFALWYSQA GTPVLDAQGR LKNNVFELTI KQTVPPPTDM ADKQPMMPV
251 KIGLLNCNGE AVAFDYQGR ATEAVLLLE AEQTFQFESV TEAVVPSLLR
301 GFSAPVHLNY PYSDDLLLL LAHDSDAFTR WEAQAQTLYRR AVAANLAALS
351 DGVELPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDILAVRFLP KWHELNROAA KOENQSYEYS PEAAGWRTL
451 NVCRAFLVRA DPAHETVAE KYAEMAQNM HEWGILSAVN GNESDTRNRL
501 LAQFADKFS DALVMDKYFA LVGSSRRSDT LQQVQTALQH PKFSLENPNK
551 ARSLIGSFSS NVPHFAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQIR AQEGLSKDVG EIVGKILD*

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m665/a665 97.3% identity in 638 aa overlap

m665.pep	10	20	30	40	50	60
	MKWDETRFGLEYDLDFMVVAVGDFNMGAMENKGLNIFNTKFLVADSRTATDTDFEGIES					
a665	MKWDETRFGLEYDLDFMVVAVGDFNMGAMENKGLNIFNTKFLVADSRTATDTDFEGIES					
	10	20	30	40	50	60
m665.pep	70	80	90	100	110	120
	VVGHEYFHNWVTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF					
a665	VVGHEYFHNWVTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF					
	70	80	90	100	110	120
m665.pep	130	140	150	160	170	180
	PEDAGPTAHPVRPASYEEMNPFYTMTVYEKGAEVVRMYHTLLGEEGFQKGKMKLYFQRHDG					
a665	PEDAGPTAHPVRPARYEEMNPFYTMTVYEKGAEVVRMYHTLLGEEGFQKGKMKLYFQRHDG					
	130	140	150	160	170	180
m665.pep	190	200	210	220	230	240
	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPPPTDM					
a665	QAVTCDDFRAAMVDANGINLDQFALWYSQAGTPVLDAQGRKNNVFELTIKQTVPPPTDM					
	190	200	210	220	230	240
m665.pep	250	260	270	280	290	300
	TDKQPMMPVKVGLLNRRGEAVAFDYQGRATEAVLLLEAEQTFILEGVTEAVVPSLLR					
a665	ADKQPMMPVKIGLLNCNGEAVAFDYQGRATEAVLLLEAEQTFQFESVTEAVVPSLLR					
	250	260	270	280	290	300
m665.pep	310	320	330	340	350	360
	GFSAPVHLNYPYSDDLLLLLAHDSDAFTRWEAAQTLYRRAVAANLATLSGVELPKHEK					
a665	GFSAPVHLNYPYSDDLLLLLAHDSDAFTRWEAAQTLYRRAVAANLAALS DGVELPKHEK					
	310	320	330	340	350	360

1062

	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLP					
a 665	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDILAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNRQAQKQENQSYEYSPEAAGWRTLNRNVCRAFLVLRADFAHIETVAEKYGEMAQNMT					
a 665	KWHELNRQAQKQENQSYEYSPEAAGWRTLNRNVCRAFLVLRADFAHIETVAEKYAEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
a 665	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFNRNVPFHAEADGSGYRFIADKVIIDRFNPQVAARLVQAFNL					
a 665	PKFSLENPNKARSLIGSFNRNVPFHAEADGSGYRFIADKVIIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQIRAQEGLSKDVGEIVGKILD					
a 665	CNKLEPHRKNLVKQALQIRAQEGLSKDVGEIVGKILD					
	610	620	630			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2165>:

g665-1.seq

```

1  ATGAGCAAAA CCGTCCGTTA TCTGAAAGAT TACCAAACGC CTGCCTACCG
51  CATTCTTGAA ACCGAACTGC ATTTTCGACAT TGCCGAACCG CAAACCGTCG
101  TGAAGTCGCG TTTGACGGTC GAGCCGCAGA GGGCGGGCGA GCCCTGGTG
151  TTGGACGGTT CGGCAAAACT CTTGTCCGTC AAAATCAACG GCGCGGCGGC
201  GGATTATGTG TTGGAAGGCG AGACGCTGAC GATTGCAGAC GTACCGTCCG
251  AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGCG GGAACCAAAA
301  TCGCTGATGG GGCTGTATGC TTCCGGCGGC AATCTGTTTA CCCAGTGCGA
351  GCCGGAGGGC TTCCGCAAAA TCACGTTCTA CATCGACCGT CCGGATGTGA
401  TGTCCAAGTT CACGACCACC ATCGTCGCGG ACAAAAAACG CTATCCCGTT
451  TTGCTTTCCA ACGGCAACAA AATCGACGGC GGCGAGTTT CAGACGGCCG
501  CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551  CTTTGGTCGC GGGCGATTG GCGGTAACGG AAGACCGTTT CACCACCATG
601  AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAACC
651  CAAGTCGGC TTTGCCCTGG AATCGTTGAA AAACGCGATG AAGTGGGACG
701  AAACGCGCTT CGGTTTGAA TATGACTTGG ATATTTTCAT GGTCTGCGCC
751  GTAGGCGATT TCAATATGGG CCGATGGAA AACAGGGTT TGAACATTTT
801  TAACACCAAG TTCGTCCTCG CCGACAGCCG CACCGCCACC GATACCGATT
851  TCGAAGGCAT TGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901  GGCAACCGCG TAACCTGCGG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951  GCTGACCGTG TTCCGCGACC AAGAGTTTTC CGGCGACCGC GCCGGCCGCG
1001 CCGTCCGCGC CATCGAGAAC ATCCGCTGCG TGCGCCAGAA CCAGTTCCCG
1051 GAAGACGCGG GCCCGACCGC CCATCCGGTG CGCCCCGTCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAAAAAGGC GCGGAAGTGG
1151 TGCGGATGTA TCATACCTCG CTCGCGAAG AGGGCTTCCA AAAAGGCATG
1201 AAGCTATATT TCCAACGCCA CGACGGACAG GCAGTGACCT GCGACGATTT
1251 CCGCGCGCGG ATGGCGGATG CGAACGGCAT CAATCTCGAC CAGTTCCGCT
1301 TGTGGTACAG CCAGGCGGGC ACGCCCGTTT TGGAAGCCGA AGGCCGTCTG
1351 AAAACAATG TTTTCGAGTT AACCATTAAA CAAACCGTGC CGCCACGCCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAA GTCCGGCTTC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTCT ATTATCAGGG CAAACGCGCA
1501 ACCGAAGCCG TGTGCTGAT GACCGAAGCC GAACAGGCTT TCCCGCTCGA
1551 AGGTGTAAAC GAAGCCGTCG TTCCCTCGCT GCTCGCGGGG TTCAGCGCGC
1601 CAGTGTATCT GAACATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCCACGACA GCGACGCTTT CACGTGCTGG GAAGCCGCCC AAACGCTCTA
1701 CCGTGCGCCG GTCGCCGCCA ACCTTGCCGC GCTTTCAGAC GGCATCGGGT

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1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAACT CATTTCAGAC
1801 GACCTCTTGG ACAACGCCCTT CAAAGCCCTG CTTTGGGCG TGCCGTCCGA
1851 AGCCGAACCTG TGGGACGGCA CGGAAACAT CGACCCGCTG CGTACCATC
1901 AGGCGCGCGA AGCCTTGTGT GATACCTTG CCGTCCGCTT CCTGCCGAAA
1951 TGGCAGCAAT TGGACCGTCA GCGCGCGAAG CAGGAAACCC AAAGTTACGA
2001 ATACAGCCCC GAAACCGCCG ACTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCCGAC CCCGCGCACA TCGAACTGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CTGCCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTCCGCTT
2251 ATCGGCTCAA GCCGCCGAG CGACACCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAATTCAGTC TCGAAACCC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TTCACGCACA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCCACC GCTTCAACCC
2451 GCAGGTCGCG GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAAGCTCG
2501 AGCCGCACCG CAAAAACTTG GTGAAACAG AATTGCAGTG CATTGCGGCG
2551 CAGGAAGGAT GTTCGAAAGA CGTGGCGCAA ATCGTCGGCA AGATTTTGGG
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2166; ORF 665-1.ng>:

g665-1.pep

```

1 MSKTVRYLKD YOTPAYRILE TELHFDIAEP QTVVKSRLTV EPQRAGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAD VPSEFRTVEV ETEILPAENK
101 SLMLGYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSNDRHWV KWEDPFAPKS YLFALVAGDL AVTEDRFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYLDLIFMVVA
251 VGDFNMGAME NKGNIFFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR AGRVVRRIEN IRLLRQNFPP
351 EDAGPTAHPV RPSVYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNVFELTIK QTVPTPDMA DKQPMIIVK VGLLRNNGEA VAFDYQKRA
501 TEAVLLMTEA EQAFPLEGVT EAVVPSLLRG FSAFVLYNYP YSDDDLLLLL
551 AHSDAFTCW EAAQTLYRRA VAANLAALSD GIGLPKHEKL LAAVEKVIDS
601 DLLDNALFAL LLGVPSAEAL WDGTEINIDPL RYHQAREALL DTLAVRFLPK
651 WHELDROAAK QENQSYEYSP ETADWRTLRLN VCRAFVLRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNCLL AQFADKFSDD ALVMDKYFAL
751 IGSSRRSDTL QQVQTAHQHP KFSLENPNKA RSLIGSFERN VPHFHAQDGS
801 GYRFIADKVI EIDRENQVA ARLVQA7NLC NKLEPHRKNL VKQELQCIRA
851 QEGLSKDVGE IVGKILG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2167>:

m665-1.seq

```

1 ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51 TATTCTCAAA ACCGATTAC ATTTTGATAT TAATGAACCG CAAACCGTCG
101 TGAAGTCGCG TTTGACGGTT GAGCCGCGA GGGTAGGGGA GCCGTGGTG
151 TTGACGGTT CGGCGAACT CTTGTCCGTC AAAATCAACG GGGCGGCGGC
201 GGATTATGTG TTGGAAGGAG AGACGCTGAC GATTGCGGGC GTGCCGTCCG
251 AACGCTTAC CGTCGAAGTG GAAACCGAAA TCCTGCGCGC GAAAAACAAA
301 TCGCTGATGG GGCTGTATGC TTCCGGCGGC AATTGTGTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACATTTTA CATCGACCGT CCGGATGTGA
401 TGTCCTAAGT CACCACCACC ATCGTCGCGC ACAAACACG CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GCGAGTTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTC CAAACCGAGC TATCTGTTTG
551 CTTTGGTTCG GGGCGATTG GCGGTAACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAGCC
651 CAAGGTCGCG TTTGCCGTGG AATCGTTGAA AAACGCGATG AAATGGGACG
701 AAACGCGCTT CGGTTTGGAA TACGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTGGCGGATT TCAATATGGG CGCGATGGAA AACAAAGGTT TGAACATCTT
801 TAACACCAAG TTCGTCTTGG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT CGAATCCGTG GTCGGACACG AGTATTTCCA CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTCCG TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAATTTTC CGGCGACCGC GCCAGCCGCG
1001 CCGTGGCGCG CATCGAAAAC ATCCGCTGCG TGCGCCAGCA CCACTTCCCC
1051 GAAGACGCGC GCCCGACCGC CCATCCGGTG CGCCCCGCCA GCTATGAGGA
1101 GATGAACAAAT TTCTACACCA TGACCGTTTA TGAAAAAGGC GCGGAAGTAG
1151 TGGCGATGTA TCACACCTG CTCGGCGAAG AGGCTTCCA GAAAGGCATG
1201 AAGCTCTATT TCCACCGCCA CGACGGACAG GCGGTACCTT GCGACGATT
1251 CCGCGCGCGC ATGGCGGACG CGAACGGCAT CAATCTCGAC CAGTTCGCCT
1301 TGTGGTACAG CAGGCGGGC ACGCCGTTT TGAAGCGGA AGGTCGCTCTG
1351 AAAAAAATA TTTTCGAGTT GACCGTCAAA CAAACCGTGC CGCCACGCGC
1401 CGATATGACG GATAAACAGC CGATGATGAT TCCGCTCAAG GTCGGGCTGC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTCC ACTATCAGGG CAAACCGCGC

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1501 ACCGAAGCCG TGTTGCTGCT GACCGAAGCC GAACAGACCT TCCTGCTCGA
 1551 AGGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
 1601 CGGTGCATCT GAACATATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
 1651 GCCCATGACA GCGACGCCCTT CACGCGCTGG GAAGCCGCCC AAACGCTCTA
 1701 CCGCCGCGCC GTCGCCGCCA ACCTTGCCAC GCTTTCAGAC GGCCTTGAGC
 1751 TGCCGAAACA CGAAAACTG CTTGCCGCGG TCGAAAAAGT CATTTCAGAC
 1801 GACCTCTTAG ACAACGCCCTT CAAAGCCCTG CTTTGGGCG TGCCATCCGA
 1851 AGCCGAGCTG TGGGACGGCG CAGAAAAATC CGACCCGCTG CGCTACCATC
 1901 AGGCGCGCGA AGCCTTGTTG GATACGCTTG CCGTCCACTT CCTGCCGAAA
 1951 TGGCAGCAAT TGAACCGTCA GCGCGCSAAG CAGGAAAACC AAAGCTACGA
 2001 ATACAGCCCC GAAGCCGCGG GCTGGCGCAC GCTGCGCAAC GTCTGCCGCG
 2051 CCTTTGTCTT GCGCGCGGAC CCCGCGCACA TCGAAACCGT TGCCGAAAAA
 2101 TACGCGGAAA TGGCGCAAAA CATGACCACG GAATGGGGCA TCCTGTCCGC
 2151 CGTCAACGGC AACGAAAGCG ATACCGCGAA CCGCCTGCTG GCGCAGTTTG
 2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTTGCCCTC
 2251 GTCGGCTCAA GCCGCCGCG CAGACCCCTG CAACAGGTTC GAACCGCCTT
 2301 GCAGCATCCG AAATTCAGCC TCGAAAAACC CAACAAAGCC CGTTCGCTCA
 2351 TCGCGAGCTT CAGCCGCAAC GTCCCGCATT TCCACGCAGA AGACGGCAGC
 2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
 2451 GCAGGTCGCC GCCCGCTTAG TGCAGGCGTT CAACCTCTGC AACAGCTCG
 2501 AGCCGCACCG CAAAACTTG GTGAAACAAG CATTCGACGG CATTCGGGCG
 2551 CAGGAAGGAT TGTGAAAGA CGTGGGCGAA ATCGTCGCGA AAATTTTGA
 2601 TTGA

This corresponds to the amino acid sequence <SEQ ID 2168; ORF 665-1>:

m665-1.pep

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTVVKSRLTV EPQRVGEPLV
 51 LDGSAKLLSV KINGAADYV LEGETLTIAG VPSEFTVEV ETEILPAENK
 101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
 151 LLSNGNKIDG GEFSDGRHWV KWEDPFSKPS YLFALVAGDL AVTEDYFTTM
 201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYLDIFMVVA
 251 VGDENMGAME NKGNIIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
 301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLLRQHQP
 351 EDAGPTAHVP RPASYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
 401 KLYFQRHDGQ AVTCDDFRAA MADANGINLD OFALWYSQAG TPVLEAEGRL
 451 KNNIFELTVK QTVPTPDMT DKQPMIIPVK VGLNLRNGEA VAFDYQKRA
 501 TEAVLLLTEA EQTFLLLEGVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
 551 AHDSDAFTRW EAAQTLYRRA VAANLATLSD GVLEPKHEKL LAAVEKVISD
 601 DLLDNAFKAL LLGVPSAEAL WDGAENIDPL RYHQAREALL DTLAVHFLPK
 651 WHELNROAAK QENOSYEYSP EAAGWRTLNR VCRAFVLRAD PAHIETVAEK
 701 YGEMAQNMTH EWGILSAVNG NESDTRNRL AOFADKFSDD ALVMDRYFAL
 751 VGSSRRSDTL QQVRTALQHP KFSLENPNKA RSLIGSFSRN VPHFHAEDGS
 801 GYRFIADKVI EIDRFNPQVA ARLVQAENLC NKLEPHRKNL VKQALQRIRA
 851 QEGLSKDVGE IVGKILD*

m665-1/g665-1 96.1% identity in 866 aa overlap

	10	20	30	40	50	60
m665-1.pep	MSKTVHYLKYDQTPAYHILKTDLHFDINEPQTVVKSRLTVEPQRVGEPLVLDGSAKLLSV					
g665-1	MSKTVRYLKDQYTPAYRILETDLHFDIAEPQTVVKSRLTVEPQAGEPLVLDGSAKLLSV					
	10	20	30	40	50	60
m665-1.pep	70	80	90	100	110	120
g665-1	KINGAADYVLEGETLTIAGVPSEFTVEVETEILPAENKSLMGLYASGGNLFTQCEPEG					
	70	80	90	100	110	120
m665-1.pep	KINGAADYVLEGETLTIADVPSEFTVEVETEILPAENKSLMGLYASGGNLFTQCEPEG					
g665-1	KINGAADYVLEGETLTIADVPSEFTVEVETEILPAENKSLMGLYASGGNLFTQCEPEG					
	130	140	150	160	170	180
m665-1.pep	FRKITFYIDRDPVMSKFTTTIVADKKRYPVLLSNGNKIDGGEFSDGRHWVKWEDPFSKPS					
g665-1	FRKITFYIDRDPVMSKFTTTIVADKKRYPVLLSNGNKIDGGEFSDGRHWVKWEDPFAKPS					
	130	140	150	160	170	180
m665-1.pep	190	200	210	220	230	240
g665-1	YLFALVAGDLAVTEDYFTTMSGRNVKIEFYTTTEADKPKVGFAVESLKNAMKWDETRFGL					
	190	200	210	220	230	240
m665-1.pep	YLFALVAGDLAVTEDRFTTMSGRNVKIEFYTTTEADKPKVGFAVESLKNAMKWDETRFGL					
g665-1	YLFALVAGDLAVTEDRFTTMSGRNVKIEFYTTTEADKPKVGFAVESLKNAMKWDETRFGL					
	250	260	270	280	290	300
m665-1.pep	YLDIFMVVAVGDFNMGAMENKGLNIFNTKFVLADSRATDITDFEGIESVVGHEYFHNWT					
g665-1	YLDIFMVVAVGDFNMGAMENKGLNIFNTKFVLADSRATDITDFEGIESVVGHEYFHNWT					

1065

	250	260	270	280	290	300
m665-1.pep	310	320	330	340	350	360
	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQPEDAGPTAHPV					
g665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRRIENIRLLRQHQFPEDAGPTAHPV					
	310	320	330	340	350	360
m665-1.pep	370	380	390	400	410	420
	RPASYEEMNNFYMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDGQAVTCDDFRAA					
g665-1	RPVSYEEMNNFYMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDGQAVTCDDFRAA					
	370	380	390	400	410	420
m665-1.pep	430	440	450	460	470	480
	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTPPTPDMTDKQPMPIPVK					
g665-1	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTPPTPDMADKQPMPIPVK					
	430	440	450	460	470	480
m665-1.pep	490	500	510	520	530	540
	VGLLNRRNGEAVAFDYQGKRATEAVLLMTEAEQTFLEGVTEAVVPSLLRGFSAPVHLNYP					
g665-1	VGLLNRRNGEAVAFDYQGKRATEAVLLMTEAEQAFPLEGVTEAVVPSLLRGFSAPVYLNYP					
	490	500	510	520	530	540
m665-1.pep	550	560	570	580	590	600
	YSDDDLLLLLAHDSDAFTWEEAAQTLRYRAVAANLATLSGVELPKHEKLLAAVEKVISD					
g665-1	YSDDDLLLLLAHDSDAFTCWEAAQTLRYRAVAANLAALSDGIGLPHKEKLLAAVEKVISD					
	550	560	570	580	590	600
m665-1.pep	610	620	630	640	650	660
	DLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLPKWHELNQAAK					
g665-1	DLLDNAFKALLLGVPSAEELWDGTENIDPLRYHQAREALLDTLAVRFLPKWHELDQAAK					
	610	620	630	640	650	660
m665-1.pep	670	680	690	700	710	720
	QENQSYEYSPAAAGWRTLNRVCRFVLRADPAHIETVAEKYGEMAQNMTHWEGILSAVNG					
g665-1	QENQSYEYSPETADWRTLNRVCRFVLRADPAHIETVAEKYGEMAQNMTHWEGILSAVNG					
	670	680	690	700	710	720
m665-1.pep	730	740	750	760	770	780
	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVRTALQHPKFSLENPNKA					
g665-1	NESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQHPKFSLENPNKA					
	730	740	750	760	770	780
m665-1.pep	790	800	810	820	830	840
	RSLIGSFSSRNVPFHAEADGSGYRFIADKVIIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
g665-1	RSLIGSFSSRNVPFHAEADGSGYRFIADKVIIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
	790	800	810	820	830	840
m665-1.pep	850	860				
	VKQALQIRAQEGLSKDVGEIVGKILDX					
g665-1	VKQELQCIRAQEGLSKDVGEIVGKILGX					
	850	860				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2169>:

a665-1.seq

```

1  ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51  TATTCTCAA ACCGATTAC ATTTGATAT TAACGAACCG CAAACCATG
101 TGAAGTCGCG TTTGACGGTC GAGCCGAAGA GGGTGGGAGA GCCGCTGGTG
151 TTGGACGGTT CGGCGAAACT CTGTCCGTC AAAATCAACG GCGTGGCGGC
201 GGATTATGTG TTGGAAGCGC AGACGCTGAC GATTGCGGAC GTGCCGTCGG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAAACAAA
301 TCGCTGATGG GGCTGATGC GTCCGCCGGT AACCTGTTTA CCCAGTCCGA
351 GCCGGAGGGC TTCGCAAAA TCACGTTCTA TATCGACCGT CCGGATGTCA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG ACAAAAAACG CTATCCCGTT
451 TTGCTCTCCA ACGGCAACAA AATCGACGGC GCGGAGTATT CAGACGGCCG

```

501 CCATTGGGTG AATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
 551 CTTTGGTCGC GGGCGATTG GCGGTCACGG AAGACTATTT CACCACCATG
 601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAGCC
 651 CAASGTCGGC TTGCGCTGG AATCGCTGAA AAACGCAATG AAGTGGGACG
 701 AAACGCGCTT CGGTTTGAA TACGACTTGG ATATTTTCAT GGTCGTCGCC
 751 GTGGGCGATT TCAATATGGG TCGGATGGAA AACAAGGGTT TGAACATCTT
 801 TAACACCAAG TTCGTCTTG CCGACAGCCG TACCGCCACC GATACCGATT
 851 TTGAAGGCAT CGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
 901 GGCAACCGCG TGACCTGCCG CGACTGGTTC CAGCTTTTCG TGAAGGAAGG
 951 GTTGACCGG TTCCGCGACC AAGAATTTTC CGGCGACCGC GCCAGCCGCG
 1001 CCGTGCGCCG TATCGAAAAC ATCCGCTTGC TCGCCAGCA CCAGTTCCCC
 1051 GAAGACGCAG GTCCGACCGC ACATCCGGTG CGCCCCGCCG GATATGAGGA
 1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGA AAAAGGCG GCGGAAGTGG
 1151 TCGGATGTA TCACACCTTG CTCGGCGAAG AGGGCTTCCA AAAAGGTATG
 1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCTGTACCT GCGACGATT
 1251 CCGCGCGGCG ATGGTGGACG CGAACGGCAT CAACCTCGAC CAATTCGCCT
 1301 TGTGGTACAG CCAAGCAGGT ACGCCGGTTT TAGATGCTCA AGGGCGTCTG
 1351 AAAACAATG TGTTCCAGTT AACCATCAAA CAAACCGTGC CGCCACGCCG
 1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAAA ATCGGGCTGC
 1451 TGAAGTCAA CGGCGAAGCG GTGGCATTG ATTATCAGGG CAAACGCGCG
 1501 ACCGAAGCCG TGTTGCTGCT GACCGAAGCC GAACAGACCT TCCAGTTCGA
 1551 AAGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
 1601 CGGTGCATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTTCTGCTC
 1651 GCCCATGACA GCGACGCCCT CACGCGCTGG GAAGCCGCAC AAACGCTCTA
 1701 CCGCCGTGCC GTCCCGGCCA ACCTTGCCGC GCTTTCAGAC GGGCTCGAGT
 1751 TGCCGAAAAA CGAAAAACTG CTTGCCGCGC TCGAAAAAGT CATTTCAGAC
 1801 GACCTCTTAG ACAACGCTTT CAAAGCCCTG CTTTGGGTG TGCCGTCTGA
 1851 AGCCGAGCTG TGGGACGGCG CGGAAACAT CGACCCGCTG CGCTACCATC
 1901 AGGCGCGCGA AGCCTTGTTG GATATACTTG CCGTCCGCTT TCTGCCGAAA
 1951 TGGCAGGAAT TGAACCGTCA GCGCGCGAAG CAGGAAACC AAAGCTACGA
 2001 GTACAGCCCC GAAGCCGCCG GTTGGCGCAC GCTGCGCAAT GTCTGCCGCG
 2051 CTTTCTGCTC GCGCGCCGAT CCCGCGCACA TCGAAACCGT TGCCGAGAAA
 2101 TACGCCGAAA TGGCGCAAAA CATGACCCAC GAATGGGCA TCCTGTCCGC
 2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCTGCTG GCGCAGTTTG
 2201 CCGACAAGTT TTCAGACGAC GCGCTGCTGA TGGACAAATA TTTCCGCCCTC
 2251 GTCGGCTCAA GCGCGCGCAG CGACACCTG CAACAGGTTT AAACCGCCTT
 2301 GCAGCATCCG AAGTTCAGCC TCGAAAATCC CAACAAAGCC CCCTCGCTCA
 2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TCCACGCGA AGACGGCAGC
 2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTTAACCC
 2451 GCAGGTCCGC GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAGCTCG
 2501 AGCCGACCGC CAAAACCTTG CTGAAACAAG CATTGCAGCG CATTGCGGCG
 2551 CAGGAAGGAT TGTCGAAAGA CGTGGCGGAA ATCGTCCGCA AAATTTTGGA
 2601 TTGA

This corresponds to the amino acid sequence <SEQ ID 2170; ORF 665-1.a>:

a665-1.pep

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIIVKSRLTV EPKRVGEPLV
 51 LDGSAKLLSV KINGVAADYV LEGETLTID VPSEFRTVEV ETEILPAENK
 101 SLMLYASAG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
 151 LLSNGNKIDG GEYS DGRHWV KWEDPFAKPS YLFALVAGDL AVTEDYFTTM
 201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYLDIFMVVA
 251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTDFEGIESV VGHEYFHNWT
 301 GNRVTCRDWF QLSLKEGLTV FRDQFESGDR ASRAVRRIEN IRLLRQHQP
 351 EDAGPTAHVP RPARYEEMNN FYTMTVYERK AEVVRMYHTL LGEEGFQKGM
 401 KLYFORHDGQ AVTCDDFRAA MVDANGINLD QFALWYSQAG TPVLDAQGRL
 451 KNNVFELTIK QTVPTPDMA DKQPMIIPVK IGLLNCNGEA VAFDYQGKRA
 501 TEAVLLLTEA EQTFQFESVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
 551 AHDSDAFTRW EAAQTLYRRA VAANLAALSD GVELEPKHEKL LAAVEKVISD
 601 DLLDNAFKAL LLGVPSEAEI WDGAENIDPL RYHQAREALL DILAVRFLPK
 651 WHELNRAQAK QENQSYEYSP EAAGWRTLRLN VCRAFLVLRAD PAHIETVAEK
 701 YAEQAQNMTH EWGILSAVNG NESDTRNRLI AQFADKFSDD ALVMDKYFAL
 751 VGSSRRSDTL QOVQALQHP KFSLENPNKA RSLIGSFSRN VPFHAEEDGS
 801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQRIRA
 851 QEGLSKDVG EIVGKILD*

a665-1/m665-1 97.2% identity in 867 aa overlap

	10	20	30	40	50	60
a665-1.pep	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	QTIIVKSRLT	VEPKRVGEPL	VLDGSAKLLSV
m665-1	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	CTIVKSRLT	VEPQRVGEPL	VLDGSAKLLSV
	10	20	30	40	50	60
	70	80	90	100	110	120

a665-1.pep	KINGVAADYVLEGETLTIADVPSEKFTVEVETEILPAENKSLMGLYASAGNLFTQCEPEG
m665-1	KINGAADYVLEGETLTIAGVPSEKFTVEVETEILPAENKSLMGLYASAGNLFTQCEPEG
	70 80 90 100 110 120
a665-1.pep	130 140 150 160 170 180
m665-1	FRKITFYIDRPDVMSKFTTTIVADKKRYPVLLSNGNKIDGGEYS DGRHWVKWEDPFAKPS
	130 140 150 160 170 180
a665-1.pep	190 200 210 220 230 240
m665-1	YLFALVAGDLAVTEDYFTTMSGRNVKIEFYITTEADKPKVGF AVESLKNAMKWDETRFGLE
	190 200 210 220 230 240
a665-1.pep	250 260 270 280 290 300
m665-1	YOLDIFMVVAVGDFNMGAMENKGLNIFNTKFLVADSRTATD TDFEGIESVVGHEYFHNWT
	250 260 270 280 290 300
a665-1.pep	310 320 330 340 350 360
m665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIEN IRLLRQHQPEDAGFTAHPV
	310 320 330 340 350 360
a665-1.pep	370 380 390 400 410 420
m665-1	RPARYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKGM KLYFQRHGDQAVTCDDFRAA
	370 380 390 400 410 420
a665-1.pep	430 440 450 460 470 480
m665-1	MVDANGINLDQFALWYSOAGTPVLDAQRLKNNVFELTIKQ TVPPTDMADKQPMIIPVK
	430 440 450 460 470 480
a665-1.pep	490 500 510 520 530 540
m665-1	IGLLNCGEAVAFDYQGKRATEAVLLLEAEQTFQFESVTEA VVPSLLRGFSAPVHLNYP
	490 500 510 520 530 540
a665-1.pep	550 560 570 580 590 600
m665-1	YSDDDLLLHDSOAFTRWEAAQTLYRRVAANLAALS DGVLPKHEKLLAAVEKVISD
	550 560 570 580 590 600
a665-1.pep	610 620 630 640 650 660
m665-1	DLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALL DILAVRFLPKWHELNROAAK
	610 620 630 640 650 660
a665-1.pep	670 680 690 700 710 720
m665-1	QENQSYEYSPEAAGWRTLNRNVCRAFLRADFAHIETVAE KYAEMAQNMTHEWGILSAVNG
	670 680 690 700 710 720
a665-1.pep	730 740 750 760 770 780
m665-1	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSD TLOQVQTALQHPKFSLENPNKA
	730 740 750 760 770 780
a665-1.pep	790 800 810 820 830 840
m665-1	RSLIGSFSRNVPHFAEDGSGYRFIADKVI EIDRFNPQVAARLVQAFNLCNKLEPHRKNL

1068

	790	800	810	820	830	840
	850	860				
a665-1.pep	VKQALQIRIRAQEGLSKDVGEIVGKILDX					
m665-1	VKQALQIRIRAQEGLSKDVGEIVGKILDX					
	850	860				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2171>:

```

g666.seq
1   ATGCTTTGTA TGAATTATCA ATCAAACCTCA GCGGAAGGAG TGCTTGTAGC
51  TAAACATAT TTATTGACTG CATTGATAAT GTCTATGGTA ATCTCCGGAT
101 GTCAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTAA TTCTGCTGTC
151 ATCGCAGGTG CAGACGCTCA CACGCCTGAA CATGTAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT AGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGGTGGTG CATTCTGTT GTATTGGGAC AATACCGCCA
401 AACATTGAC CACATTGAT GGGCGTGAGA CGGCACCGAT GCGTGCACG
451 CCAGAAATTAT TTTGGATAA AGATGGTTAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGCT CGGTAGGTAC GCCTGCTATC CCTAAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2172; ORF 666.ng>:

```

g666.pep
1   MLCMNYQSNS GEGVLVAKTY LLTALIMSMV ISGCQVIHAN QGKVNTHSAV
51  IAGADAHTPE HVTGLTEQKQ VIASDFIVAS ANPLATQAGY DILKQGSAA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GRETAPMRAT
151 PELFLDKDGX PLKFMEAVVA RXVRLLSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2173>:

```

m666.seq
1   ATGCCTTGTA TGAATCATCA ATCAAACCTCA GCGGAAGGAG TGCTTGTCGC
51  TAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTCAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC
151 ATCACAGGTG CAGACGCTCA CACGCCTGAA CATGCAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGGTGGTG CATTCTGTT GTATTGGGAT AATACCGCCA
401 AACATTGAC CACATTGAT GGGCGTGAGA CGGCACCGAT GCGTGCACG
451 CCGGAATTAT TTTGGATAA AGATGGTCAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGTG GTCGCTCGGT GGTACGCCT GCTATCCCTA AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2174; ORF 666>:

```

m666.pep
1   MPCMNHQSNS GEGVLVAKTY LLTALIMSMT ISGCQVIHAN QGKVNTHSAV
51  ITGADAHTPE HATGLTEQKQ VIASDFIVAS ANPLATQAGY DILKQGSAA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GRETAPMRAT
151 PELFLDKDGQ PLKFMEAVVV VARVRLLSL N*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m666/g666 93.9% identity in 181 aa overlap

	10	20	30	40	50	60
m666.pep	MPCMNHQSNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE					
g666	MLCMNYQSNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m666.pep	HATGLTEQKQVIASDFIVASANPLATQAGYDILKQGSAAADAMVAVQTTLSEVEPQSSGL					

```

g666      |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
HVTGLTEQKQVIASDFIVASANPLATQAGYDILKQGGSAAADAMVAVQTTLSLVEPOSSGL
              70              80              90              100             110             120

              130             140             150             160             170             180
m666.pep  GGGAFVLYWDNTAKLTTFDGRETA PMRATPELFLDKDGQPLKFMEAVVVVARWVRLLSL
           |||||
g666      GGGAFVLYWDNTAKLTTFDGRETA PMRATPELFLDKDGXPLKFMEAVV--ARXVRLLSL
              130             140             150             160             170

m666.pep  NX
           ||
g666      NX
           180

```

a666.seq

```
1 ATGCCTTGTA TGAATCATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTTGGC
51 TAAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTCACAGTCA CCATGCCAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC
151 ATCAACAGGT CAGACGCTCA CACGCCCTGAA CATGCAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GGCGGTGGTG CATTTGTGTT GTATTGGGAT AATACCGCCA
401 AAACATTGAC CACATTTGAT GGGCGTGA CA CGGCACCGAT GCGTGCGACG
451 CCGGAATTAT TTTTGGATAA AGATGGTCAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCTGG GTCTGCTCGGT GGGTACGCCT GCTATCCCTA AACTGA
```

```
a666.ppe
1 MPCMNHQSNS GEGVLVAKTY LLTALIMSMT ISGQVIHAN QGKVNTHSVA
51 ITGADAHTPE HATGLTEQKQ VIASDFMVAS ANPLATQAGY DILKQGGGSA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GREAPMRAT
151 PELFLDKDGO PLKFMEAVVV VARWVRLSL N*
```

		10	20	30	40	50	60
m666.pep		MPCMNHQNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE					
a666		MPCMNHQNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE					
		10	20	30	40	50	60
		70	80	90	100	110	120
m666.pep		HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGGSAADAMVAVQTTLSLVEPQSSGL					
a666		HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGGSAADAMVAVQTTLSLVEPQSSGL					
		70	80	90	100	110	120
		130	140	150	160	170	180
m666.pep		GGGAFVLYWDNTAKTLTTFDGRETAPMRATPELFLDKDGQPLKFMEAVVVVARWVRLLSL					
a666		GGGAFVLYWDNTAKTLTTFDGRETAPMRATPELFLDKDGQPLKFMEAVVVVARWVRLLSL					
		130	140	150	160	170	180
m666.pep	NX						
a666	NX						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2177>:

```

g667.seq
1   atgcggtttg tcttctgttt gggcgGAGAG ATAGtttctg atccgtgtga
51  tttccAtttg gtattcgtcc gcgtcgaatc tgccgctgAc CAGAcagaaa
101 cgCAGataca tCaaatacgt attcacggca tcggtttcgc aatAAttgcg
151 GAtttccttc agcgtgcccg cgtgGAacgc tccccacact ttgtgccgt
201 ccataCCCAg ctTGCCCGGA AAGCCGCACA GTTTCgcCat atcgtccagC
251 GGCACATTcg ccctcggtG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCActtg AAATCGCGGC
351 tgtcgccgAA ATCGccgTCG CCCGTATCCC AATAGCCGCG GCGGTTGATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGGTCGA AACCGCCGCC
451 GTTCCAGCTG ACCAGTTGCG GCGTATGTTT TTCAACCAAT TCGAAAAACT
501 TGGCAATCAC GACTTCTTCG CCATCGTCCA TCTCGCCGAT GGTGCCGACA
551 TGAACCTTGT CCTGCCCCCA GCGCATACAG CAGGAAACCG CCACAACCTG
601 ATGAGAGTGG TGCTGCATAA AATCGCCGCC GGTCTGTGCG CGGCGTTTCT
651 GCTGCGCGAA CAGCACCCTG TCGTCATCCG GCAGGGAAGA CGGCAAGTCA
701 TACACGTAC GGATACCCTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTA TTCATGGCag tACCTTGCAT tcaAAAACAG ActTGCGCCT
801 ATTgTgtcaT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2178; ORF 667.ng>:

```

g667.pep
1   MRFVFCLGGE IVSDPCDFHL VFVRVESAAD QTETQIHQIR IHGIGFAIIA
51  DFLQRRARVER FPHFAAVHTQ LARKAAQFRH IVQRHIRPRL VKREQIHQIA
101 VALVITADV VPLEIAAVAE IAVARIPIAR GVDVYQGAV MQYGQVETAA
151 VPADQLRRMF FNQFEKLG NH DFFAIVHLAD GADMNLVLP AHTAGNRHNL
201 MEVVLHKIAA GLCAAFLLRE QHHEVIRQGR RQVIQRTDTL EIGYGFNIES
251 QNRHGSTLH SKTDLRLLLCH *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2179>:

```

m667.seq (PARTIAL)
1   ATGCGGCTTT TCCCCGGCTT GTGCGGACAG GTAATTCGCG ATCGGTTTGA
51  TTTCCATTTC GTATTCTGTC GCATCCAGCC TGCCGCTGAC CAGACAGAAA
101 CGCAGGTACA TCAGATAAGT GTTTGCCGCG TCGGTTTCGC AATAATTGCG
151 GATTTCCTTC AGCCTGCCCG TATGGAATGC CTCCCAAACC TTGCTGCCGT
201 CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAGC
251 GGCACGTTTG CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351 TGTCGCCGAA ATCGCCGTCG CCCATATCCC AATAGCGCGC GCGGTTGATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGATCGA AACCGCCGCC
451 GTTCCAACCTG ACCAGTTGCG GCGTATGTTT TTCAATCAAT TCGAAAAATT
501 TAGCAATGAC CACTTCTCTG CCGTCATCCA TCTCGCCGAT GGTGCCGACA
551 TGTACTTTAT CCTGCCCCCA ACGCATGCAG CACGAAATCG CCACAACCTG
601 ATGAAGATGA TGCTGCATAA AATCGCCGCC CGTCTGAGCA CGGCGTTTGT
651 GCTGGGCAAT CAGCACCCT TG...

```

This corresponds to the amino acid sequence <SEQ ID 2180; ORF 667>:

```

m667.pep (partial)
1   MRLFPGLCGQ VIPHPDFHF VFVRIQPAAD QTETQVHQIS VCRVGFALIA
51  DFLQPARMEC LPNLAAVHTQ LARKTAQFRH IVQRHVCPRL VKREQIHQIA
101 VALVITADV VPLEIAAVAE IAVAHIPIAR GVDVYQGAV MQYGQIETAA
151 VPTDQLRRMF FNQFEKFSND HFLAVIHLAD GADMYFILPP THAARNRHNH
201 MKMMLHKIAA RLSTAFVLGN QHHL...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m667/g667 75.0% identity in 224 aa overlap

```

          10      20      30      40      50      60
m667.pep  MRLFPGLCGQVIPHPDFHFVFVRIQPAADQTETQVHQISVCRVGFALIAADFLQPARMEC
          ||:  | |:::  | |||:||||: |||||:| | : : ||||| ||:|

```

```

g667      MRFVFCLGGEIVSDPCDFHIVFVRVESAADOTETQIHQIRIHGIGFAIADFLQRARVER
              10          20          30          40          50          60

              70          80          90          100         110         120
m667.pep  LPNLAAVHTQLARKTAQFRHIVQRHVCPRLVKREQIHQIAVALVITADVVVPLEIAAAVE
              : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
g667      FPHEAAVHTQLARKAAQFRHIVQRHIRPRLVKREQIHQIAVALVITADVVVPLEIAAAVE
              70          80          90          100         110         120

              130         140         150         160         170         180
m667.pep  IAVAHIPIARGVDVAVYQGAVMQYQGIETAAVPTDQLRRMFFNQFEKFSNDHFLAVIHLAD
              | | | : | | | | | | | | | | | | | | | | | | | | | | : | | : | : | | |
g667      IAVARIPIARGVDVAVYQGAVMQYQGVETAAPADQLRRMFFNQFEKLGNDFFAIVHLAD
              130         140         150         160         170         180

              190         200         210         220
m667.pep  GADMYFILPPTHAARNRHNLMKMLHKIAARLSTAFVLGNQHHL
              | | | : | | | : | | | | | | | | | | | | | | : | | : | | :
g667      GADMNLVLPAAHTAGNRHNLMDEVVLHKIAAGLCAAFILREQHHFVIRQGRQVIQRTDTL
              190         200         210         220         230         240

g667      HIGYGFNIESQNRHIGSTLHESKTDLRLCHX
              250         260         270

```

a667.seq

```
1 ATGCGGTTTG TCTTCTGTTT GGGCGGAGAG ATAGTTTCTG ATCCGCTTGA
51 TTCCATTTC GTATTCGTCT GCGTCGAATC TGCCGCTGAC CAGACAGAAA
101 CCGCATACA TCAGATAGGT ATTTACCGCA CTGGTTTCGC AATAATTTCG
151 GATTTCTTC AGCCTGCCCG CCGGAACGC CTCCCACAC TTGCTGCCGT
201 CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAAC
251 GGCACATTCC CCCTCGGCTG GTAAAGCGCG AGCAAATCA TCAAATCGCA
301 ATGACGTTGG TGGTAGCGGC TGTATGTATT GTTCCACTTG AAATCGCGGC
351 TGTGCGCGAA ATCGCCGCTG CCGATATCCC AATGCGCGC GCGCTTGTATG
401 CCGTGTAGCA GCGAACGGA ATGCGAGAACC GAGAGGTGCA AACCGCGCC
451 GTTCCAAC TGACGTTGCG GCGTATGTTT TTCAATCAAC TCGAAAAATT
501 TGGCGATAAC CACTTCCTCG CCGTCATCCA TCTCGCGCAT TGTACCGACA
551 TGGACTTTAT CCTGCCCCCA ACGCATGCAG CACGAAATCG CCACAATCTG
601 ATGAAGATGA TGTGTCATAA ATCCCCACC CGTGTAGCA GCGCGTTTTT
651 GCTGGGCAAA CAGCACC ACTCATGTCG GCAGCGAGGA CGGCAAGTCA
701 TACAGCGTAC GGATACACTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTG GTCATGACAG CACCTTGTAT TTAAAA.CAG ACTTGCCCTT
801 ATTTGTGTCAT TAA
```

a667.pep

1	MRFVFCFLGGE	IVSDPLDFHF	VFVCVESAAD	QTETQIHQIG	IYRIGFAIIA
51	DFLQPARVER	LPHLAAVHTQ	LARKTAQFRH	IVQRHIRPRL	VKREQIHQIA
101	MTLVVAADV	VPLEIAAAVE	IAVAHIPTAR	GVDVA*QRTV	MQNRQVETAA
151	VPTDQLRRMF	FNQLEKFGDN	HFLAVIHLAD	CTDMDFILPP	THAARNRHNH
201	MKMMLHKIPT	RLSTAFLLGK	QHHFIVGQRG	RQVIQRTDTL	HIGYGENIES
251	QNRGHDSTLY	LKXDLRLLLH	*		

	10	20	30	40	50	60
m667.pep	MRLFPGLCGQVIPHPDFHFVVRIQPAADQTETQVHQISVCRVGF	F	A	I	A	D
a667	MRFVFCLGGEIVSDPLDHFVFVCVESAA	D	T	E	T	Q
	10	20	30	40	50	60
m667.pep	LPNLAAVHTQLARKTAQFRHIVQRHVCPRLVKREQIHQIAVAL	VITADVVPLEIAVAE				
a667	LPHLAAVHTQLARKTAQFRHIVQRHIRPRLVKREQIHQIAMTLV	VAADVVPLEIAVAE				

1072

	70	80	90	100	110	120
m667.pep	130	140	150	160	170	180
	I A V A H I P I A R G V D A V Y Q G A V M Q Y G Q I E T A A V P T D Q L R R M F F N Q F E K F S N D H F L A V I H L A D					
a667	130	140	150	160	170	180
	I A V A H I P I A R G V D A V X Q R T V M O N R Q V E T A A V P T D Q L R R M F F N Q L E K F G D N H F L A V I H L A D					
m667.pep	190	200	210	220		
	G A D M Y F I L P P T H A A R N R H N L M K M M L H K I A A R L S T A F V L G N Q H H L					
a667	190	200	210	220	230	240
	C T D M D F I L P P T H A A R N R H N L M K M M L H K I P T R L S T A F L L G K Q H H F I V G Q R G R Q V I Q R T D T L					
a667	250	260	270			
	H I G Y G F N I E S Q N R G H D S T L Y L K X D L R L L C H X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2183>:

```

g669.seq
1   ATGCGCGCA TCGTTAAAA ACACGAGCCC GTAAACGCGC CACATATCGT
51  TTTGGAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGCGGCGA ACACGGGATC
151 GAAGGGATGG GTTTCGATT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AGCGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2184; ORF 669.ng>:

```

g669.pep
1   MRRIVKKHQP VNAPHIVLEI RIMKLHRAFV FLGRKRPHHH DRSLRRQHGI
51  EGMGFDFKQI FRHVQSSNRQ SGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2185>:

```

m669.seq
1   ATGCGCGCA TCATTAAAA ACACGAGCCC ATAAACGCGC CACATATCGT
51  TTTGGAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACAGCAGCC TTCGGCGGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2186; ORF 669>:

```

m669.pep
1   MRRIIKKHQP INAPHIVLEI RIMKLHRAFV FLGRKRPHHH DSSLRRQHGI
51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m669/g669 96.2% identity in 106 aa overlap

	10	20	30	40	50	60
m669.pep	M R R I I K K H Q P I N A P H I V L E I R I M K L H R A F V F L G R K R P H H H D S S L R R Q H G I E G M G F D F K Q I					
g669	M R R I V K K H Q P V N A P H I V L E I R I M K L H R A F V F L G R K R P H H H D R S L R R Q H G I E G M G F D F K Q I					
	10	20	30	40	50	60
	70	80	90	100		

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```

m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g669        FRHVQSSNRQSGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2187>:

```

a669.seq
1  ATGCGCCGCA TCATTAATAA ACACCAGCCC GTAAACGCGC CACATATCGT
51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAACGTC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGAATC
151 GAAGGGATGG GTTTCGATT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATT TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2188; ORF 669.a>:

```

a669.pep
1  MRRIKKHQF VNAPHIVLEI RIMKLHRAV FLGRKRPHHH DRSLRRQHGI
51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

m669/a669 98.1% identity in 106 aa overlap

```

m669.pep    10      20      30      40      50      60
             MRRIKKHQFVNAPHIVLEIRIMKLHRAVFLGRKRPHHHDRSLRRQHGI
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a669        10      20      30      40      50      60
             MRRIKKHQFVNAPHIVLEIRIMKLHRAVFLGRKRPHHHDRSLRRQHGI
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

m669.pep    70      80      90      100
             FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a669        70      80      90      100
             FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2189>:

```

g670.seq
1  ATGACTTGTT GCAGGAACGT CTGGCGCGT TCGTGTTCG GGTGGTGAA
51  AAACGCTTCC GCGGTTTCGT CTTCAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGTCGA GTGCGGAAGT CGGCTCGTCA AACAGCATCA
251 CGCGCGGCTC CATCGCCAGC CCGCGCGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAG GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTCC GCATTTGCC
401 CCTTAACCTT CATCGGTGCG AGGGTGATGT TGTCCAACAC GGTGAGGTGC
451 GGCTAG

```

This corresponds to the amino acid sequence <SEQ ID 2190; ORF 670.ng>:

```

g670.pep
1  MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITSATS RANPISWVTH
51  IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NSITRGSIAS PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMLSNTVRC
151 G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2191>:

```

m670.seq
1  ATGACCTGTT GCAGGAACGT CTGGCGCGT TCGTGTTCG GGTGGTGAAA
51  AAACGCTTCC GCGGTTTCGT CTTCAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC TGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGTCGA GTGCGGAGGT CGGTTCTGTC AACAACTTA

```

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```

251 CGCGCGGTTC CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTGCC
401 CCTTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTGAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2192; ORF 670>:

```

m670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
 51 IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCRW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMFSNTVRC
151 G*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m670/g670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
              |||||
g670           MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
              10      20      30      40      50      60

              70      80      90      100     110     120
m670.pep      FITFNTSPTISGSSAEVGSSNNITRGSIAKPRAIATRCRWPPESWEGKASFLCASPTRSK
              |||||
g670           FITFNTSPTISGSSAEVGSSNNITRGSIAKPRAIATRCRWPPESWEGKASFLCASPTRSK
              70      80      90      100     110     120

              130     140     150
m670.pep      SSIAFFSACS AFCPLTFIGARVMFSNTVRCGX
              |||||
g670           SSIAFFSACS AFCPLTFIGARVMSNTVRCGX
              130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2193>:

```

a670.seq
  1 ATGACCTGTT GCAGGAACGT CTTGGCGCGT TCGTGTTTCG GGTGTTGTAAG
 51 AAACGCTTCC GGCCTTTTCT CTTCGAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATGGTCA TACCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTGGA GTGCGGAGGT CGGTTCTGCA AACAAACATTA
251 CGCGCGGTTC CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGTTCCATCG CTTTTTCTC TGCCTGTTCC GCATTTTGAC
401 CTTTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTGAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2194; ORF 670.a>:

```

a670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
 51 IMVIPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCRW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AF*PLTFIGA RVMFSNTVRC
151 G*

```

m670/a670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
              |||||
a670           MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIMVIPLSAKS
              10      20      30      40      50      60

```

1075

	70	80	90	100	110	120
m670.pep	FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK					
a670	FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK					
	70	80	90	100	110	120
	130	140	150			
m670.pep	SSIAFFSACSAFCPLTFIGARVMFSNTVRCGX					
a670	SSIAFFSACSAFXPLTFIGARVMFSNTVRCGX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2195>:

g671.seq

1	ATGATCAGCA	GGTAACAAT	CAAAACGCCT	TTCAATGCAC	CGAATACACC
51	GCCCAAAATG	CGGTTGGCAA	AGCCCAGACC	GACCGCCGAA	ACTGCGCCGG
101	TCAGCAGCGA	ACGAGGCATT	TTCTGGATCA	GACAGGCAAT	GACGAACAGG
151	GAAATGAATG	ACAGagccaa	TGCAAAACag	cggggTTGGA	ACGagGCAAA
201	GGCGAGGTcg	gcgaaggGTG	CGGCaaAGAG	TTTggcaaAA	AAGAagGAAA
251	ccaccCATGC	cACCATCgaa	ccTGCTTCGG	CAATCACGCC	GCGCATCGTG
301	GAAATGACGA	TGCAGGCGGC	GATGACGGcg	gAGGCGAGGA	GGTCGGCAAT
351	GGGGAGGCTA	TTCATTCGTT	ACCTGGCCGG	CGATGCCGTG	CACGCGCAGT
401	TTGTTCAAAT	CGCGTTCGGC	ATCCCTTGCG	TTTTTATAGT	TGCTTGA

This corresponds to the amino acid sequence <SEQ ID 2196; ORF 671.ng>:

g671.pep

1	MISRVTIKTP	FNAPNTPPKM	RLAKPRPTAE	TAPVSSERSI	FWIRQAMTNR
51	EMNDRANANR	RGWNEAKARS	AKGAAKSLAK	KKETTHATIE	PASAITPRIV
101	ENTMQAAMTA	EARRSAMGRL	FIRYLAGDAV	HAQFVQIAFG	IPCVFIVA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2197>:

m671.seq

1	ATGACCAGCA	GGTAACAAT	CAAAACGCCT	TTCAATGCAC	CGAATACGCC
51	GCCCAAAATG	CGGTTGGCAA	AGCCCAAACC	GACCGCCGAA	ACTGCGCTGG
101	TCAGCAGCGA	ACGAGGCATT	TTCTGGATCA	GACAGGCAAT	GACGAACAGG
151	GAAATGAACG	ACAGAGCCAA	TGCAAAACAG	CGGGGTTGGA	ACGAGGCAAA
201	GGCGAGGTCG	GCGAAGGAGG	CGGCAAGAG	TTTGGCGAAA	AAGAAGGAAA
251	CCACCCATGC	CGCCATTGAG	CCTGCCTCCG	CAATCACGCC	GCGCATCGCG
301	GATAGCACGA	TGCAGGCGGC	GATGACGGCG	GAGACGAGGA	GGTCGGCAAT
351	GGGGAGGCTA	TTCATTCGTT	ACCTGACCGG	CGATACCGTG	TACGCGCAAT
401	TTGTTCAAAT	CGCGTTCGCG	ATCCCTTGCG	TTTTTATAGT	TGCTTGA

This corresponds to the amino acid sequence <SEQ ID 2198; ORF 671>:

m671.pep

1	MTSRVTIKTP	FNAPNTPEKM	RLAKPKPTAE	TALVSSERSI	FWIRQAMTNR
51	EMNDRANANR	RGWNEAKARS	AKEAAKSLAK	KKETTHAAIE	PASAITPRIA
101	DSTMQAAMTA	ETRRSAMGRL	FIRYLTGDTV	YAQFVQIAFG	IPCVFIVA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m671/g671 91.9% identity in 148 aa overlap

	10	20	30	40	50	60
m671.pep	MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR					
g671	MISRVTIKTPFNAPNTPPKMRLAKPRPTAETAPVSSERSIFWIRQAMTNREMNDRANANR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m671.pep	RGWNEAKARSAKEAAKSLAKKKETTHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL					

```

g671      ||||| | | | | | : | | | | | : | | | | | : | | | | |
          RGWNEAKARSAKGAASKLAKKETTHATIEPASAITRIVEMTMQAAMTAEARRSAMGRL
              70           80           90           100          110          120

                130           14C           149
m671.pep   FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
            ||||| : ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g671       FIRYLAGDAVHAQFVQIAFGIPCVFIVAX
                130           14C

```

a671.seq

```
1  ATGACCAGCA GGGTAATAAT CAAATGCGT TTCAATGCAC CGAATACGCC
51  GCCCAAAATG CGGTGGCAA AGCCCAAACC GACCGCGGAA ACTGCCCGG
101 TCAGCAGCGA CGGGAGTATT TTCTGGATCA GACAGGCAAT GACGAATAGG
151 GAAATGAACG ACAGAGCCAA TGCAAACAGG CGGGGTTGTA ACGATGCAA
201 GCGCATGTCT GCGAAGGGTG CGGCAAAGAG TTGGCGAAA AAAAAGGCAA
251 CCACCCATGC CGCCATTGAG CCAGCCTCCG CAATCACGCC GCGCATCGCG
301 GATGAGCACA TGCAGGCGCG CATGATGGCG GAGACGAGGA GGTGCGCAAC
351 GGAGAGGTTA TTCATTCTTT ACCTGACCGC CGATACCGTG TACGCGCAAT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTCCG TTTTATAGT TGCTTGA
```

```
a671.pep
1  MTSRVIKMP  FNAPNTPPKM  RLAKPKPTAE  TAPVSSERSI  FWIRQAMTNR
51  EMNDRANANR  RGWNDAKAMS  AKGAAKSLAK  KKATTHAAIE  PASAITPRIA
101 DSTMQAAMMA  ETRRSATGRL  FIRYLTGDTV  YAQFVQIAFG  IPCVFIVA*
```

	10	20	30	40	50	60
m671.pep	MTSRVTIKTFPNAPNTPPKMLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR					
a671	MTSRVLIKMPFNAPNTPPKMLAKPKPTAETAPVSSERSIFWIRQAMTNREMNDRANANR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m671.pep	RGWNEAKARSAKEAAKSLAKKKETHAAIEFPASAITPRIADSTMQAAMTAETRRSAMGRL					
a671	RGWNDAKAMSAKGAASKLAKKKATTHAAIEFPASAITPRIADSTMQAAMMAETRRSATGRL					
	70	80	90	100	110	120
	130	140	149			
m671.pep	FIRYLTGDTVYAQFVQIAFGIPCVFIVAX					
a671	FIRYLTGDTVYAQFVQIAFGIPCVFIVAX					
	130	140				

```

9672.seq
1  ATGAGGAAAA  TCCGCACCAA  AATCTGCGGC  ATCACCACAC  CGGAAGACGC
51  ACTGTATGCC  GCCCGCCCG  GCGCAGACGC  ATTGGGACTG  GTTTTTCAC
101 CCAAAGCCC  CCGCGCTATC  GACATCATTA  AAGCAAAATA  AATCGCGCC
151 GCATCTGCCG  CGTTTGTGAC  CSTTTCGCC  CTTTTCGTCA  ACGAAAGCGC
201 GCAAAACATC  CGCCGCATCC  TTGCCGAAGT  GCGCATACAC  ATCATCCAAT
251 TCCACGGCGA  CGAAGACGAT  GCATTCTGCC  GCGAGTTCGA  CGGCCCTAT
301 ATTAAGCCA  TTCGTGTTCA  GACGGCATCA  GACATCCGAA  ACGCCGCCAC
351 GCGCTTCCCC  AACGCTCAG  CATGCTGTT  CGATGCCTAT  gaccttTCGG
401 AATACGGCG  CACCGGACAC  CGCTTCGact  GGagctgtt  gccggaATAT
451 TCGGGCAAG  CGTGGGTGCT  TGCCGCGGG  CTGACCCCTG  AAAACGTCGG
501 CGAAGCCGT  CGCATCACCG  GAGCGGAAG  GGTGCACGTA  TCCGGCGGCG
551 TGAAGCGTC  TAAAGGCAA  AAGACCCCG  CCAAAGTCGC  GCCTTTATC
601 GCAACCGCCA  ACCGCCATC  CGGTAA

```

1077

This corresponds to the amino acid sequence <SEQ ID 2202; ORF 672.ng>:

```

g672.pep
  1 MRKIRTKICG ITTPEDALYA AHAGADALGL VFYFQSPRAI DIIKAQKIAA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFDRPY
101 IKAIRVQTAS DIRNAATREF NAQALLFDAY HPSEYGGTGH RFDWTLAEY
151 SGKPWVLAGG LTPENVGEAV RITGAEAVDV SGGVEASKGK KDKAKVAAFI
201 ATANRLSR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2203>:

```

m672.seq
  1 ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
 51 AGCTGCCGCC GCAGCGGCAG GTGCGGATGC CGTCGGGCTG GTCTTTTTC
101 AAGGCAGCAG CCGGGCCGTC GATATTGCCG CGGCCAAAAA AATCACCGCC
151 GCACCTGCCGC CGTTTGTCAG CGTTGTCGCC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT GCCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCTAT
301 ATCAAAGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCAC
351 GCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGAAAC CGCTTCGACT GGACGCTGCT GCGGGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGG
501 CGAAGCCGTC CGCATCACCG GAGCGGAATC GGTCGATGTA TCCGGCGGTG
551 TGGAAGCGTC TAAAGGCAAA AAAGATGCCG CCAAAGTCGC CGCCTTTATC
601 GCAACGCCCA ACCGCCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2204; ORF 672>:

```

m672.pep
  1 MRKIRTKICG ITTPEDAAAA AAAGADAVGL VFFQSSRAV DIARAKKITA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAATREF DAQALLFDAY HPSEYGGTGN RFDWTLAEY
151 SGKPWVLAGG LTPENVGEAV RITGAESVDV SGGVEASKGK KDKAKVAAFI
201 ATANRLSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m672/g672 91.3% identity in 208 aa overlap

	10	20	30	40	50	60
m672.pep	MRKIRTKICG	ITTPEDAAAA	AAAGADAVGL	VFFQSSRAV	DIARAKKITA	ALPPFVSVVA
g672	MRKIRTKICG	ITTPEDALYA	AHAGADALGL	VFYFQSPRAI	DIIKAQKIAA	ALPPFVSVVA
	10	20	30	40	50	60
	70	80	90	100	110	120
m672.pep	LFVNEAQNIR	RRILAEVPIH	IIQFHGDEDD	AFCRQFHRPY	IKAIRVQTAS	DIRNAATREF
g672	LFVNEAQNIR	RRILAEVPIH	IIQFHGDEDD	AFCRQFDRPY	IKAIRVQTAS	DIRNAATREF
	70	80	90	100	110	120
	130	140	150	160	170	180
m672.pep	DAQALLFDAY	HPSEYGGTGN	RFDWTLAEY	SGKPWVLAGG	LTPENVGEAV	RITGAESVDV
g672	NAQALLFDAY	HPSEYGGTGH	RFDWTLAEY	SGKPWVLAGG	LTPENVGEAV	RITGAEAVDV
	130	140	150	160	170	180
	190	200	209			
m672.pep	SGGVEASKGK	KDKAKVAAFI	ATANRLSRX			
g672	SGGVEASKGK	KDKAKVAAFI	ATANRLSRX			
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2205>:

a672.seq

1078

```

1  ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
51  ACTGTATGCC GCCCAGCGCG GCGCAGACGC ATTGGGACTG GTTTTTTACC
101 CCCAAAGCCC CCGCGCTGTC GACATCATT AAGCACAAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTCTG CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT ACCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCTAT
301 ATCAAGGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCGA
351 CCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGACAC CGCTTCGACT GGACGCTGTT GCGGGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTGCA
501 CGAAGCCATC CGCATCACCG GAGCGGAAGC GGTCGATGTA TCCGGCGGCG
551 TGGAAGCGTC TAAAGGCAAA AAAGACCCAG CCAAAGTTGC CGCCTTTATC
601 GCAACGCCCA ACCGCCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2206; ORF 672.a>:

```

a672.pep
1  MRKIRTKICG ITPEDALYA AHAGADALGL VFYPQSPRAV DIIKAQKITA
51  ALPPFVSVA LFNESAQNI RRILAEPVPIH IIQFHGDEDD AFRCQFHRPY
101 IKAIRVQTAS DIRNAADREF DAQALLFDAY HPSEYGGTGH RFDWTLLEAY
151 SGKEPWLGG LTPENVDEAI RITGAEAVDV SGGVEASKGK KDPKVAEFI
201 ATANRLSR*

```

m672/a672 91.8% identity in 208 aa overlap

	10	20	30	40	50	60
m672.pep	MRKIRTKICG	ITPEDAAAAA	AGADAVGLV	FFQGSRAVD	DIARAKKITA	ALPPFVSVA
a672	MRKIRTKICG	ITPEDALYA	AHAGADALGL	VFYPQSPRAVD	IKAQKITAAL	PPFVSVA
	10	20	30	40	50	60
	70	80	90	100	110	120
m672.pep	LFVNESAQNI	RRILAEPVPIH	IIQFHGDEDD	AFRCQFHRPY	IKAIRVQTAS	DIRNAATREF
a672	LFVNESAQNI	RRILAEPVPIH	IIQFHGDEDD	AFRCQFHRPY	IKAIRVQTAS	DIRNAADREF
	70	80	90	100	110	120
	130	140	150	160	170	180
m672.pep	DAQALLFDAY	HPSEYGGTGN	RFDWTLLEAY	SGKPPWLAGGL	TENVGEAVRIT	GAEVSDV
a672	DAQALLFDAY	HPSEYGGTGH	RFDWTLLEAY	SGKPPWLAGGL	TENVDEAIRIT	GAEVSDV
	130	140	150	160	170	180
	190	200	209			
m672.pep	SGGVEASKGK	DAAKVAAFI	ATANRLSRX			
a672	SGGVEASKGK	DAKVAEFI	ATANRLSRX			
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2207>:

```

g673.seq
1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51  TTGCGGCTTC GTGGCGATTG TCGGTCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAGGCG
151 CAGACGACGC GCAACCGCCT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CGGGCTTTCA AACCACCACG CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGCGCTCGG CGGTGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GCGATGCGC CTTACCGATG CCGACGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCATTTTA GTGATCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTGTT
451 GCCCAAGTGC GCGCCGAATT TGAATTGCG GCGGCGGAGG CGGTCAGTGC
501 GAAACACGGT TTGCGGATTG CCAACCTGTT GGAGCTGCTC AAGCCGTATC
551 TGCCCGAAAG CGTACCGATG TATCCGAAG ACATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCCT GAAAACTCT TCCGCTATT

```

1079

```

651 GGGCGAGGAG CTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGGAGACGG TTTGAACCGC ATCTACatcg cCGTTTTGGT CGACAAAGAA
751 AGCCAAAAGG CGATTTTGAT CGGTAAAGGC GGGGAGCGTT TGAATAAAT
801 TTCCACCGAA GCGCGGCTGG ATATGGAAAA ACTGTTTGAT AACAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCAGA CGACATTCGC
901 TTCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2208; ORF 673.ng>:

g673.pep

```

1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVVFVEAMR LTDADRVVLK QLPKHTPVIL VINKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELL KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFRYLGE E LPYAMNVEVE QFEEGDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD NKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2209>:

m673.seq

```

1 ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CCGGCTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGGCGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GCGCATGCGC TTTACCGATG CCGACGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCATTTTA GTGGTCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGTGTGTT
451 GCCCAAGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CCGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTIAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCCT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTTGGT CGATAAGGAA
751 AGCCAAAAGG CAATTTTAAT CGGTAAAGGC GGAGAACGTT TGAAGAAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2210; ORF 673>:

m673.pep

```

1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVVFVEAMR LTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFRYLGE E LPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD TKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m673/g673 98.4% identity in 307 aa overlap

```

          10      20      30      40      50      60
m673.pep MDIETFLAGERAAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTRNRVTGI
          |||||||
g673      MDIETFLAGERAAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTRNRVTGI
          10      20      30      40      50      60

          70      80      90     100     110     120
m673.pep YTDDTAQFVFVDTPGFQTDHNRNALNDRLNQNVTEALGGVDVVVFVEAMRFTDADRVVLK
          |||||||

```


1080

```

g673      YTDDTAQVFVVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRLTDADRVVLK
           70      80      90      100     110     120

           130     140     150     160     170     180
m673.pep  QLPKHTPVILVVKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI
           |||||
g673      QLPKHTPVILVINKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI
           130     140     150     160     170     180

           190     200     210     220     230     240
m673.pep  KPYPLESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEDGLNR
           |||||
g673      KPYPLESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEDGLNR
           190     200     210     220     230     240

           250     260     270     280     290     300
m673.pep  IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFLKVWVKVKS GWADDIR
           |||||
g673      IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDNKVFLKVWVKVKS GWADDIR
           250     260     270     280     290     300

m673.pep  FLRELGLX
           |||||
g673      FLRELGLX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2211>:

```

a673.seq
1  ATGGATATTG AACCTTCCT TGCAGGGGAA CGCGCCGCCG ACGGATACCG
51  TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAATCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTGTGTTT GTCGATACGC CCGGTTTTC AACCGACCAC CGCAACGCGC
251 TCAACGACCG TTTGAATCAA AACGTTACCG AGGCACTCGG CGCGGTGGAT
301 GTGGTGGTTT TCGTCGTGGA AGCGATGCGT TTTACCGATG CCGACCGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCATTTTA GTGGTCAACA
401 AAATCGATAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGTTTGT
451 GCCCAGGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAAGCG
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TAGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTGGT CGATAAGGAA
751 AGCCAAAAGG CGATTTTAAT CGGCAAAGGC GGGGAGCGTT TGAAGAAAAT
801 TTCCACCGAA GCGCGGTGG ATATGGAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCTGCGCG AGCTGGGTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2212; ORF 673.a>:

```

a673.pep
1  MDIETFLAGE RAADGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51  QTRNRVTGI YTDQTAQVFV VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVVFVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYPLESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLF DT KVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

m673/a673 99.7% identity in 307 aa overlap

```

           10      20      30      40      50      60
m673.pep  MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTRNRVTGI
           |||||
a673      MDIETFLAGERAADGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTRNRVTGI
           10      20      30      40      50      60

```

1081

	70	80	90	100	110	120
m673.pep	YTDDTAQFVFVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRFTDADRVLK					
a673	YTDDTAQFVFVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRFTDADRVLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m673.pep	QLPKHTPVILVVKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
a673	QLPKHTPVILVVKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m673.pep	KPYLPESVPMYPEDMVTDKSAREFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEDGLNR					
a673	KPYLPESVPMYPEDMVTDKSAREFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEDGLNR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m673.pep	IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFVKVWVKVSGWADDIR					
a673	IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFVKVWVKVSGWADDIR					
	250	260	270	280	290	300
m673.pep	FLRELGLX					
a673	FLRELGLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2213>:

```

g674.seq
1  ATGAAAACAG CCCGCCGCGG TTCCCGCGAG CTGCGCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CGCCGCGGCC CGAAATTGCT AAAAACATCC
101 GCGAAATGTC CGACTTTGCC AAGCGGACG AAGAATTGTT CAACAACTC
151 TTCTTCGGCA CACAAACCAA TGCAGCGGAC TACATCCAAA AAATCCGCCC
201 GCTGCTCGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACGCG CTGCCACGAG CTTTCGCTA TGCCCGAAAC GCCCTACCCC
301 GTATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCAGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2214; ORF 674.ng>:

```

g674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL
51  FFGTQTNAAD YIQKIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
101 VIINEAIEVT KTEGGTDGKH FVNGILDKLA AQIRPDEPKR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2215>:

```

m674.seq
1  ATGAAAACAG CCCGCCGCGG TTCCCGCGAG CTGCGCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CGCCGCGGCC CGAAATTGCT AAAAACATCC
101 GCGAAATGTC CGACTTTGCC AAGCGGACG AAGAATTGTT CAACAACTT
151 TTCTTCGGCA CGCAAACCAA TGCAGCGGAC TATATCCGAC AAATCCGCCC
201 GCTACTTGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACGCG CTGCCACGAG CTGTCGCGCA TGCCCGAAAC GCCCTACCCC
301 GTATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCCGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2216; ORF 674>:

```

m674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL

```

1082

51 FFGTQTNAAE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
 101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m674/g674 97.9% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAE					
g674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
g674	YIQKIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
g674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2217>:

a674.seq
 1 ATGAAACAG CCCGCCGCGC TTCCCGCGAG CTGCGGTAC AAGCCGTTTA
 51 CCAATCCCTT ATCAACC3CA CCGCCGCGCC CGAGATTGCT AAAAACATCC
 101 GCGAAATGCC CGACTTTGCC AAGGCAGACG AAGAATTGTT CAACAACTT
 151 TTCTTCGGCA CGCAAACCAA TGCGGCAGAG TACATCCGAC AAATCCGCCC
 201 CCTGCTCGAC CGCGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTCC
 251 TGCTGACCGC CTGCCACGAG CTGTCCGCCA TGCCCGAAAC GCCCTACCCC
 301 GTCATCATCA ACGAAGCCAT CGAAGTAACC AAAACCTTCG GCGGCACGGA
 351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
 401 GTCCCGACGA GCCCAAACGC CGTTGA

This corresponds to the amino acid sequence <SEQ ID 2218; ORF 674.a>:

a674.pep
 1 MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMPDFA KADEELFNKL
 51 FFGTQTNAAE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
 101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

m674/a674 99.3% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAE					
a674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMPDFAKADEELFNKLFFGTQTNAAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
a674	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
a674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2219>:

```
g675.seq
  1  ATGAACACCA TCGCCCCcaa cctcgacgGC AAACACCTCC GCATCGGCAT
 51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCCAAATG CTCAAAGTCT
101  GCTGCCGCAC CCTCCAAGAA TTGGGCGTAG CAGACGAAAa catcaccgtc
151  gCCACCGTAC CCGGCGCGCT TGAATCCCC ATCGCGCTGA TGAACTTTGC
201  CTCTTCCGAA AAATTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251  GCGAAACCTA CCATTTCGAG CTGGTTGCCA ACGAATCCGG CGCAGGGATC
301  GGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAACG CCGTCCTGAC
351  CACCGAAAAC GACGCGCAGG CAATTGAACG GATTGGAGAA AAAGCCTCGG
401  ATGCCGCCAA AGTCGCCGTA GAATCGGCCA ACCTCGTCAA CCTTCTGCTC
451  GAAGAACAGT TTGAAGACGA AGAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2220; ORF 675.ng>:

1084

g675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSQM LKVCCTRLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVANESGAGI
101 GRVALDYNIP IANAVLTEN DAQAIERIGE KASDAKVAV ECANLVNLLL
151 EEQFEDEE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2221>:

m675.seq

```

1  ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
151 GCCACCGTAC CCGGCGCGCT TGAATCCCC ATCGCGCTGA TGAACCTTGC
201 CTCTTCCGAA AAGTTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251 GCGAAACCTA CCATTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGCGTC
301 AGCCGCGTCG CACTCGACTA CAATATCCCG ATTGCCAATG CCGTCCTAAC
351 CACGGAACAC GACGCGCAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCGGTC GAATGCGCCA ACCTCGTCAA CCTGCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2222; ORF 675>:

m675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCTRLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNEGAGV
101 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAKVAV ECANLVNLLL
151 EEQFEDEE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m675/g675 96.8% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCTRLQELGVADENITVATVPGALEIP					
g675	MNTIAPNLDGKHLRIGIVQARFTNEIGSQMLKVCCTRLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFE LVSNEGAGVSRVALDYNIPIANAVLTEN					
g675	IALMNFASSEKFDALIAIGVVIRGETYHFE LVANESGAGIGRVALDYNIPIANAVLTEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAKVAVECANLVNLLLEEQFEDEEX					
g675	DAQAIERIGEKASDAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2223>:

a675.seq

```

1  ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
151 GCCACCGTAC CCGGCGCGCT TGAATCCCC ATCGCGCTGA TGAACCTTGC
201 CTCTTCTGAA AAATTGACG CACTGATTGC CATCGGCGTC GTTATCCGTG
251 GCGAAACCTA CCATTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGGGTC
301 AGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAATG CCGTCCTGAC
351 CACGGAACAC GACGCACAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCGGTA GAATGCGCCA ACCTCGTCAA CCTCCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2224; ORF 675.a>:

a675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCTRLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNEGAGV

```

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101 SRVALDYNIP IANAVLT TEN DAQAIERIEE KASDAKVAV ECANLVNLLL
 151 EEQFEDEE*

m675/a675 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVC	CRTLQELGVADENITVATVPGALEIP				
a675	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVC	CRTLQELGVADENITVATVPGALEIP				
	10	20	30	40	50	60
m675.pep	IALMNFASSSEKFDALIAIGVVIRGETYHFELVS	SNESGAGVSRVALDYNIPIANAVLT TEN				
a675	IALMNFASSSEKFDALIAIGVVIRGETYHFELVS	SNESGAGVSRVALDYNIPIANAVLT TEN				
	70	80	90	100	110	120
m675.pep	DAQAIERIEEKASDAKVAVECANLVNLLLEE	QFEDEEX				
a675	DAQAIERIEEKASDAKVAVECANLVNLLLEE	QFEDEEX				
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAKVAVECANLVNLLLEE	QFEDEEX				
a675	DAQAIERIEEKASDAKVAVECANLVNLLLEE	QFEDEEX				
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2225>:

g677.seq
 1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CTTTATTtg
 51 ggAAACGGTG CGCTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
 101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGGC CTTCGGCGCT
 151 GTTCAAAACC ACTTCGTCGC CTTCGGCGCG TTTAATCAGG CAACGCGCCA
 201 ACGGCGAAAT CCAAGAAATT TTGTTTTGCG CGGTATCGAT TTCATCGACG
 251 CCGACGATT TGACGGTTTG CTCGGCCCCG TCGCCGCGCA ACAGACCGAC
 301 GGTCCGCGCG AAAAATACTT GGTCCGTGCG TTCGCGCAAT TCGGGATCGA
 351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTGCG
 401 ATTTCCGCGCA TACGGCGTTT GCCGTAAAGA TAGTCGCCGT TTTCCGTGCG
 451 GTCGCGGTTG CCTGCCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
 501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
 551 GGCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2226; ORF 677.ng>:

g677.pep
 1 MPQILVRIFL IRYFSIWETV RLCRFRHRSR SVDFDVDRK DFNFLTAFRR
 51 VQNHFAFAR FNQATRRRRN PRNFVLRGID FIDADDFDGL LAPVAAQOTD
 101 GRAEYLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHAF AVKIVAVFAA
 151 VAVACRPVDD LDDFGAFFID QLIKLVFQCL PSGRNVVFG FGTHIVCG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2227>:

m677.seq
 1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CTTTATTtg
 51 GGAAACGGCG CGCTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
 101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGCC CTTCGGCGCT
 151 GTTCAAAACC ACTTCGTCGC CTTCGGCGCG TTTAATCAGA CAACGAGCCA
 201 GCGGCGAAAT CCAAGAAATT TTGTTTTGCG CGGTATCGAT TTCATCGATG
 251 CCGACGATT TGACGGTTTG CTCGGCCCCG TCGTCGCGCA ACAGTCGAC
 301 CGTCGCGCGG AAAAATACTT GGTCCGTGCG TTCGCGCAAT TCGGGATCGA
 351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTGCG
 401 ATTTCCGCGCA TACGGCGTTT GCCGTAAAGA TAGTCGCCGT TTTCCGTGCG
 451 GTCGCGGTTG CCTGCCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
 501 CTTTGTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
 551 GCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2228; ORF 677>:

m677.pep
 1 MPQILVRIFL IRYFSIWETA RLCRFRHRSR SVDFDVDRK DFNFLTFRR

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51 VQNHVFAR FNQTSQRRN PRNFVLRGID FIDADDFDGL LAPVVAQSD
 101 RRAEKHLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA
 151 VAVACRPVDD LDDFGAFFVD QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m677/g677 94.9% identity in 198 aa overlap

	10	20	30	40	50	60
m677.pep	MPQILVRIFLIRYSFIWETARFCRFRHRSRSVDFDVFDRKDFNFLT	PFRRVQNHVFAR				
g677	MPQILVRIFLIRYSFIWETVRLCRFRHRSRSVDFDVFDRKDFNFLT	AFRRVQNHVFAR				
	10	20	30	40	50	60
	70	80	90	100	110	120
m677.pep	FNQTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQSDRRAEKHLVGRFAQFGIDDDG					
g677	FNQATRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQTGGRAEKYLVRFAQFGIDDDG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m677.pep	SLQTFGQETDAAVDFAHTAFVAVFAAVAVACRPVDDLDDFGAFFVDQLIKLVFQCL					
g677	SLQTFGQETDAAVDFAHTAFVAVFAAVAVACRPVDDLDDFGAFFIDQLIKLVFQCL					
	130	140	150	160	170	180
	190	199				
m677.pep	PSGGRNVVFGFGTHIVCGX					
g677	PSGGRNVVFGFGTHIVCGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2229>:

a677.seq

1	ATGCCGCAGA	TTTTGGTGCG	GATTTTCCTC	ATTCGGTATT	CCTTTATTTG
51	GGAAACGGCG	CGTTTGTGCC	GTTTCAGACG	GCATTCCCGA	TCAGTCGATT
101	TTGATGTATT	CGACAGAAAG	GATTTCAATT	TCCTCACGCC	CTTCCGGCGT
151	GTTTAAACC	ACTTCGTCGC	CTTCACGCGC	TTAATCAGA	CAACGAGCCA
201	GCGGCGAAAT	CCAAGAAATT	TTGTTTTGCG	CGGTATCGAT	TCATCGATG
251	CCGACGATT	TGACGGTTTG	CTCGCGCCCG	TCGCCGCGCA	ACAGACCGAC
301	GGTCGCGCCG	AAAAACACTT	GGTCGGTCGC	TTCCGCGCAAT	TCGGGATCAA
351	CGACGACGCG	GGCTTCCAAA	CGCTTGGTCA	GGAAACGGAT	GCGGCGGTCTG
401	ATTTCGCGCA	TACGGCGTTT	GCCGTAAAGG	TAGTCGCCGT	TTTCGCTGCG
451	GTCGCCGTTG	CCTGCCGCC	AGTTGACGAT	TTGGACGATT	TCGGGGCGTT
501	CTTTATTAAAC	CAGTTGATAA	AGCTCGTCTT	TCAATGCCTG	CCATCCGCGC
551	GGCGTAATGT	AGTTTTTGGT	TTCGGTACTC	ATATTGTGTG	CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2230; ORF 677.a>:

a677.pep

1	MPQILVRIFL	IRYSFIWETA	RLCRFRHRSR	SVDFDVFDRK	DFNFLT	PFRR
51	V*NHFVAFTR	FNQTSQRRN	PRNFVLRGID	FIDADDFDGL	LAPVAAQQT	D
101	GRAEKHLVGR	FAQFGINDDG	GFQTLGQETD	AAVDFAHTAF	AVKVVAVFAA	
151	VAVACRPVDD	LDDFGAFFIN	QLIKLVFQCL	PSGGRNVVFG	FGTHIVCG*	

m677/a677 93.4% identity in 198 aa overlap

	10	20	30	40	50	60
m677.pep	MPQILVRIFLIRYSFIWETARFCRFRHRSRSVDFDVFDRKDFNFLT	PFRRVQNHVFAR				
a677	MPQILVRIFLIRYSFIWETARLCRFRHRSRSVDFDVFDRKDFNFLT	PFRRVXNHVFATR				
	10	20	30	40	50	60
	70	80	90	100	110	120

```

m677.pep      FNQTTSORNPRNFVLRGIDFIDADDFDGLLAPVVAQSDRRAEKHLVGRFAQFGIDDDG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a677          FNQTTSORNPRNFVLRGIDFIDADDFDGLLAPVAAQQTdGRAEKHLVGRFAQFGINDDG
              70          80          90          100         110         120

              130         140         150         160         170         180
m677.pep      SLQTFGQETDAAVDFAHTAFAVKIVAVFAAVAVACRPVDDLDDFGAFFVDQLIKLVFQCL
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a677          GFQTLGQETDAAVDFAHTAFAVKVAVFAAVAVACRPVDDLDDFGAFFINQLIKLVFQCL
              130         140         150         160         170         180

              190         199
m677.pep      PSGGRNVVFGFGTHIVCGX
|||||:|||||:|||||:|||||:|||||:
a677          PSGGRNVVFGFGTHIVCGX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2231>:

g678.seq

1	ATGAATAGCC	TCCCCATTGC	CGACCTCCTC	GCCTcgcCG	TCATCGCCGC
51	CTGCATCGTC	ATTTCCACGA	TGCGCGGCGT	GATTGCGGAA	GCAGgttcGA
101	TGGTgGCATC	ggtggTTTcc	tCTTTTTttg	ccAAACTCTt	tGCCGCACcc
151	ttcgccgACC	TCGCCTTTGc	ctCGTTCcA	ccccgcTGT	TTGCATtggc
201	tCTGCATTC	ATTTCCCTGT	TCGTCATTGC	CTGTCTGATC	CAGAAAATGC
251	TCCGTTCGCT	GCTGACCGGC	GCAGTTTCGG	CGGTcGGTCT	GGGCTTTGCC
301	AACCGCATT	TGGGCGGTGT	ATTcGGTGCA	TTGAAAGCG	TTTTGATTGT
351	TACCTGCTG	ATCATGCTTG	CTTCAAAAAC	CGACCTCGCC	GATACCAAGG
401	AATGCCAACA	GTCCTATACC	GTACCGTTTT	TCGATCGCCT	TTCCGGAAGC
451	TGTGTTAAAC	atacggacAA	CGCaccgaa	tCCCTcgaqc	accgactaa

This corresponds to the amino acid sequence <SEQ ID 2232; ORF 678.ng>:

g678.pep

1	<u>MNSLPIADLL</u>	<u>ASAVIAACIV</u>	<u>ISTMRGVIAE</u>	<u>AGSMVAWVVS</u>	<u>FFFAKLFAAP</u>
51	<u>FADLAFASFQ</u>	<u>PRLFALALS</u>	<u>ISLFVIACLI</u>	<u>QKMLRSLITG</u>	<u>AVSAVGLGFA</u>
101	<u>NRILGGVFGA</u>	<u>LKGVLIIVTLL</u>	<u>IMLASKTDLP</u>	<u>DTEEWQQSYT</u>	<u>VPFFVSLSEA</u>
151	<u>VLNHTDNAPE</u>	<u>SLDDN*</u>			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2233>:

m678.seq

```
1  ATGAATAGCC TCCCATTCG CGACCTCCTC GTCTCCGCCG TCATCGCCGC
51  CTGCATCGTG CTATCCGCGA TGC CGGGCGT GATTGCGGAG GCAGGGCTCAA
101 TGGCGGCATG GGTGGTTTCC TTCTTTTTCG CCAAACCTCT TGCCGCGCTCC
151 TTCGCGGACC TCGCCTTTGC CTGCTTCCAA CCCCCTGTG TGCATTTGGC
201 TCTGTCTGTT ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTTCGCT GCTGACCAGC GCAGTTTCGG CGGTTCGTTT GGGCTTTTGC
301 AACCCGATTT TGGCGGGCGT ATTCGGTGCA TTGAAAGCGG TTTTGATTGT
351 TACCCTGCTG GTCATGCTTG CTTCAAAAAC CGACCTGCCG GATACCGAAG
401 AATGCGCGCA ATCTTACACA CTGCGCTTTT TCGTATCGCT TTCGGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGGAAG ACGATTGA
```

This corresponds to the amino acid sequence <SEQ ID 2234; ORF 678>:

m678.pep

1	MNSLP	ADIADLL	VSAVIAACIV	LSAMRGVIAE	AGSMAAWVVS	FFFAKLFAAS
51	FADLAFASFQ	PRLFALALS	ISLFVIACL	IQLNLRSLITS	AVSAVELGFA	
101	NRIILGGVFGA	LKGVLIIVTLL	VMLASKTDLP	DTEEWRSQSYT	LPFFVSLSEA	
151	VLNHSGGTAE	TPEDD*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m678/g678 89.7% identity in 165 aa overlap

1088

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ					
g678	MNSLPIADLLASAVIAACIVISTMRGVIAEAGSMVAWVVSFFFAKLFAAPFADLAFASFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
g678	PRLFALALSFISLFVIACLIQKMLRSLTGAWSAVGLGFANRILGGVFGALKGVLIIVTLL					
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLASKTDLDPTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
g678	IMLASKTDLDPTEEWQSYTVPFFVSLSEAVLNHTDNAPESLDDDX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2235>:

```

a678.seq
1  ATGAATAACC TCCCCGTTGC CGACCTCCTC GTCTCCGCCA TCATCGCCGC
51  CTGCATCGTG CTATCCGCGA TGCGCGGCGT GATTGCGGAG GCTGGCTCAA
101 TGGCGGCATG GGTGGTTGCC TTTTTCG CCAAACTCTT TGCCGCACCC
151 TTGCGCGACA TCGCCTTTCG ATCGTTCCAA CCCCGCCTGT TTGCATTGGC
201 TCTGTCGTTT ATTTCCCTAT TCGTCATTGC CTGTCTGATC CAGAAAATAC
251 TCCGCTCGCT GCTGACCGGG GCAGTTTCGG CGGTCGGTTT GGGCTTTGCC
301 AACCGCATTT TGGGCGGCGT ATTCGGTGCA TTGAAAGGCA TTTGATTAT
351 TACCCTGCTG GTCATGCTCG CTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2236; ORF 678.a>:

```

a678.pep
1  MNNLPVADLL VSAIIAACIV LSAMRGVIAE AGSMAAWVVA FFFAKLFAAP
51  FADIAFASFQ PRLFALALSF ISLFVIACLI QKILRSLLTG AVSAVGLGFA
101 NRILGGVEGA LKGILIIITLL VMLASKTDLF DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

m678/a678 93.9% identity in 165 aa overlap

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ					
a678	MNNLPVADLLVSAIIAACIVLSAMRGVIAEAGSMAAWVVAFFFAKLFAAPFADIAFASFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
a678	PRLFALALSFISLFVIACLIQKILRSLTGAWSAVGLGFANRILGGVFGALKGILIIITLL					
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLASKTDLDPTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
a678	VMLASKTDLDPTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2237>:

```

g680.seq
1  ATGACGAAGG GCAGTTCGGC GATGTCCAGC CCACGCGCGG CGATATCGGT
51  GGCGACGAGG ACGCGCAGGC TGCCGTCTTT GAAGGCGTTG AGTGTTTCGA
101 GCCTGCTTGG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG

```

1089

```

151 CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTtttgCA
201 AAAGACGATA ACTTGGTTCA TATGCAGATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT TTGGAAGGTA TCGACGGCGA TGATGTgttg ttcGACGTTG
301 GCGTTGGTGG TGTTTTGGGC GGCAACCTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGTGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAACC CCATATCCAA CATGCGGTCT GCTTCGTCCA GAACGACGAT
501 TTCGGCTTTG TTTAAACTGA TGTTTTTCTG TTTCACATGG TCGAGCAGCC
551 GTCCGACGGT GCGCAGCACT ATTTGCGAGC CGGCACGCAG GTCGGCGGTT
601 TGTTTTGTCCA TGTTGACACC GCCGAAGAGG ACGGTATGCC GCAGCGGCAG
651 GTTTTTTAATg tag

```

This corresponds to the amino acid sequence <SEQ ID 2238; ORF 680.ng>:

```

g680.pep
1 MTKGSSAMSS PRAAISVATR TRRLPSLKAL SVSSLLCWER SPCACADRL
51 RRTSSRVTRS TLCLVLQKTI TWFICRSTIS RSSRLRFWKV STAMMCCSTL
101 ALVVFWAATS TVSGAFMKSC ASLRIGAELV AEKSRVVRWR GSICMILRMS
151 SINPISNMRS ASSRTTISAL FKLMPFCFTW SSSRPTVATT ISQPARRSAV
201 CLSMLTPPKR TVCRSGRFLM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2239>:

```

m680.seq
1 ATGACGAAGG GCAGTTCGGC AATGTCCAGC CCGCGCGCGG CGATGTCGGT
51 GGCGACGAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTTTTGCA
201 GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301 GCGTTGGTGG TGTTTTGGCG GCGCACTTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAACC CCATATCCAG CATACGGTCG GCTTCGTCCA AAACGACGAT
501 TTCGACTTTG TTCAAATGGA TGTTTTTCTG TTTCACGTGG TCGAGCAGCC
551 TTCCGACGGT GCGCAGCACT ATTTGCGAGC CGGCACGCAG GTCGGCGGTC
601 TGTTTTGTCCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTGTATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2240; ORF 680>:

```

m680.pep
1 MTKGSSAMSS PRAAMSVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
51 RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101 ALVVFCAATS TVSGAFMKSC ASLRIGAELV AEKSRVVRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPPNK TVWRSGRFLM *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```

m680/g680 90.9% identity in 220 aa overlap

          10      20      30      40      50      60
m680.pep  MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
          |||
g680      MTKGSSAMSSPRAAISVATRTRRLPSLKALSVSSLLCWERSPCACADRLRRTSSRVTRS
          10      20      30      40      50      60

          70      80      90      100     110     120
m680.pep  TLCLVLQNTMTWFICKSTISRSSRLRFKXVSTAMMCCSTLALVVFCAATSTVSGAFMKSC
          |||
g680      TLCLVLQKTIITWFICRSTISRSSRLRFWKVSTAMMCCSTLALVVFCAATSTVSGAFMKSC
          70      80      90      100     110     120

          130     140     150     160     170     180
m680.pep  ASLRIGAELVAEKSRVVRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKMFFCFTW

```

1090

```

g680      |||||
          ASLRIGAEKVAEKSRVWRWRSICMILRMSSINPISNMRSASSRTTISALFKLMFFCFTW
          130      140      150      160      170      180

          190      200      210      220
m680.pep  SSSRPTVATTISQPARRSAVCLSI FIPNKT VWRSGRFLMX
          |||||
g680      SSSRPTVATTISQPARRSAVCLSM LTPPKRTVCRSGRFLMX
          190      200      210      220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2241>:

```

a680.seq
1  ATGACGAAGG GCAGTTCGGC AATATCCAGC CCCCGCGCGG CGATATCGGT
51  GCGGACGAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CGGCGCACCA GTTCGCGCGT TACGCGGTGC ACGCTTTGTT TGGTTTTCGA
201 GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCGCT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301 CGCTTGGTGG TGTCTTGGCG GCGGACTTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAAAC CCATATCCAG CATA CGGTTCG GCTTCGTCCA AAACGACGAT
501 TTCGACTTTG TTCAAATGGA TGTTTTCTG TTTCACGTGG TCGAGCAGCC
551 GTCCGACGGT GCGGACGACG ATTCGCGAGC CGGCACGCAG GTCGCGGTC
601 TGTTCGTCCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTGTATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2242; ORF 680.a>:

```

a680.pep
1  MTKGSSAISS PRAAISVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
51  RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSLRF*MV STAMMCCSTL
101 ALVVSCAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKWMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPNKT TVWRSGRFLM *

```

m680/a680 98.6% identity in 220 aa overlap

```

          10      20      30      40      50      60
m680.pep  MTKGSSAMSSPRAAMS VATRTRRLPSLKALSVSSRLCWERSPCIACADRLRRTSSRVTRS
          |||||
a680      MTKGSSAISSPRAAISVATRTRRLPSLKALSVSSRLCWERSPCIACADRLRRTSSRVTRS
          10      20      30      40      50      60

          70      80      90      100     110     120
m680.pep  TLCLVLQNTMTWFICKSTISRSSLRFXMVSTAMMCCSTLALVVFCAATSTVSGAFMKSC
          |||||
a680      TLCLVLQNTMTWFICKSTISRSSLRFXMVSTAMMCCSTLALVVS CAATSTVSGAFMKSC
          70      80      90      100     110     120

          130     140     150     160     170     180
m680.pep  ASLRIGAEKVAEKSRVWRWRSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW
          |||||
a680      ASLRIGAEKVAEKSRVWRWRSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW
          130     140     150     160     170     180

          190     200     210     220
m680.pep  SSSRPTVATTISQPARRSAVCLSI FIPNKT VWRSGRFLMX
          |||||
a680      SSSRPTVATTISQPARRSAVCLSI FIPNKT VWRSGRFLMX
          190     200     210     220

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2243>:

```

g681.seq
1  ATGACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCGG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGcgacgg

```

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```

101  tgatgtTTTC GTCTGCTACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151  TTGAGCATTT GGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201  GATGCGGAGG TGTTTGCcgt cgaggttgGG GGCGATGGTG TTCATTGGGT
251  GTCCTTTGGT ATTCGGGGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301  CGGCTGCCAG TCGGCAACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351  ACGCGCTGCC TTCGGGTTGG GAAAGCAGTG CGGCGGTTTC AGGGTTGGTT
401  TTGGTGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GGTCTGCGGT
451  GTATTCTCGC GTTTCGTGCG CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501  CAAAAACGGG GCCTTCGCGG TAAAGGAAGC CGACGGGCCG GTTTTGTTTG
551  GCGACGGTGT TGGTGGCGAT GCAGCGTTCG AGTGCCGAGG AAAGTGCTTG
601  TGCAATGCG TTCATTGCGG GAATACGTTG GGGGGGGGGA AACTTGCGGA
651  TTTTACCAG ATTCGCCGTG TGTCGGCAGA CGGCGGCGGT TTGGTGGTAC
701  AATGTGCCCC GTTTGCAGCC TTAAGGTGTT TCTGTATTTT TGGAGTATGG
751  AAACGCATTC GGGCTGTTTT TTGCGGAAGA CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2244; ORF 681>:

```

g681.pep
1  MTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSIWLPISLV KRACTMPMR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVGNGLC AVFGKLPRAA FGLGKQCGGF RVGFGDVGEA DDAEVGVVVG
151 VFVGFVAAEE TPAAVVFKNG GFAVKEADGP VLFGDGVGGD AAVECRGKCL
201 CKCVHCGNTL GGGKLADFTT IFALSADGGG LVVQCAPFAA LRCFCIFGVW
251 KRIRAVFCGR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2245>:

```

m681.seq
1  ATGACGACGC CGATGGCAAT CAGTGCCTCA AACTTTTTCG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTT GTCTGCCACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCCGT CGAGGTTGGG GGCGATGGTG TTCATTGGGT
251 GTCCTTTGGT ATTCGGAGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301 CGSCTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351 ATGCGCTGCC TTCGGGTTGG GAGAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 TTGGCGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GATCTGCGGT
451 GTATTCTCGC GTCTCGTTCG CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAAACGGG GCCTTCGCGG TAGAGGAAGC CGACGGGCCG GTTTTGTTTG
551 GCGACGGTGT TGGTGGCGAT ACAGCGTTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAATGCG TTCATTACGG GAATACGTTG GGGG.AAAAC TTACGGATT
651 TACCACGATT CGTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGAAA
751 CGCATTCGGG CTGTTTTTTG CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2246; ORF 681>:

```

m681.pep
1  MTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSISLPISLV KRACTMPMR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVGDGLEC AVFGKLPCAA FGLGEQCGGF RVGFGDVGEA DDAEVVRIVG
151 VFVGLVAAEE TPAAVVFKNG GFAVEEADGP VLFGDGVGGD TAVECRGKCL
201 CKCVHYGNTL GXKLTDFTT RALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGR *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 681 shows 94.6% identity over a 261 aa overlap with a predicted ORF (ORF681.a) from *N. gonorrhoeae*:

m681/g681

```

          10      20      30      40      50      60
m681.pep  MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV
          |||
g681       MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSIWLPISLV
          10      20      30      40      50      60

```

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	70	80	90	100	110	120
m681.pep	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRCLKVSVLRPLVPGDGLECAVFGKLPCAA					
	: : : : :					
g681	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRCLKVSVLRPLVPGNGLECAVFGKLPRAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGFVDVGEADDAEVVRIVGVFVGLVAAEETPAAVVFKNGGFAVEEADGP					
	: : : : : :					
g681	FGLGKQCGGFRVGFVDVGEADDAEVVGVGVFVGLVAAEETPAAVVFKNGGFVAVEADGP					
	130	140	150	160	170	180
	190	200	210	220	230	239
m681.pep	VLFGDGVGGDTAVECRGKCLKCVHYGNTLGX-KLTDFTTIRALSADGGGLVVQCAPFAA					
	: : : : : :					
g681	VLFGDGVGGDAAVECRGKCLKCVHCGNTLGGGKLADFTTIPALSADGGGLVVQCAPFAA					
	190	200	210	220	230	240
	240	250	260			
m681.pep	LRCFCIFGVWKRIRAVFCGRRX					
	: : : :					
g681	LRCFCIFGVWKRIRAVFCGRRX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2247>:

```

a681.seq
1   ATAACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCAG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTT GTCTGCCACG CCAATTCTT GGAGGGTGC GACGAGACT
151 TTGAGCATT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTGCCGT CGAGTTGGG GCGATGGTG TTCATTGAGT
251 GTCCTTTGGT ATTCGGAGGT TTCGGAATGC CGCTGAAGG GTCAGTCCTT
301 AGGTGCCCAG TCGCGACCG TTTGGAATGT GCCGTCTTCT GCCAATTCCC
351 ACGCGCTGCC TTCAGGTTGG GAGAGCAGTG CGCGGTTTC AGGGTTGGTT
401 TTGGTGATAT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GGTGCTCGGT
451 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTT
501 CAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCTG GTTTTGTGTT
551 GCGACGGTGT TGGTGGCGAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAAAATGC TTCAATGCGG GAATACGTT GGGGAAAAC TTGCGGATTT
651 TACCACGATT CTGCGTTGT CGGCAGACGG CGCGGTTTG GTGGTACAAT
701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGAAA
751 CGCATTCGGG CTGTTTTTTC CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2248; ORF 681.a>:

```

a681.pep
1   ITPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSISLPISLV KRACTMPMRR CLPSRLGAMV FIECPLVFGG FGMPSEGSVL
101 RLPVGDGLEC AVFCQFPRAA FRLGEQCGGF RVGFGDIGEA DDAEVVRVVG
151 VFVGLVAAEE TPAAVVFKNG GFAVEEADGL VLFGDGVGGD AAVECRGKCL
201 CKCVHCGNTX GGLADFTTI LALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGRR *

```

m681/a681 90.8% identity in 260 aa overlap

	10	20	30	40	50	60
m681.pep	MTTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV					
	: : : : : :					
a681	ITTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m681.pep	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRCLKVSVLRPLVPGDGLECAVFGKLPCAA					
	: : : : :					
a681	KRACTMPMRRCLPSRLGAMVFIECPLVFGGFGMPSEGSVLRLPLVPGDGLECAVFCQFPRAA					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGF	GDVGEADDAEVVR	IVGVFVGLVAAEET	PAAVVFKNGGFAVEE	ADGP	
a681	FRLGEQCGGFRVGF	DIGEADDAEVVR	VGVFVGLVAAEET	PAAVVFKNGGFAVEE	ADGL	
	130	140	150	160	170	180
	190	200	210	220	230	240
m681.pep	VLFGDGVGGDTAVE	CRGKCLCKCVHYG	NLTGXLTDFTTIR	ALSADGGGLVVQCA	PPFAAL	
a681	VLFGDGVGGDAAVE	CRGKCLCKCVHCG	NLTGXLTDFTTIR	ALSADGGGLVVQCA	PPFAAL	
	190	200	210	220	230	240
	250	260				
m681.pep	RCFCIFGVWKRIR	AVFCGRRX				
a681	RCFCIFGVWKRIR	AVFCGRRX				
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2249>:

g682.seq

```

1  ATGCGCGATT TCGCCGTATG GGTGCCTTAC GGGGAACGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCC CGCACCTTAT TCGCCTGAGC CCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCC ATTTGACGAT GCACTACTGT CCTATTTGA TTTTAATTGA
201 CTATATTGTG GTGAATGATG AAATAAAAT GCCGTCTGAA CCCGATTGGA
251 TTCAGACGGC ATTTTGTATG GCAGGATTTA TTCGCTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCAGTC AGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2250; ORF 682>:

g682.pep

```

1  MRDFAVWVPY GERRKNWDIR YCLPHLIRLS PTRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDYIC VNDEIKMPSE PDWIQTAFCM AGFIREPTDR
101 PILTRQSGVV RISPRTGFRY PTRSLPKSKK AYG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2251>:

m682.seq

```

1  ATGCGTGATT TCACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCC ATTTGACGAT GCACTACTGT CCTATTTGA TTTTAATTGA
201 CTAT..... GAAA TGGCAATGCC GTCTGAACCC GATTGGATTC
251 AGACGGCATT TTGTATGGCG TACGGATTTA TTCGGTTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCAGTC AGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2252; ORF 682>:

m682.pep

```

1  MRDFTVWVSY GKWRKNWDIR YCLLHLIHLS STRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDY.. ..EMAMFSEP DWIQTAFDMA YGFIREPTDR
101 PIRTRQSGVV RISPRTGFRY PTRSLPKSKK AYG*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 682 shows 88.1% identity over a 134 aa overlap with a predicted ORF (ORF682.a) from *N. gonorrhoeae*:

m682/g682

```

      10      20      30      40      50      60
m682.pep  MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          |||::||| ||: ||||| |||: || ||||| ||||| ||||| ||||| |||||
g682      MRDFAVWVPYGERRKNWDIRYCLPHLIRLSPTRLRKCGRILSGICEPFCLITPDLTMHYC
          10      20      30      40      50      60

      70      80      90      100     110
m682.pep  PILILIDY----EMAMPSEFPDWIQTAFCMAYGFIRFPTDRPIRTRQSGVVRISPRTGFR
          ||||| ||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g682      PILILIDYICVNDEIKMPSEFPDWIQTAFCMA-GFIRFPTDRPILTRQSGVVRISPRTGFR
          70      80      90      100     110

      120     130
m682.pep  YPTRSLPKSKKAYGX
          ||||| ||||| ||||| |||||
g682      YPTRSLPKSKKAYGX
          120     130

```

```

a682.seq
  1  ATGCGCGATT TTACCGTATG GGTGTCTTAC GGGAAATGGC GGGAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAAGT TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTC TG
151 ATTACGCCCG ATTTGACGAT GCATCTACTGT CCTATTTTGA TTTTAATTGA
201 ATAT.....
251 .....TATA TTCGGTTTCC AACTGACCGA
301 CCCATTCTGA CAAGCCGAC AGGCGTTGTT CGGATTTTCG CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

```
a682.pep
1  MRDFTVWVSY GKWRKNWDIR YCLLHLIHLN STLRKRCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIEY.. ..... ..YIRFPTDR
101 PILTRPTGVV RISPRTGERY PTRSLPKSKK AYG*
```

[illegible]

```

g683.seq
1  ATGATTAAGG  AAACCTAAT  GCGCCCAATC  TTCCTATCTT  TCGTTTACTT
51  CCTTATTTTG  ATAACCGCCT  GCGACACACC  GGACAAGTCT  GCCCGATGGG
101 AAAATATCGG  CACAATCTCA  AACGGCAATA  TTCATACATA  TATTAATAAA
151 GACAGTGTGA  GTAAAACAGG  AAATCTGTAG  ATTTTCCAAG  ATAAAAAAGT
201 TGTTACCAAT  GTGAAACAAG  AACGTTTGTG  CAACACCCCC  GCATACAAGA
251 CTGCCATTGC  CGAGTGGGAA  ATCCACTGCA  ACAACAAAC  ATACCGCTTA
301 AGTTCGCTAC  AGTTATTGTA  TACAAAAAAC  ACGGAAATTT  CGGACAAAAA
351 CTACACAGCC  TCTCCCTCC  GCCAGTAGAG  CATCTGTCCT  CCGACATTAA

```

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401 CTGAAAAACA ATATGAAACC GTATGCGGGA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2256; ORF 683 >:

g683.pep

```

1  MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPMISLS GTLTEKQYET VCGKKL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2257>:

m683.seq..

```

1  ATGATTAAGG AAACCTAAT GCGCCCAATC TTCCTATCTT TCGTTTATT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
201 TGTACCAAT CTAAACAAG AACGTTTTCG CAACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AGTTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAAAGCTCTG A
```

This corresponds to the amino acid sequence <SEQ ID 2258; ORF 683>:

m683.pep..

```

1  MIKETLMRPI FLSFVLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPMISLS GTLTEKQYET VCGKKL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 683 shows 99.3% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. gonorrhoeae*:

m683/g683 99.3% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	: : : : : : : : :					
g683	MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m683.pep	IFQDKKVVVNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
	: : : : : : : :					
g683	IFQDKKVVVNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
	70	80	90	100	110	120
	130	140				
m683.pep	SSLRPMISLSGTLTEKQYETVCGKKLX					
	: : : : :					
g683	SSLRPMISLSGTLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2259>

a683.seq

```

1  ATGATTAAGG AAACCTAAT GCGCCCAATC TTCCTATCTT TCGTTTATT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCNAG ATAAAAAAGT
201 TGTACCAAT CTAAACAAG AACGTTTTCG CNACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AATGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
351 NTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAAAGCTCTG A
```

This corresponds to the amino acid sequence <SEQ ID 2260; ORF 683.a>:

a683.pep

```

1  MIKETLMRPI FLSFVLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFXDKKVVVN LKQERFAXTP AYKTAIAEWE IHCNNKTYRL
```


101 SSLQLFDTKN TEISTQXYTA SSLRPMSILS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 683 shows 97.9% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. meningitidis*:

m683/a683 97.9% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPIFLSFVLF	PILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM				
a683	MIKETLMRPIFLSFVLF	PILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM				
	10	20	30	40	50	60
	70	80	90	100	110	120
m683.pep	IFQDKKVVVTLNKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
a683	IFXDKKVVVTLNKQERFAXTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQXYTA					
	70	80	90	100	110	120
	130	140				
m683.pep	SSLRPMSILSGTLTEKQYETVCGKKLX					
a683	SSLRPMSILSGTLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2261>

g684.seq

1	ATGCGCCTTT	TCCCATCGC	CGCCGCCCTG	ACGCTTGCCG	CCTGCGGTAC
51	TGTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACCGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAAACC	GACCCCTACC	GCATCAACAC
201	CGCACAAAAC	CATGTTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAC	CTTTGTTCTT
301	GCCTCACGCA	GCGGCAGTAC	CGACAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CCATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2262; ORF 684>:

g684.pep

1	MRLFP	IAAAL	TAA	CGTVQS	TOYFVLPDSR	YIRPATQGGG	TAVEVRLAEP
51	LKR	GLVYQT	DPYRLNTAQN	HVWADTLDDM	LEAALSNAFN	RLDSTRTFVP	
101	ASR	SGSTDKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD	
151	GAA	AMTAAL	QGLKQAAQOM	VE*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2263>:

m684.seq

1	ATGCGCCTTT	TCCCGATTGC	CGCCGCCCTG	TCGCTTGCCG	CCTGCGGTAC
51	TGTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACTGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAAACC	GACCCCTACC	GCCTCAACAC
201	CGCACAAAAC	CACGTCTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAT	CTTTGTTCTT
301	GCCTCACGCA	GCGGCAGTAC	CGAAAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CGATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2264; ORF 684>:

m684.pep

1	MRLFP	IAAAL	SLAACGTVQS	TOYFVLPDSR	YIRPATQGGG	TAVEVRLAEP
51	LKR	GGVYQT	DPYRLNTAQN	HVWADTLDDM	LEAALSNAFN	RLDSTRIFVP
101	ASR	SGSTEKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD

151 GYAAMTAALE QGLKQAAQOM VE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 684 shows 97.7% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. gonorrhoeae*:

m684/g684 97.7% identity in 172 aa overlap

	10	20	30	40	50	60
m684.pep	MRLFPFAAALSLAACGTQSTQYFVLPDSRYIRPATQGGTAVEVRLAEPLKRGGLVYQT					
g684	MRLFPFAAALSLAACGTQSTQYFVLPDSRYIRPATQGGTAVEVRLAEPLKRGGLVYQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRLNTAQNHVWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS					
g684	DPYRLNTAQNHVWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS					
	70	80	90	100	110	120
	130	140	150	160	170	
m684.pep	YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX					
g684	YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2265>

a684.seq

1	ATGCGCCTCT	TCCCGATTGC	CGCCGCCCTG	ACGCTTGCCG	CCTGCGGTAC
51	TGTGCAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACTGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCCTCAACAC
201	CGCACAAAAC	CACGTCTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGACCAA	TGCATTCAAC	CGTTTGACA	GCACACGCAT	CTTTGTTCTT
301	GCCTCACGCA	GCGGCAGTAC	CGAAAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CCATAGCCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2266; ORF 684.a>:

a684.pep

1	MRLFPFAAAL	TLAACGTVQS	TOYFVLPDSR	YIRPATQGGT	TAVEVRLAEP
51	LKRGGLVYQT	DPYRLNTAQN	HVWADTLDDM	LEAALSNAFN	RDLSTRIFVP
101	ASRSGSTKWT	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD
151	GYAAMTAALE	QGLKQAAQOM	VE*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 684 shows 99.4% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. meningitidis*

m684/a684 99.4% identity in 172 aa overlap

	10	20	30	40	50	60
m684.pep	MRLFPFAAALSLAACGTQSTQYFVLPDSRYIRPATQGGTAVEVRLAEPLKRGGLVYQT					
a684	MRLFPFAAALSLAACGTQSTQYFVLPDSRYIRPATQGGTAVEVRLAEPLKRGGLVYQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRLNTAQNHVWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS					
a684	DPYRLNTAQNHVWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVYIDAFQGS					
	70	80	90	100	110	120
	130	140	150	160	170	

```

g685.seq
1      TTGTTTGGCC  GTATCGGGAA  TTTTGC GTTT  TGC GCGTGG  TTTCTGCAGG
5      TTGTTTGCTT  AATAAATAAC  ATTCTATTCT  GTATGCAAAAG  GAACCGCACA
101    CCGTGAACCA    CGCTTTTTAT  TGGGCAAGcct  CGCGCGTCTCT  CGCGCGCGCC
151    TGTTCGCCCG    AACCTGCCGC  CGAAAAAACT  GTATcgcCGG  CATCCCAAGC
201    CGCATCCACA    CCTGTCCGCA  CGCTGACCGT  GCCGACCCGC  CGGGCGCGTAGT
251    CGGTTGTGCC    GAAGAAATCCC  GAACgcgtcg  cegtgtAcga  CtggcGGCGG
301    TtggatACGC    TGACCCGATG  GGGCGTGAAT  GTGGGCGCAA  CCACCGCGCC
351    GGTGCGCGTGC    GACTATTGTC  AGCCTGCATT  TGACAAGGCC  GCAACCGGTGG
401    GGACGCTGTT    TGAGCCCGAT  TGCGAATCCC  TGCACCGCCA  CAATCCGAGT
451    TTTGTCAATTA    CCGCGGGGCC  GGGTGC GGAA  GCGTATGAAC  AATTGGCGAA
501    AARCGCGGACC    ACCATAGATT  TGACGGTGGa  CAACGGCAAT  ATCCGCACCA
551    CGGGCGAGAA    GCAGATTGGAG  ACCCTGTCGC  GGATTTTCGG  TAAGGAAGCG
601    CGCGTGGCGG    AATTGAATGC  GCAGATTGAC  GCGCTGTGTC  CCAAAAAGCG
651    CGAAGCCGCG    ARAAGCAAAg  GACGCGGGCT  GGTGCTGTGC  GTTACAGCCA
701    ACAAGGTGTC    CGCCTTCGCG  ACGCAATCCG  GGTGGCAAG  TTGGATACAC
751    GGCACATCG     CGCTCGCGCC  CCGTGACGAA  TCTTTACCA  ACGAAGGCGA
801    CGGGCAGGCC    GTTTCCTTCG  AATACATCAA  AGAGAAAAAC  CCCGCTTGGa
851    TTTTCAATCAT    CGAGCCGACC  GCCGCCATCG  GGCAGGAAGG  CGCCGCTGCC
901    TGTGAAGTGT    TGGATAACCG  CGTGTATGCG  GCGACGAACG  CTTGGAAGCG
951    CAAGCAAACT    ATCGTATATC  CTGCGCGGAA  CTACATTGTC  GCGGGCGGCG
1001   CGCGCGCACT    GTACACGGCG  GCGGAACAGT  TGAAGCGGGC  GTTTGAAAAG
1051   GCAGAACCCG    TATCGCGCGA  GTAG

```

g685.pap

1	LFCRIGNFAF	CGVVSAGCLL	NNKHSYSYAK	EPHTVKPRFY	WAACAVLPAA
51	CSPEPAAEKT	VSASQAAST	PVATLTVPAT	RGDAVVPKNP	ERVAVYDWAQ
101	LDLTTEPGVN	VGATTAPVRV	DYLPAPFDKA	ATVGLTFEPD	CESLHRHNQP
151	FVITGGPGAE	AEYQLAKNT	TLDTLVGNLN	IRTSGEKOME	TLSRIFGKEA
201	RVAEELNAQF	ALFAQKREAA	KGKGKGLVLS	VTGNKVSAFG	TQSRLASWII
251	GDIGLPPVDE	SLRNEGHGQP	VSFEYIKEKN	PGWIFIIDRT	AAIGQEGPAA
301	VEVLDAALVC	GTNAWKRKQI	IVMPAANYIV	AGGARQLIQA	AEQLKAAFEK
351	AEPPAA*				

```

m685.seq
1      TTGTTTTGCC GTATCGGGAA TTTTGC GTTT TGCGCGGTGG TTTCTGCAGG
5      TTGTTTGTCT AATAATAAAC ATTCTTATTC GTATGCAAAAG GAACCGCACA
101    CCGTGAACCTT GCGTTTTTAT TTGGGACGCT GCGCGGTCTCT GTCAGCCGCC
151    TGTTCGCGCGG AACCTCGCCG CGAAAAAATC GTATCCGCGC CATCCGCATC
201    TGCCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCGCA
251    AGAATCCCGA ACSCGTGCGG GTGTACGACT GGGCGGCGGT GGATACGCTG
301    ACCGAAATTGG CCGTGAATGT GGGCGCAACC ACCGCGCCGG TGCGCGTGGA
351    TTATTTTGAC CTTCGATTTT ACAAGGCGCG AACCGTGGGG ACGCTGTTTCG
401    AGCCCGATTA CGAAGCCCTG CRCCGCTACA ATCCTCAGCT TGTCAATTAC
451    GCGGGGCGCG GCGCGGAAGC GTATGAACAG TTAGCGAAAA ACGCGAATCC
501    CATAGATCTG ACCGTTGGACA ACGGCAATAT CCGCACCCAG GCGGAAAGCG
551    AGATGGAGAC CTTTGC GCGG APTTTTCGCGA AGGAAGCGCG CGCGGCGGAA
601    TTGAAGGCGC AGATTGACGC GCTGTTTCGC CAACCGCGCG AAGCGCGCAA
651    AGGCAAAAGGA CGCGGGCTGG TGCTGTTCGTT TACGGGCAAC AAGGTGTCCG
701    CCTTCGGCAC CGACTCGCGG TTGGCAAGTT GGATACACGC CGCATCTCGG
751    CTACCGCCCTG TAGACGAATC TTTAGCAAC GAGGGGACAG GCGACGCTGT
801    TTCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG
851    ACCGTACCGC CGCCATCGGG CAGGAAGGCG CGGCGGCTGT CGAAGTATTC
901    GACGACGCGC TGGTACGCGG CACGAACGCT TGGAAAGCGA AGCAATCAT
951    CGTCATGCCT CGCGCAACT ACATTGTGCG GGGCGGCGCG CGGCAGTTGA
1001   TTTCAGGCGCG GAGGAGTTG AAGGCGCGCT TTAATAAGGC AGAACCCGTT
1051   GCGCGGGGGA AAAAGTAG

```

m685.pgp

1099

```

1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51 CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLO PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPGEAEAYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKGKG RGLVLSVTGN KVSAGTQSR LASWIHGDI
251 LPPVDESLRN EGHGQPVSE YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGA RQLIQAAEQL KAAFKKAEPV
351 AAGKK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 685 shows 94.4% identity over a 356 aa overlap with a predicted ORF (ORF 685) from *N. gonorrhoeae*:

m685/g685 94.4% identity in 356 aa overlap

```

m685.pep      10      20      30      40      50      60
LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPPEAAEKT
g685          10      20      30      40      50      60
LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLPAACSPPEAAEKT

m685.pep      70      80      90      100     110
VSAASASA----ATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRV
g685          70      80      90      100     110     120
VSAASQAASTPVATLTVPTARGDAVVPKNPERVAVYDWAALDTLTPGVNVGATTAPVRV

m685.pep     120     130     140     150     160     170
DYLOPAFDKAAATVGTLEFEPDYEALHRYNPQLVITGGPGAAYEQLAKNATTIDLTVDNGN
g685         120     130     140     150     160     170     180
DYLOPAFDKAAATVGTLEFEPDCESLHRNPQFVITGGPGAAYEQLAKNATTIDLTVDNGN

m685.pep     180     190     200     210     220     230
IRTSGEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGKGRGLVLSVTGNKVSAGF
g685         180     190     200     210     220     230     240
IRTSGEKQMETLSRIFGKEARVAELNAQIDALFAKREAAKGKGRGLVLSVTGNKVSAGF

m685.pep     240     250     260     270     280     290
TQSRLASWIHGDIPLPPVDESLRNECHGQPVSEYIYEKNPDWIFIIDRTAAIGQEGPAA
g685         240     250     260     270     280     290     300
TQSRLASWIHGDIPLPPVDESLRNECHGQPVSEYIYEKNPDWIFIIDRTAAIGQEGPAA

m685.pep     300     310     320     330     340     350
VEVLNANALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKKAEPVAAKKX
g685         300     310     320     330     340     350
VEVLNANALVCGTNWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFEKAEPVAAQX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2271>

```

a685.seq
1  TTGTTTGGCC GTATCGGGAA TTTTGCCTTT TGCAGCGTGG TTTCTGCAGG
51 TTGTTTGGCTT AATATAAACC ATCTTATTTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCAGCGTCCT GCTGACCGCC
151 TGTTCGCCCC AACCTGCCGC CGAAAAACT GTATCCGCCG CATCCGCATC
201 TGCCGCCACA CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GTGTGAATGT GGGCGCAACC ACCGCGCCGG TCGCGTGGGA
351 TTATTTCGAG CCTGCATTTC ACAAGCGGCG AACGGTGGGG ACCTGTTCG
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTCATTACC
451 GCGCGGCCGG GCGCGGAAGC GTATGAACAG TTGGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCATAT CCGCACCAGC GCGGAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGAAGCGCG CGCGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCGCC CAAACGCGCG AAGCCGCCAA
651 AGGCAAGGGA CGCGGGCTGG TGCTGTCCGT TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GSATACACGG CGACATCGGC
751 CTACCCCTG TAGACGAATC TTTACGCAAC GAGGGGACCG GGCAGCGCTG
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG

```

1100

```

851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGGAAAGCGCA AGCAAAATCAT
951 CGTCATGCCT GCCGCGAACT ACATTGTCGC GGGCGGCTCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGGAGGCGT TTGAAAAGGC AGAACCCGTT
1051 CCGCGGGGA AAGAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2272; ORF 685.a>:

```

a685.pep
1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51  CSPEPAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLO PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPGEAEYEQ LAKNATTIDL TVDNGNIRTS GEKOMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKGKG RGLVLSVTGN KVSAGTQSR LASWIHGDIG
251 LPPVDESIRN EGHGQPVSEF YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGS RQLIQAAEQL KEAFEKAEPV
351 AAGKE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 685 shows 98.9% identity over a 355 aa overlap with a predicted ORF (ORF 685) from *N. meningitidis*:

```

m685/a685 98.9% identity in 355 aa overlap

m685.pep      10      20      30      40      50      60
LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAEKT
a685          10      20      30      40      50      60
LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAEKT

m685.pep      70      80      90      100     110     120
VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ
a685          70      80      90      100     110     120
VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ

m685.pep     130     140     150     160     170     180
PAFDKAATVGTLEFPDYEALHRYNPQLVITGGPGEAEYEQALAKNATTIDLTVDNGNIRTS
a685         130     140     150     160     170     180
PAFDKAATVGTLEFPDYEALHRYNPQLVITGGPGEAEYEQALAKNATTIDLTVDNGNIRTS

m685.pep     190     200     210     220     230     240
GEKOMETLARIFGKEARAAELKAQIDALFAQTREAAKGKRGRLVSVTGNKVSAGTQSR
a685         190     200     210     220     230     240
GEKOMETLARIFGKEARAAELKAQIDALFAQTREAAKGKRGRLVSVTGNKVSAGTQSR

m685.pep     250     260     270     280     290     300
LASWIHGDIGLPPVDESIRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL
a685         250     260     270     280     290     300
LASWIHGDIGLPPVDESIRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL

m685.pep     310     320     330     340     350
DNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKKAEPVAAGKKX
a685         310     320     330     340     350
DNALVRGTNAWKRKQIIVMPAANYIVAGGSRLIQAAEQLKAAFEKAEPVAAGKEX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2273>

```

g686.seq (partial)
1  ..AATTTCCTCT GCCGCGCCGA TGATGTTTTT GACGATATCT GCAGTGCCGT
51  TGAAGGGCTTC ggcgcATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 TTGGCGCGTT TGAATCCGTC GCCTACTCCT TGCCTCAGCA TAGCGCCGGC
151 ATTGTGGAAG CCGTCGGCAA GCCGTTGTCC GGTGCTGCGG TTGTCGGTCA
201 GGTGTAGGCG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
251 TCCTTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301 GCCGTCGGCG GGATGGTGTT CGTATCCGTC CCAATGGATG CGGTAAAGGC
351 TGAATCCGTC AACGGGACTA CCGGCTTCGT CAGAATCGGA ATGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2274; ORF 686 >:

```
g686.pep (partial)
1  ..NFSCRADDVF DDICSAVEGF GGIARSVQLG AVSGGAFESV AYSLRQHSAG
51  IVETVGRPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI
101 AVGGMVFVSV PMDAVKAESV NGTTGFVRIG M'
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2275>:

```
m686.seq.
1  ATGATGTTGA AAAAATTCGT ACTCGGCGGT ATTGCCGCAT TGCTTTTGGC
51  GGCCTGCGGC GGTTCGGAAG GCGGCAGCGG AGCGNNNNNN NNNNNNAATT
101 TCTCCTCAG CGCCGATGAT GTTTTAAACG ATATCTGCAG TGCCGTTGAA
151 GGCTTCGGCG GCATTGCCCG ATCTGTCCAG CTCGGGGCTG TATCGGGTGG
201 CGCGTTTGAA TCCGTCGCCT ACTCCTTCCG TCAGCATACT ACCGGCATTG
251 TGGAAACGGT CGGCAAGCCG TTGTCCGGTG CTGCGGTTGT CGGTCAGGIT
301 GAGGCGGATA TTTTGGGCAA CGCCTTTTAT CTCGTAGCTG TATATATCCC
351 TCGCGCCTTT GGGAGCGGGA TAGCCGCCCG CCTGTGGCCC GTCATAGCCG
401 TCGGCGGGAT GGTGTTTCGTA TCCGTCCCAA TGGATCGCGT AAAGGCTAAA
451 TCCGTCAACG GGACTACCGG CTCATCAGA ATCGGAATGT GA
```

This corresponds to the amino acid sequence <SEQ ID 2276; ORF 686>:

```
m686.pep
1  MMLKKEVLGG IAAVLAAACG GSEGGSGAXX XXNFSCSADD VFNDICSAVE
51  GFGGIARSVQ LGAVSGGAFE SVAYSIRQHT TGIVETVGRP LSGAAVVGQV
101 EADILGNAFY VVAVYIPRAF GSGIAAALWF VIAVGGMVFY SVPMDAVKAK
151 SVNGTTGFIR IGM'
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 686 shows 95.4% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. gonorrhoeae*

g686/m686 95.4% identity in 131 aa overlap

g686.pep				10	20	30
				NFSCRADDVFDDICSAVEGFGGIARSVQLG		
m686	LKRFEVLGGIAALVLAACGSGEGSGAXX	XXXXNFSCSADDVFNDICSAVEGFGGIARSVQLG				
	10	20	30	40	50	60
g686.pep		40	50	60	70	80
		AVSGGAFESVAYSRLQHSAGIVETVGRPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS				
m686		AVSGGAFESVAYSRLQHTTGIVETVGRPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS				
	70	80	90	100	110	120
g686.pep		100	110	120	130	
		GIAAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFVRIGMX				
m686		GIAAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFVRIGMX				
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2277>

```
a686.seq (partial)
1  ..AATTTCCTT GCGCGCCGA TGATGTTTT GACGATATCT GCAGTGCCGT
51  TGAAGCTTC GCGGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 GTGGCGCGT TGAATCCGTC GCCTACTCCT TCGGTCAACA TACTACCGGT
151 ATTGTGGAAC CGGTCGACAA GCCGTTGTCC GGTGCTGCGG TTGTCGGTCA
201 GGTGAGGCG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
251 TCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301 GCCGTCGCGG GGATGGTGTT CGTATCCGTC CCAATGGATG CGGTAAGGC
351 TGAATCCGTC AACGGGACTA CCGGCTTCAT CAGAATCGGA ATGTGA
```

This corresponds to the amino acid sequence <SEQ ID 2278; ORF 686.a>:

```
a686.pep (partial)
```

1102

```

1  ..NFSCRADDVF DDICSAVESF GGIARSVOLG AVSGGAFESV AYSLRQHTTG
51  IVETVDKPLS GAAVVGQVEA DELGNIFYV AVYIPRAFGS GIAAALWPVI
101 AVGGMVFVSV PMDAVKAESV NGTTGFIRIG M*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 686 shows 96.2% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N meningitidis*:

m686/a686 96.2% identity in 131 aa overlap

```

              10      20      30      40      50      60
m686.pep      LKKFVLGGIAALVLAACGGSEGGSGAXXXNFSCSADDVFNDICSAVEGFGGIARSVQLG
a686              ||| |||||:|||||:|||||:|||||
              NFSCRADDVFDDICSAVESFGGIARSVQLG
                      10      20      30

              70      80      90      100     110     120
m686.pep      AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNIFYVVAVYIPRAFGS
a686              ||| |||||:|||||:|||||:|||||:|||||:|||||
              AVSGGAFESVAYSLRQHTTGIVETVDKPLSGAAVVGQVEADILGNIFYVVAVYIPRAFGS
                      40      50      60      70      80      90

              130     140     150     160
m686.pep      GIAAALWPVIAVGGMVFVSVPMDAVKAKSVNGTTGFIRIGMX
a686              ||| |||||:|||||:|||||:|||||:|||||
              GIAAALWPVIAVGGMVFVSVPMDAVKAESVNGTTGFIRIGMX
                      100     110     120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2279>

```

g687.seq
1  ATGAATCCA GACACCTCGC CCTCGCCCTC GCGGTGCGC CCCTGTTCGC
51  CCTTGCCGCG TGCGACAGCA AAGTCCAAC CAGCGTCCC GCCGACAGCG
101 CGCCTGCCGC TTCGGCAGCC GCCGCCCGG CAGGACTGGT CGAAGGCCAA
151 AACTACACCG TCCTTGCCAA CCGGATTCCC CAACAGCAGG CAGGCAAGGT
201 TGAAGTGCTT GAGTTTTCG GCTATTTTG TCCGCACTGC GCCCGCCTcg
251 AACCTGTTTT GAGCAAACAC GCCAAGTCTT TTAAAGACGA TATGTACCTG
301 CGTACCGAAC ACGTGCTCTG GCAGAAAGAA ATGCTGCCGC TGGCAGCCct
351 cGCCGCGGCC GTCGATATGG CTGCCGCCGA AAGCAAAGAT GTGGCGAACA
401 GCCATATTTT CGATGCGATG GTCAACCAAA AAATCAAGCT GCAAGAGCCG
451 GAAGTCCTCA AAAAATGGCT GGGCGAACaa ACcgcttTG ACGGCAAAAA
501 AGTCCTTGCC GCCTACGAAT CCCCAGAAAG TCAGGCGCGC GCcggcAAAA
551 TGCAGGAGCT GACCGAAACC TTCCAAATCG ACGGTACGCC CACGGTTATC
601 GTCGGCGGCA AATATAAAGT CGAATTGCGC GACTGGGAGT CCGGTATGAA
651 CACCATCGAC CTTTGGCGG ACAAAGTACG TGAAGAACAA AAAGCCGCGC
701 AGTAG

```

This corresponds to the amino acid sequence <2280 ID 724; ORF 687>:

```

g687.pep
1  MKSRHLALAL GVAALFALAA CDSKVQTSVP ADSAPAASAA AAPAGLVEGQ
51  NYTVLANPIP QQOAGKVEVL EFFGYFCPHC ARLEPVLSKH AKSFKDDMYL
101 RTEHVWQKE MLPLARLAAA VDMAAESKD VANSIFDAM VNQIKLQEP
151 EVLKKWLGEQ TAFDGKKVLA AYESPESQAR AGKMQLTET FQIDGTPTVI
201 VGGRYKVEFA DWESGMNTID LLADKVREEQ KAAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2281>:

```

m687.seq
1  ATGAATCCA GACACCTTGC CCTCGGCGTT GCGGCCCTGT TCGCCCTTGC
51  CGCGTGCGAC AGCAAAGTCC AAACCAGCGT CCCCGCCGAC AGCGCGCTG
101 CCGCTTCGCG AGCCGCCGCC CCGGAGGGC TGGTCGAAGG GCAAACACTAT
151 ACCGTCCTTG CCAACCCGAT TCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCAC CTCGAACCTG
251 TTTTAAGCAA ACACGCCAAG TCTTTAAAG ACGATATGTA CCTGCGTACC
301 GAACACGTCG TCTGGCAGAA AGAAATGCTG ACGCTGGCAC GCCTCGCCCG
351 CGCCGTTCGAT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAAATCA AGCTGCAAAA TCCGGAAGTC
451 CTCAAAAAT GGCTGGGCGA ACAAACCGCC TTTGACGGCA AAAAAGTCCT

```

1103

```

501 TGCCGCCTAC GAGTCCCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACCGGT TATCGTCGGC
601 GGTAATATA AAGTTGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA ACAAAAAGCC GCGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2282; ORF 687>:

```

m687.pep
  1 MKSRHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
  51 TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
 101 EHVWVQKEML TLARLAAAVD MAAADSKDVA NSHIFDAMVN QKIKLQNPVEV
 151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFO IDGTPTVIVG
 201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 687 shows 97.0% identity over a 234 aa overlap with a predicted ORF (ORF 687) from *N. gonorrhoeae*:

```

m687/g687 97.0% identity in 234 aa overlap

      10      20      30      40      50
m687.pep MKSRHLAL--GVAALFALAACDSKVQTSVPADSAPAASAAAAAPAGLVEGQNYTVLANPIP
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g687      MKSRHLALALGVAALFALAACDSKVQTSVPADSAPAASAAAAAPAGLVEGQNYTVLANPIP
          10      20      30      40      50      60

      60      70      80      90      100     110
m687.pep QQQAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTEHVWVQKEMLTLARLAAA
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g687      QQQAGKVEVLEFFGYFCPHCARLEPVLSKHAKSFKDDMYLRTEHVWVQKEMPLARLAAA
          70      80      90      100     110     120

      120     130     140     150     160     170
m687.pep VDMAAADSKDVANSHIFDAMVNQKIKLQNPVLLKKWLGEQTAFDGKKVLAAYESPESQAR
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g687      VDMAAADSKDVANSHIFDAMVNQKIKLQNPVLLKKWLGEQTAFDGKKVLAAYESPESQAR
          130     140     150     160     170     180

      180     190     200     210     220     230
m687.pep ADKMQLTETTFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g687      AGKMQLTETTFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
          190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2283>

```

a687.seq
  1 ATGAAATCCA AACACCTCGC CCTCGGCGTT GCCGCCCTGT TCGCACTTGC
  51 CGCGTGCCGAC AGCAAAGTCC AAACCAGCGT CCCGCGCGAC AGCGCGCCTG
 101 CCGCTTCGGC AGCGCGCGCC CCGGCAGGGC TGGTCGAAGG GCAAACTAT
 151 ACTGTCCTTG CCAACCCGAT TCCCAACAG CAGGCAGGCA AAGTCGAAGT
 201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCAC CTCGAACCTG
 251 TTTTAAGCAA ACACGCCAAG TCTTTTAAAG ACGATATGTA CCTGCGTACC
 301 GAACACGTCG TCTGGCAGAA AGAAATGCTG ACGCTCGCAC GCCTCGCCGC
 351 CGCGTTCGAT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
 401 TTTTCGATGC GATGGTCAAC CAAAAATCA AGCTGCAAGA GCCGGAAGTC
 451 CTCAAAAAAT GGCTGGGCGA ACAAACCGCC TTTGACGGCA AAAAAGTCCT
 501 TGCCGCTTAC GAATCTCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
 551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACCGGT TATCGTCGGC
 601 GGCAAAATATA AAGTCGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
 651 CGACCTTTTG GCGGACAAAG TACGCGAAGA ACAAAAAGCC GCGCACTAA

```

This corresponds to the amino acid sequence <SEQ ID 2284; ORF 687.a>:

```

a687.pep
  1 MKSKHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
  51 TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
 101 EHVWVQKEML TLARLAAAVD MAAADSKDVA NSHIFDAMVN QKIKLQPEV
 151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFO IDGTPTVIVG
 201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AH*

```


Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 687 shows 98.7% identity over a 232 aa overlap with a predicted ORF (ORF 687) from *N meningitidis*:

m687/a687 98.7% identity in 232 aa overlap

	10	20	30	40	50	60
m687.pep	MKSRHLALGV	ALFALAACDSKVQTSVP	ADSAAPASAAAAPAGL	VEGONYTVLANPI	PQQ	
a687	MKSKHLALGV	ALFALAACDSKVQTSVP	ADSAAPASAAAAPAGL	VEGONYTVLANPI	PQQ	
	70	80	90	100	110	120
m687.pep	QAGKVEVLEFF	GYFCPHCAHLEPVLSKHAKS	FKDDMYLRTEHV	VVWQKEMTLARL	AAAVD	
a687	QAGKVEVLEFF	GYFCPHCAHLEPVLSKHAKS	FKDDMYLRTEHV	VVWQKEMTLARL	AAAVD	
	130	140	150	160	170	180
m687.pep	MAAADSKDVANSH	IFDAMVNQIKLQNP	EVLLKWLGEQTA	FDGKKVLAAYES	PESQARAD	
a687	MAAADSKDVANSH	IFDAMVNQIKLQNP	EVLLKWLGEQTA	FDGKKVLAAYES	PESQARAD	
	190	200	210	220	230	
m687.pep	KMQELTET	FQIDGTPVIVGGKYK	VEFADWESGMNT	IDLLADKVVREE	QKAAQX	
a687	KMQELTET	FQIDGTPVIVGGKYK	VEFADWESGMNT	IDLLADKVVREE	QKAAHX	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2285>

g688.seq

1	GTGCTACACT	AGACATCCCG	ATTTGCACAG	AAAGGTTCTC	CCGTGAACAA
51	AACCTCATC	CTCGCCCTTT	CCGCCCTGTT	CAGCCTGACC	GCGTGCAGCG
101	TCGAACGCGT	CTCGCTGTTT	CCCTCCTACA	AACTCAAAT	CATCCAAGGC
151	AACGAACCTG	AACCGCGCGC	CGTTGCCGCC	CTGCGCCCGC	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCTTTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAACCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGCCCTCC	AAAATGCCGC	CGAAGCCCTC	CGCGCGAAAC
401	AAAACGCAGA	CAAACAATAA			

This corresponds to the amino acid sequence <SEQ ID 2286; ORF 688 >:

g688.pep

1	VLH*TSRFAQ	KGSPVNKTLI	LALSALFSLT	ACSVVERVSLF	PSYKLKIIQG
51	NELEPRVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGVLVRTEG	DALQNAEAL	RAKQNAQKQ*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2287>:

m688.seq

1	GTGTTACACT	ACCCATCCCG	ATTTGCACAG	AAAGGCATT	CCGTGAACAA
51	AACCTCATC	CTCGCCCTTT	CCGCCCTCCT	CGGCTTGCC	GCGTGCAGTG
101	CCGAACGCGT	TTCAGTGTC	CCCTCGTACA	AACTCAAAT	CATACAGGGC
151	AACGAACCTG	AACCGCGCGC	CGTTGCCGCC	CTCCGCCCGC	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCATTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAATCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGCTCTGC	AAACGCTGC	CGAAGCCCTC	AAAGACGGCC
401	AAAACACAGA	CAAACCATAA			

This corresponds to the amino acid sequence <SEQ ID 2288; ORF 688>:

m688.pep

1	VLHYPSRFAQ	KGISVNKTLI	LALSALLGLA	ACSAERVSLF	PSYKLKIIQG
51	NELEPRVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGVLVRTEG	DVLQNAEAL	KDRQNTDKP*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 688 shows 90.6% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. gonorrhoeae*:

m688/g688 90.6% identity in 138 aa overlap

```

      10      20      30      40      50      60
m688.pep  VLHYPSRFAQKGISVNKTLILALSALLGLAACSVERVSLFPSYKLKIIQGNELEPRVAA
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g688       VLHXTSRFAQKGSVPNKTLLILALSALFSLTACSVERVSLFPSYKLKIIQGNELEPRVAA
          10      20      30      40      50      60

      70      80      90     100     110     120
m688.pep  LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g688       LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
          70      80      90     100     110     120

      130     140
m688.pep  DVLQNAAEALKDRQNTDKPX
          ||| ||||| ||||| |||||
g688       DALQNAAEALRAKQNAADKQX
          130     140

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2289>

```

a688.seq
1  GTGTTACACT ACCCATCCCG ATTTGCACAG AAAGGCATTT CCGTGAACAA
51 AACCCTCATC CTCGCCCTTT CGGCCCTCCT CGGCCTTGCC GCGTGCAGCG
101 TCGAACCGGT TTCACTGTTC CCCTCGTACA AACTCAAAAT CATACAGGGC
151 AACGAACTCG AACCTCGCGC CGTCGCCTCC CTCCGCCCCG GTATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCATTCC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCCGCAA CGGCATCATC
301 AAAGACCGAA GCAATCTGAC CGTCTATTTT GAAAACGGCG TGCTCGTCCG
351 CACCGAAGGC AACGCCCTGC AAAATGCCGC CGAAGCCCTC CGCGTAAAC
401 AAAACGCAGA CAAACAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2290; ORF 688.a>:

```

a688.pep
1  VLHYPSRFAQ KGISVNKTLI LALSALLGLA ACSVERVSLF PSYKLKIIQG
51 NELEPRAVAS LRPGMTKDQV LLLLGSPILR DAFHTDRWDY TFNTSRNGII
101 KDRSNLTVYF ENGVLVRTEG NALQNAEAL RVKQNAADKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 688 shows 93.5% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. meningitidis*

m688/a688 93.5% identity in 138 aa overlap

```

      10      20      30      40      50      60
m688.pep  VLHYPSRFAQKGISVNKTLILALSALLGLAACSVERVSLFPSYKLKIIQGNELEPRVAA
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a688       VLHYPSRFAQKGISVNKTLILALSALLGLAACSVERVSLFPSYKLKIIQGNELEPRAVAS
          10      20      30      40      50      60

      70      80      90     100     110     120
m688.pep  LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a688       LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
          70      80      90     100     110     120

      130     140
m688.pep  DVLQNAAEALKDRQNTDKPX
          ||| ||||| ||||| |||||
a688       NALQNAAEALRVKQNAADKQX
          130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2291>

```

g689.seq (partial)
1  ..TCTCCGCCCC TTCCTCCGAT GAGCGGAAAA CTGATGGCGG TTTTGATGGC
51  GGTACTGGTC GCGCTGATGC CGTTTTCAT CGATGCCTAC CTGCCCAGCA
101 TTCCCGAAAT GCGCAGCCG CTGAACGCGG ATATCCACCG TATCGAATAG
151 AGTCTGAGTT TGTTTATGTT CGSCACGGCG TTCGGGCAAG TGGCCGCGCG
201 CGCGGTGTCC GACATCAAAG GCGCAAACC CGTCGCCCTG ACCGGTTTGA
251 TTGTATATTG CCTTGCCGTT GCCGCCATCG TATTTGCTTC GAGTACCGAA
301 CAGCTCCTTA ACCTGCGTGC GGTACAGGCG TTCGGCGCAG GCATGGCTGT
351 AGTCATCGTC ggtgcatggy tgcgcgatTA TTATTCCGGA CGCAAAGCCG
401 cgcAGATGTT TGCCCTTATC GGCATCATTG TGATGGTTGT GCCGTGGCC
451 GCACCCATGG TCGGCGCATT GTTGCAGGGA TTGGGCGGAT GCGGGCGCAT
501 TTTCGTTTTC ttggcGgcgT ATTCGCCGGT GCTGCCCGGT TTGGTACAGT
551 ATTTCTCTGC CAATCCCGCC GTCGGCGGCA AAATCGGCAG GGATGTGTTC
601 GGGCTGGTGG CGGGGCGGTT CAAGCGCGTA TTGAAAACCC GTGCCGCGAT
651 GGGTtatCTG TTTTTCAGG CATTCACTT CGGTTTCGATG TTCGCCTTTC
701 TGACCGAATC TTCCTTCGTG TACCGGCAGC TCTACCACGT TACGCCGCAC
751 CCGTACGCAT GGGTGTTCG ACTCAACATC ATCACGATGA TGTTTTTCAG
801 CGCGGTTACC GCGTGGCGGC TTAACACCGG CGCGCATCCG CAAAGCATCC
851 TGCTGCGGGG GATTGTCGTC CAATTGCGG CCAACCCGTC CCAACTCGCC
901 GCCGTGCTGT TTTTCGCGTT GCCCCCGTTT TGGGTGCCGG TCGCGTGCCT
951 GATGTTTTTC GTCGGTACGC AGGGCCTGGT CGGTGCGGAC ACGCAGGCAT
1001 GCTTTATGTC TTATTTCAAA GAAGAGGGCG GCAGCGCGAA CGCGGTGTTCG
1051 GGTGTATTCC GGTCTTAAT CGGCGCGGCG GTGGTCATGG CGGCAACCGT
1101 GATGGCGGCA ACCATGACCG CGTCCGCTC TGCGGCAATT GCGCTTTTGT
1151 GGCTCTGCTC GCACAAGGCG TGGAGGAAA ACGAAAAAA GCGAATACTT

```

This corresponds to the amino acid sequence <SEQ ID 2292; ORF 689>:

```

g689.pep (partial)
1  ..SPPLPPMSGK LMAVLMALV ALMPFSIDAY LPAIPEMAQP LNADIHRIE*
51  SISLFMFSTA FGQVAGGAVS DIKGRKPVAL TGLIVYCLAV ARIVFASSTE
101 QLLNLRAVQA FGAGMAVVIV GAMVRDYSG RKAQMFLI GILMVVPLA
151 APMVGALLQG LGGWRAIFVF LAAYSPLVPG LVQYFLPNFA VGGKIGRDVF
201 GLVAGRFRKRV LKTRAAMGYL FFOAFSFGSM FAFLETSEFV YRQLYHVTPH
251 RYAWVFALNI ITMFFSRVT ANRLKTGAHP QSILLRGIVV QFAANPSQLA
301 AVLFFGLPEF WLPVACVMFS VGTQGLVGAD TOACFMSYFK EEGGSANAVS
351 GVFRSLIGAG VVMAATVMAA TMTASASCGI ALLWLCSHKA WKENEKKRIL

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2293>:

```

m689.seq
1  TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
51 GTTGCCGCGT GTTGTGCGG GTGTGTAA AATTTCCGTT TCCGCGTATT
101 GTGTTTTCCG CCGCCGGGCG GTTGTGTTG GAATCGGACG AGAATTTATG
151 CCTTCGTCGC ATTATCCTGA AATGAGCGAA AACTGATGG CGGTTTTGAT
201 GCGGATGCTG GTTACGCTGA TGCCGTTTC CATCGATGCC TACCTGCCCG
251 CGATTCGCGA AATGGCGCAA TCGCTGAACG CGGATGTTCA CCGCATCGAA
301 CAGAGTTTGA GTTGTGTTAT GTTCGGCACG GCGTTCCGAC AGGTGGTCCG
351 CCGTTCCGGT TCCGACATCA AAGGGCGCAA ACCCGTCGCC CTGACCGGTT
401 TGATTGTATA TTGCCCTTGC GTTGCCGCCA TCGATTGTTT TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGACG GCATTCCGGT CGGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGCAGCA TTATTATTCC GGACGCAAAG
551 CCGCCAGAT GTTTGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCCGCGC ATTGTTGCAG GGCTTGGGTG GCTGGCAGGC
651 GATTTTTGTT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTTTGGTAC
701 AGTATTTCCT GCCAAGCCC GCCGTCGGCG GCAAAATCGG ACGGGACGTG
751 TTCGGGCTGG TGGCGGGGCG GTTCAAGCGG GTATTGAAAA CCCGTGCTGC
801 GATGGGTTAT CTGTTTTTTC AGGCATTGAG CTTCGGTTCG ATGTTCCGCT
851 TTCTGACCGA ATCTTCTTTC GTGTACCAGC AGCTCTACCG TGTACGCCCT
901 CATCAATACG CTTGGGCGTT TGCACCTAAC ATCATCAGCA TGATGTTTTT
951 CAACCGCGTT ACCGCGTGGC GGCTCAAAAC CGGCGTGCA CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCCAACTC GTCCAACTC
1051 GCGGCCGTGC TGTTTTTCGG GTTGCCCCG TTTTGGCTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGCTT GGTCCGTGCA AACACGAGG
1151 CGTGTGTTAT GTCCATTTC AAAGAAGAGG GCGGCAGCGC AAACCCGTA
1201 TTGGGTGTAT TCCAATCTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTTCTGACAC GACGGTTCGG CAACCGTAT GCGCGCAACG ATGACCGCGT
1301 CCACCTCTTG CGGCATTGCG CTTCTGTGCG TCTGCTCGCA TCGTCCGTGG

```

m689 . per

1	LLIHYYIVPVK	PVLPGLLLP	VCAGVLKFSV	SAYCVFRRRA	VCLRIGREFM
51	PSAHYPEMSE	KIMAVLMAML	VTIMPFSDIA	YLPAPFEMQA	SLNADVHRIE
101	QSLSLFMFGT	AFGQVGVGSV	SDIKRKPVA	LTGLIVYCLA	VAIVFVSSA
151	EQLLNLRVVQ	AFGQKPTFVI	VGMVRDYYS	GRKAAQMFAL	IGIILMVVPL
201	VAPMVGALLQ	GLGGWQALFV	FLAAYSVLGL	GLVQYFLEKP	AVGGKIGRDV
251	FGLVAGFRKR	VLKTRAAMGY	LFFQAQSFSS	MFALTESSP	YVQQLRYVTP
301	HQYAWAFALN	ITTFMFNNRV	TAWRLKTGVH	PQSILLNGIV	VQFAANLSRV
351	AAVLFEGLPP	FWLLVACVMF	SVGTQGLVGA	NTQACFMSYF	KEEGGSANAV
401	LGVFQSLIGA	GVGMAATFLH	DGSATVMAAT	MTASTSCGIA	LLWLCSHRAW
451	KENGSEHYL*				

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 689 shows 88.0% identity over a 408 aa overlap with a predicted ORF (ORF 689) from *N. gonorrhoeae*:

m689/a689 88.0% identity in 408 aa overlap

	30	40	50	60	70	80
m689.pep	CAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPFMSEKLMAVLMAMHVTLMFPSIDAY					
g689	SPPLPPMSGKLMMAVLMMAVLVALMPFSIDAY					
	10	20	30			
	90	100	110	120	130	140
m689.pep	LPAIPEMAQSLNADVHRIEQSLSLFMGFTAFGQVVGGVSVDIKGRKPVALTGLIVYCLAV					
g689	LPAIPEMAQPLNAIHRIEXSLSLFMGFTAFGQVAGGAVSDIKGRKPVALTGLIVYCLAV					
	40	50	60	70	80	90
	150	160	170	180	190	200
m689.pep	AAIVFVSSAEQLNLNRVVQAFGAGMTTVVIVGAMVRDYYSGRKAAQMFAFIGIILMVVPLV					
g689	AAIVFASSTEQLLNLRVAQAFGAGMAVVIWGAMVRDYYSGRKAAQMFAFIGIILXVPLA					
	100	110	120	130	140	150
	210	220	230	240	250	260
m689.pep	APMVGALLQLGGWQAI FVFLAAYS LVLGLVQY FLPKPAVGGKIGRDVFGLVAGRFRKV					
g689	APMVGALLQLGGWR AIFVFLAAY SPVLPGLVQY FLPNPAVGGKIGRDVFGLVAGRFRKV					
	160	170	180	190	200	210
	270	280	290	300	310	320
m689.pep	LKTRAAMGYLFFQAFSFGSMFAFLT ESSFVYQQLYRVTPHQYAWAFALNIITMMFFNRVT					
g689	LKTRAAMGYLFFQAFSFGSMFAFLT ESSFVYRQLYHVTPHRYAWVFALNIITMMFFSRVT					
	220	230	240	250	260	270
	330	340	350	360	370	380
m689.pep	AWRLKTGVHPQSILLWGIVVQFAANLSQLAAVLFFGLPPFWLLVACVMFESVGTQGLVGAN					
g689	AWRLKTGAHPQSILLRGIVVQFAANPSQLAAVLFFGLPPFWLPVACVMFESVGTQGLVGAD					
	280	290	300	310	320	330
	390	400	410	420	430	440
m689.pep	TQACFMSYFKKEEGGSANAVLG VFSQLIGAGVGMATFLHDGSATVMAATMTASTSCGIAL					
g689	TQACFMSYFKKEEGGSANAVSGVFRSLIGAGVMAAT-----VMAATMTASASCGIAL					
	340	350	360		370	380
	450	460				
m689.pep	LWLCSHRWKENGQSEYLX					
g689	LWLCSHKWKENEKKRIL					
	390	400				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2295>

```
a689.seq
1   TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTCG CGGGGCTTTT
51  GTTGCCGCCT GTTTGTGCCG GTGTGTTAAA ATTTTCCGTT TCCGCGTATT
101 GTGTTTTCGG CCGCCGGGCG GTTTGTTTTC GAATCGGACG AGAATTATATG
151 CCTTCTGCCC ATTATCCTGA AATGAGCGAA AAACGTATGG CGGTTTGTAT
201 GCGGATGCTG GTTACGCTGA TGCCGTTTTC CATCGATGCC TACCTGCCCG
251 CGATTCCCGA AATGGCGCAG TCGCTGAACG CGGATGTCCA CCGCATCGAA
301 CAGAGCCTGA GTTTGTTTAT GTTCGGCAGC GCGTTCGGAC AGGTGGTCGG
351 CGGTTCGGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCG CTGACCGGAC
401 TGGCCGTCCTA CTGCCTTGCC GTTGCCGCCA TCGTATTTGC TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGCG CATTTCGGTG CGGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGGCGCA TTATTATTCC GGACGCAAG
551 CCGCCCGAGT GTTTGCCCTT ATCGGCATCA TTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTGCGAG GGCTTGGGTG GCTGGCAGGC
651 GATTTTGTGT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTTTGGTAC
701 AGTATTTCCT GCCCAAGCCC GCCGTCGGCG GCAAAATCGG CAGGGATGTG
751 TTCGGGCTGG TGGCTGGGCG GTTCAAACGC GTATTGAAA CCCGTGCCGC
801 GATGGGTTAT CTGTTTTTTC AGGCATTGAG CTTGCGTTCG ATGTTCCGCT
851 TCTTGACCCA ATCTTCCTTC GTGTACCAGC AGCTCTACCA CGTTACGCG
901 CACCAGTACG CTTGGGCGTT TGCACCAAC ATCATCAGCA TGATGTTTTT
951 CAACCGTATT ACCGCGTGGC GGCTCAAAAC CCGCGTGCA CCGCAAAGCA
1001 TCTTGTCTGT GGGGATTGTC GTCCAGTTTG CCGCCAACCT GTCCCAACTC
1051 GCCGCCGTGC TGTTTTTTCG GTTGCCCCCG TTTTGGCTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGGCTT GGTGCGTGCA AACACGAGG
1151 CGTGTTTTAT GTCCTATTTC AAAGAAGAGG CGGCGAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTTCTGCAAC GACGGTTCGG CAACCGTGAT GCGCGCAACC ATGACCGCGT
1301 CTACCTCTTC CGGCATTGCG CTTTGTGGC TCTGCTCGCA TCGTGCCTGG
1351 AAAGAAAACG GGCAAAGCGA ATACCTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2296; ORF 689.a>:

```
a689.pep
1   LLIHIVPVR PVLPGLLLPP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM
51  PSAHYPEMSE KLMAVLMAML VTLMPSIDA YLPAIPEMAQ SLNADVHRIE
101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLAVYCLA VAAIVFASSA
151 EQLLNLRVVQ AFGAGMTVVI VGAMVRDYYS GRKAAQMFAL IGIILMVVPL
201 VAPMVGALLQ GLGGWQAFV FLAAYSLVLL GLVQYFLPKP AVGKIGRDV
251 FGLVAGRFRK VLKTRAAMGY LFFQAFSFGS MFAFLTESSF VYQQLYHVT
301 HQYAWAFALN IITMFFFNRI TAWRLKTGVH PQSILLWGIV VQFANLSQL
351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTAATSCGIA LLWLCSHRAW
451 KENGQSEYL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 689 shows 99.1% identity over a 459 aa overlap with a predicted ORF (ORF 689) from *N. meningitidis*:

m689/a689 99.1% identity in 459 aa overlap

	10	20	30	40	50	60
m689.pep	LLIHIVPVRPVLPGLLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE					
a689	LLIHIVPVRPVLPGLLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE					
	10	20	30	40	50	60
m689.pep	KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV					
a689	KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV					
	70	80	90	100	110	120
m689.pep	SDIKGRKPVALTGLIVYCLAVAAIVFVSSAEQLLNLRVVQAFGAGMTVVI VGAMVRDYYS					
a689	SDIKGRKPVALTGLAVYCLAVAAIVFASSAEQLLNLRVVQAFGAGMTVVI VGAMVRDYYS					
	130	140	150	160	170	180
m689.pep	GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAFVFLAAYSLVLLGLVQYFLPKP					
a689	GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAFVFLAAYSLVLLGLVQYFLPKP					

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|||||
a689  GRKAAQMFALIGIILMVPLVAPMVGALLQGLGGWQAI FVFLAAYSLVLLGLVQYFT.PKP
      190      200      210      220      230      240

      250      260      270      280      290      300
m689.pep  AVGGKIGRDVFGVLVAGRFKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSEFVYQQLYRVTP
|||||
a689  AVGGKIGRDVFGVLVAGRFKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSEFVYQQLYHVTP
      250      260      270      280      290      300

      310      320      330      340      350      360
m689.pep  HQYAWAFALNIIITMMFFNRVTAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLF FGLPP
|||||
a689  HQYAWAFALNIIITMMFFNRITAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLF FGLPP
      310      320      330      340      350      360

      370      380      390      400      410      420
m689.pep  FWLLVACVMFSVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGM AATFLH
|||||
a689  FWLLVACVMFSVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGM AATFLH
      370      380      390      400      410      420

      430      440      450      460
m689.pep  DGSATVMAATMTASTSCGIALLLWLC SHRAWKENGQSEYLX
|||||
a689  DGSATVMAATMTASTSCGIALLLWLC SHRAWKENGQSEYLX
      430      440      450      460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2297>

```

g690.seq (partial)
1  ATGAAAAACA AAACGTCATC ACTTCCCTTA TGGCTTGCCG CAATCATGCT
51  GGCCCGCGCT TCCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCTTC GTCTTCCGCG TCATCGGCTT CTTCCCAAC CGATTTCGAA
151 CCGCCGCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCACT
201 GTGAAATTGC ACCGGCCTGC ACCCCGCGGC CGGCATTGGC GATCTCATAC
251 AGCAAAATCGC CGAACACATC GACTCGGACT GTCTGTTTGC CCTTTCCCAT
301 AACGAACTGG AAACCCGTTT CGGCTTACCC GCGCGCGGCT ATGACAACAT
351 ACAGCGGctG CTgtttCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAATCAT GCTGGCAATC GAAGACTTGC GTTACGGAAC GCGCACCATC
451 AGccgGCAGG CACAAGATGC CATAATGGAA CAGGAACGCC gcctccGaGa
501 agCGACGCTG ATGCTGACAC AGGGCAGTCA AAAAACC CGG GgACAAGCGG
551 AGGAACCGAA ACGCGCACGT TATTTTGAAG TTTCCGCAAC ATCtgCctaT
601 TTgaaccggc ACAaCaacGG ACTTggcgGC AATTTCaAT ACATCGGCCA
651 ATTGCCCGGC TATCTGAAAA TGCACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTTAGAC
751 ATCCATTTTG ACGAAAATGG CAAAATCAGC CGTATTGTGC TTTACGAAAA
801 AAATATCTAT ...

```

This corresponds to the amino acid sequence <SEQ ID 2298; ORF 690>:

```

g690.pep (partial)
1  MNKNTSSLPL WLAAIMLAAR SPSKEDKKE NGASAASSSA SSASSQTDLQ
51  PAASAPDNVK QAESAPL*NC TGLHPAAGIG DLIQQAIEHI DSDCLFALSH
101 NELETRFGLP GGYDNIQRL LFPDIRPEDP DYHQIMLAI EDLRYGTRTI
151 SRQAODAIME OERRLEATL MLTQGSQKTR GQGEPEPKRAR YFEVSATSAY
201 LNRHNNLGG NFQYIGQLPG YLKMHEMLE NQSLFRLSNR ERNPDKPFLLD
251 IHFDENGKIT RIVVYEKNY ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2299>:

```

m690.seq..
1  ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTACCG CAATCATGCT
51  GACCGCGTGT TCTCCGAGCA AAGACGATAA AACCAAGAA GTCCGTGCAT
101 CCCTGTCTTC GTCTCCGCG TCATCAGCTC CTTCCCAAC CGATTTCGAA
151 CCGACCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCGGCC
201 GTCAAAATGC ACCAGCCTGC ACCCCGCCAC CGGCATTGAC GATCTCATGC
251 AGCAAAATCGC CGAACACATT GACTCGGACT GTCTGTTTGC CCTTTCCCAT
301 CACGAACTGG AAACCCGTTT CGGCTTACCC GACGGTGGCT ATGACAACAT
351 ACAGCGGctG CTGTTTCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAATCAT ACTGGCAATT GAAGACTTGC GTTACGGAAA GCGCAGGATC
451 AGCCGGCAGG CACAAAATGC CTTGATGGAA CAGGAACGCC GCCTCCGAGA
501 AGCGACGCTG TTGCTGATAC AGGGCAGTCA AGAAACCCGC GGACAAGCGG

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551 AGGAGCCGAA ACGCAGCGGT TATTTTSAAG TTTCGGCAAC CCCTGCCTAT
601 TCGAGCCGGC ACAACAACGG ACTTGGCGGC AATTTCCAAT ACATCAGCCA
651 ATTGCCCGGC TATCTGAAAA TACACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTATAGAC
751 ATCCATTTTG ACGAAAATGG CAAAATCACG CGTATTGTCG TTTACGAAAA
801 AAACATCTAC TTCATCCAA ACACGGGGCG AATATAA

```

This corresponds to the amino acid sequence <SEQ ID 2300; ORF 690>:

```

m690.pep
1  MKNKTSLLL WLTAIMLTAC SPSKDDKTKE VGASAASSSA SSAPSQTDLQ
51  PTASAPDNVK QAESAPPSNC TSLHPATGID DLMQQAIEHI DSDCLFALSH
101 HELETRFGLP DGGYDNIQRL LFPDIRPEDP DYHQIILAI EDLRYGKRTI
151 SRQAQNALME OERRLREATL LLIQGSQETR GQGEPEPKRTR YFEVSATPAY
201 SSRHNNLGGG NFQYISQLPG YLKIHGEMLE NQSLFRLSNR ERNPKPFLD
251 IHFDENGKIT RIVVYEKNYI FNPNTGRI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 690 shows 89.3% identity over a 408 aa overlap with a predicted ORF (ORF 690) from *N. gonorrhoeae*:

```

m690/g690      89.3% identity in 408 aa overlap

          10      20      30      40      50      60
m690.pep  MKNKTSLLLWLTAIMLTACSPSKDDKTKEVGASAASSSASSAPSQTDLQPTASAPDNVK
          |||||  |||:||||: ||||:|||| |||||:|||| |||||:|||||
g690       MKNKTSLLPLWLAAIMLAARSPSKEDKTENGASAASSSASSAPSQTDLQPAASAPDNVK
          10      20      30      40      50      60

          70      80      90      100     110     120
m690.pep  QAESAPPSNCTSLHPATGIODLMQQAIEHIDSDCLFALSHHELETRFGLPDGGYDNIQRL
          |||||  |||:||||: ||||:|||| |||||:|||| |||||:|||||
g690       QAESAPLXNCTGLHPAAGIGDLIQQAIEHIDSDCLFALSHNELETRFGLPGGGYDNIQRL
          70      80      90      100     110     120

          130     140     150     160     170     180
m690.pep  LFPDIRPEDPDYHQIILAIEDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQETR
          |||||  |||||:||||| |||||:||||| |||||:||||| |||||:|||||
g690       LFPDIRPEDPDYHQIMLAIEDLRYGTRTISRQAQDAIMEQERRLREATLMLTQGSQKTR
          130     140     150     160     170     180

          190     200     210     220     230     240
m690.pep  GQGEPEPKRTRYFEVSATPAYSSRHNNLGGNFQYISQLPGYLKIHGEMLENQSLFRLSNR
          |||||  |||:||||: ||||:|||| |||||:|||| |||||:|||||
g690       GQGEPEPKRTRYFEVSATPAYLNRRHNNLGGNFQYIGQLPGYLMHGEMLENQSLFRLSNR
          190     200     210     220     230     240

          250     260     270     279
m690.pep  ERNPKPFLDIHFDENGKITRIVVYEKNYIFNPNTGRI
          |||||  |||||:||||| |||||:||||| |||||:|||||
g690       ERNPKPFLDIHFDENGKITRIVVYEKNY
          250     260     270

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2301>

```

a690.aag
1  ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTGCCG CAATGATGCT
51  GACCGCGTGT TCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCTCT GTCCACGGCA TCCGCGCTT CGTCTTCCGC GCCCAAAACC
151 GATTTGCAAC CGGCCGCATC CGCCCTGAT AACGTCAGC AGGCAGAAAG
201 CGTGCCGCCG TCAAAATTGCA CCGACCTGCA CCCC GCCACC GGCATTGACG
251 ATCTCATGCA GCAAATCGCC GAACACATTG ACTCGGACTG TCTGTTTGCC
301 CTTTCCCATC ACGAACTGGA AACCCGTTTC GGCTTACCCG GCGGCGGCTA
351 TGACAACATA CAGCGGCTGC TGTTCCTCCA CATCCGCCCT GAAGATCCCG
401 ACTACCATCA GAAAATCATA CTGGCAATG AAGACTTGC TACGGAAAG
451 CGCAGCATCA GCGGCGAGGC ACAAGATGCC TTGATGGAAC AGGAACGCCG
501 CCTCCGAGAA GCGACGCTGT TGCTGATACA GGGCAGTCAA GAAACCCGCG
551 GACAAGCGCA GGAGCCGAAA CGCAGCGCTT ATTTGAAAG TTCCGCAACC
601 CTGCGCTATT CGAGCCGGCA CAACAACGGA CTGGCGGCA ATTTCCAATA
651 CATCGGCCAA TTGCCCGGCT ATCTGAAAT ACACGGAGAA ATGCTTGAAA

```

1111

701 ACCAATCACT CTTCCGGCTG TCCAACCGTG AACGCAATCC CGACAAACCG
 751 TTTTATAGACA TCCATTTTGA CGAAATGGC AAAATCACGC GTATTGTCST
 801 TTACGAAAA AACATCTACT TCAATCCAAA CTTGGGCGA AGATAA

This corresponds to the amino acid sequence <SEQ ID 2302; ORF 690.a>:

a690.pep
 1 MKNKTSLLLL WLAAMMLTAC SPSKEDKKE NGASAASSTA SAASSAPQT
 51 DLQPAASAPD NVKQAESVFP SNCTDLHPAT GIDDLMOQIA EHIDSDCLFA
 101 LSHHELETRF GLPGGGYDNI QRLLFPDIRP EDPDYHQKII LAIEDLRYGK
 151 RTISRQAQDA LMEQERRLRE ATLLLIQGSQ ETRGQGEPEK RTRYFEVSAT
 201 PAYSSRHNN LGGNFQYIGQ LPGYLKHGE MLENQSLFRL SNRERNPKDP
 251 FLDIHFDENG KITRIVVYEK NIYFNENLGR R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 690 shows 93.9% identity over a 280 aa overlap with a predicted ORF (ORF 690) from *N. meningitidis*:

m690/a690 93.9% identity in 280 aa overlap

m690.pep	10	20	30	40	50
a690	10	20	30	40	50
m690.pep	60	70	80	90	100
a690	60	70	80	90	100
m690.pep	120	130	140	150	160
a690	120	130	140	150	160
m690.pep	180	190	200	210	220
a690	180	190	200	210	220
m690.pep	240	250	260	270	279
a690	240	250	260	270	279

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2303>

g691.seq
 1 GTGCCGCTGC CTGCTCCCTG CCGTTTTGCC AACCTGCCG CCTCTTTTT
 51 AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
 101 TCCCCCGGAA CGATTTTCAA CCGAAGTGGC ACATACGCCG GUTCGGGCTG
 151 ACACAGGGTC AGCACAATGA GCTGCGTAAA ATCCGCCGCC CCTTCAAAAT
 201 GGCGGGCGAC AGGCGCGGTT TGAAGGTTAT GCATTCCGAA CACAGCCGCC
 251 GCCGCTCTGT CGTCGAAATC ATTTCTTCGG ATGTTTTTAA TCAGAACGAG
 301 GCGCGCGATT ATGTCGAAAG CCGTACCAC TCCAGCATGG ATTTGCGGT
 351 GGACGAATTG GAAATCCAAC ACCGCTTCTT CCATATTCTC ACACCGCAAC
 401 AGCAGCAAA GTGGCTTCTT TCCTGCCTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2304; ORF 691 >:

g691.pep
 1 VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
 51 TQGGHNELRK IRAAFKMGD RARLKVHSE HSRRSVVEI ISSDVFNRE
 101 ARDYVESRYH SSMDFAVDEL EIQHRFFHIL TPOQQOMWLS SCLK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2305>:

```
m691.seq
1  GTGCCACTGC CTGCTCCCTG CCGTTTTGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GTCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCGGAA CGATTTTCAA CCGAACTGCG ACATACGCCG ACTCGGGCTG
151 ACCCAAAGTC AGCACAATGA GCTGCGTAAA ATCCGCACCG CCTTCAAAT
201 GCGGGGCGAC AGGGCGCGTT TGAAGGTAT GCATTCCGAA CACAGCCGCC
251 GCCGGTCTGT CGTCGAAATC ATTCCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTCTT CCATATCTC ACACCGCAAC
401 AGCAGCAAT GTGGCTTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2306; ORF 691>:

```
m691.pep
1  VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
51  TQSQHNELRK IRTAFKMGD RARLKMVHSE HSRRSVVEI ISSDVFNRE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. gonorrhoeae*:

```
m691/g691 97.2% identity in 144 aa overlap

      10      20      30      40      50      60
m691.pep VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFOPNCDIRRLGLTQSQHNELRK
g691      VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFOPNCDIRRLGLTQSQHNELRK
      10      20      30      40      50      60

      70      80      90     100     110     120
m691.pep IRTAFKMGADRARLKMVHSEHSRRSVVEIISSDVFNREARDYVESRYLSGMDFAVDEL
g691      IRAAFKMGADRARLKMVHSEHSRRSVVEIISSDVFNREARDYVESRYLSSMDFAVDEL
      70      80      90     100     110     120

      130     140
m691.pep EIQRFFHILTPQQQMWLSCLKX
g691      EIQRFFHILTPQQQMWLSCLKX
      130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2307>

```
a691.seq
1  GTGCCACTGC NTGCTCCCTG CCGTTTTGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCTGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGACTG
151 ACACAGGGTC AGCACAATGA ACTGCGTAAA ATCCGCGCCG CCTTCAAAT
201 GCGGGGCGAC AGGGCGCGTT TGAAGGTAT GCATTCCGAA CACAGCCGCC
251 GTCGGTCTGT CGTCGAAATC ATTCCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTCTT CCATATCTC ACACCGCAAC
401 AGCAGCAAT GTGGCTTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2308; ORF 691.a>:

```
a691.pep
1  VPLXAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPLNDFQ PNCDIRRLGL
51  TQSQHNELRK IRAAFKMGD RARLKMVHSE HSRRSVVEI ISSDVFNRE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. meningitidis*:

m691/a691 97.2% identity in 144 aa overlap

	10	20	30	40	50	60
m691.pep	VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPNDPQNCDIRRLGLTQSQHNELRK					
a691	VPLXAPCRFAKPAASFLSMALLSCQLSHAATAYIPNDPQNCDIRRLGLTQSQHNELRK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m691.pep	IRTAFKMAGDRARLKVMHSEHSRRRSVVEIISSDVFNREARDYVESRYLSGMDFAVDEL					
a691	IRAAFKMAGDRARLKVMHSEHSRRRSVVEIISSDVFNREARDYVESRYLSGMDFAVDEL					
	70	80	90	100	110	120
	130	140				
m691.pep	EIOHRFFHILTPQQQOMWLSSCLKX					
a691	EIOHRFFHILTPQQQOMWLSSCLKX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2309>

g692.seq

```

1  GTATCGCACA CACGCTGTCG CTGTTTCGGAA TCGATACGCC GGATTTCGGCG
51  GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATGCGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGCGTCGCGC
151 TTCATTCCAT GCGGCAGGGT ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTGCGCGGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGGACAGGG CTTCGGTCAG CTTTCATGCC CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC
401 AGTTGTGCGG CTTCAGGCTC GACGATTTTG ATGTTTTTCA GGTTTTCCGC
451 GATGTCGGCT TTGGATGCGG TCAGCGGATT GATGCGCTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTTACAG ATCACCAGG CGCGTGCAGG GTTGGACggG
551 TegtTGGCGG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATT
601 CAGTTTGCCT GGATACAGTC CCAAGGCGC GGTCGGCACT TGAAGGCTT
651 CGGTGATGTC CAGGTTGTGT TCTTTTTTGA AATCGTCAAG ATAGGGTTT
701 TGTTGGAAGA CGTTGATGTC CAACTCGCCC TCCGCCAATG CCAGATTTCG
751 GCGCACAATG TCggTAAATT cgaccaatTT gacgGTGTay cCTTTTTTCT
801 CCAGCTCGgc tTGGATTGTG TCTTTGACCA TATcgccgaa gtcgcccacg
851 gTCGTGCGCG agacgaTTTC TTTTTCGCG CgcgCGTTAT CGGCAGAAGG
901 GCGGCGGgca gaggctgCGG GCGCGCTGTC TTTTtgaccG ccgCAGGCTG
951 CGAGGATGAG CCGGAGtgcg gcggcggaaa ggGTTTGA GAAGGTTTTc
1001 atATTTTCTc ctga

```

This corresponds to the amino acid sequence <SEQ ID 2310; ORF 692 >:

g692.pep

```

1  VSHTRCRCSE SIRRIWRNGR EWRIGQKCR LNTDAVQTAS FYTTALFGCA
51  FIPCGRVFVA LEAFVRVCFE RVGVIGLYV FKPLAVFVGG FDGRFPVDIGK
101 ARLLEQGFQV LHAAAYGVVA VDDGKIHVGA AARQLCGFKL DDFDVQVQFR
151 DVGFGCGQRI DAVFEFDPTQ FVQHHQGACE VGRVVGGRYG AAVFDFFQRF
201 QFARIQSQR GRHLEGFGDV QVVFEEIVK IGFVLEDVDV QLALRQCQIR
251 AHIVGKFDQF DGVAFFLQLG LDLFDDHIAE VAHGRAEDDF FFRKAVIGRR
301 GGGRGCGRAV FLTAAGCEDE RECGGKGFE EGFHIFS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2311>:

m692.seq

```

1  GTGTTGCACA CGCTTTGTCG CTGTTTCGGAA TCGATACGCC GGATTTCGGCG
51  GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATACAGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGCGTCGCGC
151 TTCATTCCAT GCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTGCGCGGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGGACAGGG CTTCGGTCAG CTTTCATGCC CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC

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401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTCCTCGGC
451 GATGTCCGCT TTGGATGCGG TCAACGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTGAGC ATCACCAGA CGCGGCGAA GTTGGACGGG
551 TCGTTGGCGG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATT
601 CAGCTTGCCC GGGTACAGTC CCAAAGCGC GGTCCGCACT TGAAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTGA AGTCGTCAG ATAGGGTTTG
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 GCGTACATAG TCGGTAAACT CGACCAGTTT GACGGTGTAG CCTTTTTTCT
801 CCAGCTCGGC TTGGATTGT TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTC TTTTTCGCC GCGCCGTTGT CGGCGGCGGC
901 AGAAGCGGAT GCGGCGGGCG CGCTGTCTTT TTGACGCGC CAGGCGGCGA
951 GGATGAGCGC GAGTGGCGG GCGGAAAGG TTTGAAGAA GGTTCCTATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2312; ORF 692>:

m692.pep

```

1 VLHTLCRCSE SIRRIIRNGR EWRIKQKCR LNTDTVQTAS FYTTALFGCA
51 FIPCGRGFVA LEAFVRVGF EGVGVLGYV FKPLAVFVG FDGRPVDIGK
101 ARFLEQGFQ LHAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVFGVLG
151 DVFRCGQRI DAVFEFDPQ FVEHHQDAGE VGRVVGRCYG AAVFDFQRF
201 QLARVQSRR GRHLEDFGDV QIVFFEIVK IGFVLEDVDV QLALSCQIR
251 AYIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRRAVVG
301 RSGCGGRAVF LTAAGGEDER ECGGKGFEF GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 692 shows 91.1% identity over a 338 aa overlap with a predicted ORF (ORF 692) from *N. gonorrhoeae*:

m692/g692 91.1% identity in 338 aa overlap

m692.pep	10	20	30	40	50	60
	VLHTLCRCSESIRRIIRNGREWRIKQKCR LNTDTVQTASFYTTALFGCAFIPCGRGFVA					
g692	VSHTRCRCSESIRRIWRNGREWRIKQKCR LNTDAVQTASFYTTALFGCAFIPCGRVFVA					
m692.pep	70	80	90	100	110	120
	LEAFVRVGFERVGVLGYVFKPLAVFVGFDGRPVDIGKARFLEQGFQ LHAAYGVVA					
g692	LEAFVRVGFERVGVLGYVFKPLAVFVGFDGRPVDIGKARLLEQGFQ LHAAYGVVA					
m692.pep	130	140	150	160	170	180
	VDDGKIHVGAATRLRGFKLDDFDVFGVLEVRFGCGQRI DAVFEFDPQ FVEHHQDAGE					
g692	VDDGKIHVGAARQLCGFKLDDFDVFGVFRVFGCGQRI DAVFEFDPQ FVHHQDAGE					
m692.pep	190	200	210	220	230	240
	VGRVVGRCYGAAVDFDFQRFQLARVQSRRGRHLEDFGDVQIVFFEIVKIGFVLEDVDV					
g692	VGRVVGRCYGAAVDFDFQRFQFARIQSRRGRHLEDFGDVQVVFVEIVKIGFVLEDVDV					
m692.pep	250	260	270	280	290	
	QLALSCQIRAYIVGKLDQFDGVAFFLQLGLDLFFDHIAE VADGRAEDDF FFRRAVVG--					
g692	QLALSCQIRAHIVGKFDQFDGVAFFLQLGLDLFFDHIAE VADGRAEDDF FFRRAVIGRR					
m692.pep	300	310	320	330		
	GGRSGCGGRAVELTAAGGEDERECGGKGFEFGFHIFSX					
g692	GGGRCG-RAVELTAAGCEDERECGGKGFEFGFHIFSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2313>

a692.seq

```

1 GTGTTGCACA CGCTTTGTCG CTGTTCCGAA TCGATACGCC GGATTCGGCG

```

```

51 GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATACGGGTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT CCGGCAGGGG ATTTGTAGCC CTCGAACGCT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCGGCGGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGGAACAGGG CTTGGTCAG CTTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC
401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTTTCGGC
451 AATGTCCGCT TTGGATGCGG TCAGCGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTCGAGC ATCACCAGA CGCGGGCGAA GTTGGACGGG
551 TCCTTGGCGC CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATT
601 CAGCTTGCCC GGTACAGTC CCAAAGCGC GGTCCGCACT TGGAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAAG ATAGGGTTTG
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 CGGCACATAG TCGGTAAACT CGACCAAGTT GACGGTGTAG CCTTTTTTCT
801 CCAGCTCGGG TTGGATTGT TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTC TTTTTCGCC GCGCCGTGT CGCGCGCGGC
901 AGAAGCGGAT GCGCGGGCG CGCTATCTTT TTGACCGCCG CAGCGCGCGA
951 GGATGAGCG GAGTGGCGG GCGGAAAGGG TTTGAAGAA GGTTTTCATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2314; ORF 692.a>:

a692.pep

```

1 VLHTLCRCSE SIRRIIRNGR EWRIKQKCR LNTDTVQTAS FYTTALFGCA
51 FIPCGRGFVA LEAFVRVGF E RVGVLGLGYV FKPLAVFVCG FDGRFPVDIGK
101 ARFLEQGFQ LHAAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVQVFG
151 NVRFCCGQRI DAVFEEDPTQ FVEHHQDAGE VGRVVGGRYG AAVFDFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDDV QLALSQCQIR
251 AHIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRRAVVGGG
301 RSGCGGRAIF LTAAGGEDER ECGGGKGFEE GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 692 shows 98.8% identity over a 336 aa overlap with a predicted ORF (ORF 692) from *N. meningitidis*:

m692/a692 98.8% identity in 336 aa overlap

	10	20	30	40	50	60
m692.pep	VLHTLCRCSE	SIRRIIRNGR	EWRIKQKCR	LNTDTVQTAS	FYTTALFGCA	FIPCGRGFVA
a692	VLHTLCRCSE	SIRRIIRNGR	EWRIKQKCR	LNTDTVQTAS	FYTTALFGCA	FIPCGRGFVA
	70	80	90	100	110	120
m692.pep	LEAFVRVGF	ERVGVGLGYV	FKPLAVFV	CGFDGRFP	VDIGKARF	LEQGFQ
a692	LEAFVRVGF	ERVGVGLGYV	FKPLAVFV	CGFDGRFP	VDIGKARF	LEQGFQ
	130	140	150	160	170	180
m692.pep	VDDGKIHV	GAAATRLR	GFKLDDF	VDVQVLD	VRFVCGQ	RIDAVFE
a692	VDDGKIHV	GAAATRLR	GFKLDDF	VDVQVLD	VRFVCGQ	RIDAVFE
	190	200	210	220	230	240
m692.pep	VGRVVGGR	YGAAVDF	DFQRFQL	ARVQSQR	GRHLEDF	GDVQIV
a692	VGRVVGGR	YGAAVDF	DFQRFQL	ARVQSQR	GRHLEDF	GDVQIV
	250	260	270	280	290	300
m692.pep	QLALSQCQ	IRAYIVG	KLDQFDG	VAFFLQL	GLDLFFD	HIAEVAD
a692	QLALSQCQ	IRAYIVG	KLDQFDG	VAFFLQL	GLDLFFD	HIAEVAD
	310	320	330			
m692.pep	RSGCGGRA	IFLTAAG	GEDERE	CGGGKGF	EFGFHIFS	X
a692	RSGCGGRA	IFLTAAG	GEDERE	CGGGKGF	EFGFHIFS	X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2315>:

```

g694.seq
1   TCGGCATTG TGTGCCCCA ACATCCGATG CCTGCGTTAA CGCCTGCGTC
51  AACGTTTGCA CAAATCGGGT TTGGTTTCGC CCTCGCGGCG CAGCTCCTTG
101 GGCAGGACGA ACACGATGCT TTCTTCCGCG CCCCCCCTT CGCGCACGGT
151 TTCATGCCCC CATCCGCGTA TGGTTGCCAA TACTTCCCGC ACCAACACTT
201 CGGGCGCGGA CGCGCTGCC GTTACGCCGA CTTTGCCTTT GCCTCAAAC
251 CACGTGCGTT GCaggTAGGA CGCGTTGTCC ACCATATACG CATCGATTCC
301 CGCGGATGCC GCCACTTCGC GCAGGCGGTT GCTGTGGAC GAATTGGGCG
351 AACCGACCAC AATCAGCATG TCGCACTGTT CCGCCAGCTC TTTGACGGCG
401 GTTTGCCGGT TGGTCGTCGC ATAGCAGATG TCTTCTTGT CGCGATTGCG
451 GATATTGGGG AAACGCGCGT TCAGCGCGCG GATGATGTCT TTGGTTTCAT
501 CGACCGAGAG CGTGGTTTGG CTGACATAGG CGAGTTTGTC GGGGTTTCTG
551 ACTTCGAGTT TTGCCACATC TCCGACCGTT TCGACCAAAA GCATTTTGCC
601 CGGTGCAACG TGCCCCATCG TGCTTCGAC CTCGGCGTGC CCCTTATGCC
651 CGATCATGAT GATTTCACAG TCTTGGSCAT CCAGTCGGGC GACTTCCTTA
701 TGCACTTTTG TCACACGCGG GCAAGTCGCA TCAAATACCC GGAACCCGCG
751 CTCCGCGCGT TCCTGCTGCA CGGCCTCGA TACGCCGTGT GCCGAATAA
801 CCAGTGTGCG GCCCGGCGGC ACTTCCGCCA AGTCTTCGAT AAACACCGCG
851 CTTTTTTGCG GCAGGTTGTC CACGACGAAT TTGTTGTGGA CGACTTCGTG
901 GCGCACATAA ACCGGCGCGC CGAATTCCTC CAAAGCACGT TCGACAATAC
951 TGATTGCCCG ATCCACACCG GCGCAGAAGC CGCGCGGATT GGCAAGGATG
1001 ATGGTTTTTC CGTTCATAAG TTTTGCATTC CGTGTTCAGA CGGCATTAC
1051 GTTTTTTTGC TNNATCTTG CGATGGACGA TATTGTCAA GACCGCCAAC
1101 ACCGCACCGA CGCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2316; ORF 694>:

```

g694.pep (partial)
1   SAFVLPKHEM FALTPASTFA QIGGFALAA QLLGQDEHDA FFRAPPPAHG
51  FMPPSAYGCQ YFPHQHFRGR RACRYADFAF AFKPRALQVG RVVHHIRIDS
101 ARCRHFAQAV AVGRIGRTDH NHDVALFRQL FDGLPVGRR IADVFLVRIA
151 DIGETRVQRG DDVFGFIDRE RSLADIGFV GVSDFEFCHI SDREFQKHFA
201 RCKLPHRAFD LGVPLMPDHD DFTVLGIQSG DFLMHFRHOR ASRIKYPETA
251 LRRFLLHLRL YAVCRINOCR ARRHFRQVFD KHRAFFAQV HDEFVVDDEV
301 AHINRRAEFF QSTFDNTDCP IHTGAEAARI GKDDGFSVHK FCIPCSGDIH
351 VFLLXLCDDR YQAPPTPHR RR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2317>:

```

m694.seq
1   TTGGTTTCCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTC
51  GACGGCATTG GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGAC
101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
151 CACAATGCTT TCTTCCGCAC CCTCGCCTTC CGGTACGGTT TCGTGCCCCC
201 ATCCGCGTAT GGTGCCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
251 GCGCTTCCG TTACGCCGAC TTTGTTTTTG CCCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
351 CCATTTCCG CAAGCGGTTG CTGTTGACG AATTGGGCGA ACCGACCACA
401 ATCACGATGT CGCACTGTTT TGCCAACCTT TTGACGGCGG TTTGCCGGTT
451 GGTCTGCGCA TAGCAGATAT CTTCTTGTG CGGATTGCGG ATATTGGGGA
501 AACGCGCGT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTG GGGTTTCTGA CTTCGAGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCC GGCACAAGCT
651 GCCCCATCGT TCCTTCGACC TCGACGTGCC CCTTATGCCC GATCATGATG
701 ATTTACAGAT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACGAGCGGG CAAGTCGCAT CAAACACGCG GAACCGCGc TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCCGCGCGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGGTGTGCC ACGACGAATT TGTTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACTCTTCC AAAGCACGTT CGACAATACT GATT GCCCGA
1001 TCCACACGAG CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTCTC
1051 GTTCATAAGC CCGGTATTC GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTTAC GGTGGACGAT GTTGTCACAC ACCGCCAACA CCGCACCGAC
1151 GCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2318; ORF 694>:

```

m694.pep
1   LVSASGTRQK CRLKPVQTAFL VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNHDVALF COLFDGGLFPV

```

1117

```

151 GRIADIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPHR SFOLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFQ VFNKHTFTT
301 QVVHDEFVFN DFVAHINRRA ELFQSTFDNT DCPIHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 86.8% identity over a 372 aa overlap with a predicted ORF (ORF 694) from *N. gonorrhoeae*:

```

m694/g694      86.8% identity in 372 aa overlap

              10      20      30      40      50
m694.pep      LVSASGTRQKCRLEPVQTAFLPKHS---TPASTFAQIGFGFALAAQLFGQDEHNAFFR
              :||||| :||||| :||||| :||||| :|||||
g694          SAFVLPKHPMPALTTPASTFAQIGFGFALAAQLFGQDEHDAFFR
              10      20      30      40

              60      70      80      90     100     110
m694.pep      TLAFAYGFVPFSAYGCGYFPHOHFGRGRACRYADVFALKPCALQVACIIHHIRIDSARC
              : |||:||||| :||||| :||||| :||||| :|||||
g694          APPFAHGFMPPSAYGCGYFPHOHFGRGRACRYADFAFAKPRALQVGRVHHIRIDSARC
              50      60      70      80      90     100

              120     130     140     150     160     170
m694.pep      RHFAQAVAVGRIGRTDHNHDVALFCQLFDGGLPVGRRRIADIFLVRIADIGETRVQRGDDV
              :||||| :||||| :||||| :||||| :|||||
g694          RHFAQAVAVGRIGRTDHNHDVALFRQLFDGGLPVGRRRIADVFLVRIADIGETRVQRGDDV
              110     120     130     140     150     160

              180     190     200     210     220     230
m694.pep      FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARRKLPHRSFDLDVPLMPDHDDFT
              :||||| :||||| :||||| :||||| :|||||
g694          FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARCKLPHRAFDLGVPLMPDHDDFT
              170     180     190     200     210     220

              240     250     260     270     280     290
m694.pep      VLGIQSGDFLMHFRHQRASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFQVFNKHR
              :||||| :||||| :||||| :||||| :|||||
g694          VLGIQSGDFLMHFRHQRASRIKYPETALRRFLHRLRYAVCRINQCRARRHFQVFNKHR
              230     240     250     260     270     280

              300     310     320     330     340     350
m694.pep      TFFTQVVHDEFVVDNFVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGI
              :||||| :||||| :||||| :||||| :|||||
g694          AFFAQVVHDEFVVDNFVAHINRRAELFQSTFDNTDCPIHTGAEAARIGKDDGFSVHKFCI
              290     300     310     320     330     340

              360     370     380
m694.pep      SFSDGINIFLLGFYGGRCCTPTPTPHRRRX
              :||||| :|||||
g694          PCSDGIHVFLXXLCDGRYCAPTPHRRRX
              350     360     370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2319>:

```

a694.seq
1  TTGGTTTCGG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTCA
51 GACGGCATTT GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTGCAC
101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
151 CACRAATGCTT TCTTCCGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
201 ATCCGCGTAT GGTTCGCAGT ACTTCCGCGA CCAACACTTC GGGCGCGGAC
251 GCGCCTGCGC TTACGCGGAC TTTGTTTTTG CCCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
351 CCACTTCGCG CAAGCGGTTG CTGTTGGACG AATTGGCGCA ACCGACCACA
401 ATCAGCATGT CGCACTGTTT TGCCAACTCT TTGACGGCGG TTTGCCGGTT
451 GGTCGTCGCA TAGCAGATAT CTTCTTTGTG CGGATTGCGG ATATTGGGGA
501 AACGCGGTT CAGCGCGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTCT GGGTTTCTGA CTTGAGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCG GCGCAAGCT
651 GCCCCATCGT TCCTTCGACC TCGACGTGCC CTTATGCCG GATCATGATG

```

```

701 ATTTCACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACCTTTCGT
751 CACCAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCCGGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGGTTGTCC ACGACGAATT TGTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACTCTTCC AAAGCACGTT CGACAATACT GATTGCCCGA
1001 TCCACACCAG CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTTCTC
1051 GTTCATAAGC CCGGTATTTC GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTAC GGTGGACGAT GTTGTCACAC ACCGCCAACA CCGCACCGAC
1151 GCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2320; ORF 694.a>:

```

a694.pep
1  LVSASGTRQK CRLKPVQTAF VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPQHFF GRGRACRYAD FVFALKPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNDVALF CQLFDGGLPV
151 GRIADIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPHR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLYAVCRIN QCRARRHFRQ VFNKHRTFFT
301 QVVHDEFVFN DVAHINRRA ELFOSTFDNT DCPHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 694 shows 100% identity over a 385 aa overlap with a predicted ORF (ORF 694) from *N. meningitidis*:

```

m694/a694 100.0% identity in 385 aa overlap

      10      20      30      40      50      60
m694.pep LVSASGTRQKRLKPVQTAFVLPKHSTPASTFAQIGFGFALAAQLFGQDEHNAFFRTLAF
a694      LVSASGTRQKRLKPVQTAFVLPKHSTPASTFAQIGFGFALAAQLFGQDEHNAFFRTLAF
      10      20      30      40      50      60

      70      80      90     100     110     120
m694.pep AYGFVPPSAYGCQYFPQHFGGRGRACRYADFVFALKPCALQVACIIHHIRIDSARCRHFA
a694      AYGFVPPSAYGCQYFPQHFGGRGRACRYADFVFALKPCALQVACIIHHIRIDSARCRHFA
      70      80      90     100     110     120

      130     140     150     160     170     180
m694.pep QAVAVGRIGRTDHNHDVALFCQLFDGGLPVGRRRIADIFLVRIADIGETRVQRGDDVFGFI
a694      QAVAVGRIGRTDHNHDVALFCQLFDGGLPVGRRRIADIFLVRIADIGETRVQRGDDVFGFI
      130     140     150     160     170     180

      190     200     210     220     230     240
m694.pep DRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARRKLPHRSFDLDVPLMPDHDDFTVLGI
a694      DRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARRKLPHRSFDLDVPLMPDHDDFTVLGI
      190     200     210     220     230     240

      250     260     270     280     290     300
m694.pep QSGDFLMHFRHQRASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHRTFFT
a694      QSGDFLMHFRHQRASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHRTFFT
      250     260     270     280     290     300

      310     320     330     340     350     360
m694.pep QVVHDEFVFNDFVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGISFSD
a694      QVVHDEFVFNDFVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGISFSD
      310     320     330     340     350     360

      370     380
m694.pep GINIFLLGFYGGRCCTPPTPHRRRX
a694      GINIFLLGFYGGRCCTPPTPHRRRX
      370     380

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2321>:

```
g695.seq
1  TTGCTCAAA CTCGTCCGGC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTGAACGG AAGGGTGATG CGCGAAGCGG CTTTGTATGC GCCGCCCAGT
101 GTCAAAATTC TCAAAGATTT CAATCAAAAC CTGCCGAACG ATACGCGGAT
151 TGTCCCCATC ACCCTGCCCG TCGGCGACGG TTTGACCCTG CTTCTGAAAA
201 AATAATGAAG ACCAAATTAC CGCTTTTAT CATTGGGCTG TCTGTGTCTG
251 CCTCCTGTGC TTCCGTTTTC CCCGTTCCGG AGGGCAGCGG AACCGAAATG
301 CCGACACAGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCCACCTT
351 GCAAGACCGT TTGGACTATC TGGAAGGCAA AATCGTCCGG CTGTCGAACG
401 AAGTGGAAAT GTTAAACGGG AAAGTCAAAG CATTGGAGCA TACGAAAATA
451 CACCCTTCG GCAGGACATA CGTCCAAAA CTCGACGACC GCAAATTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACCGTCG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TCAAACGGC
601 AGGTTTCTG CCGCAGCCGC CTTGTTSAAG GGGCGGACG GCGGAGACGG
651 CCGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGGAA CTGTGAATCT GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCCGAA GTCATATTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTACGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2322; ORF 695>:

```
g695.pep
1  LPQTRPARRH HRHRQYFVER KGDARSGF*C AAQCQNSQRF QSKPAERYAD
51  CPHHPARRRR FDPASEKIMK TKLPLFLIWL SVSASCASVL PVPEGSRTM
101 PTQENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVEMLNG KVKALEHTKI
151 HPSGRITYVQK LDDRKLKEHY LNTGEGSASA HTVETAQNLY NQALKHYQNG
201 RFSAAAALLK GADGGDGGSI AQRSMYLLLO SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE VIFKIGECQY RLQOKDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2323>:

```
m695.seq
1  TTGCTCAAA CTCGTCCGTC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTGAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCCAGC
101 GTCGGCATCC TCAAAGATTT CAATCAAAAC CTGCCGAACG ACCCGCGCAT
151 CGTCCCCATC ACCCTGCCCG TCGGCGACGG CTTGACCCTG CTTCTGAAAA
201 AATAATGAAG ATCAAATTAC CGCTTTTAT CATTGGGCTG TCTGTGTCCG
251 CCTCCTGTGC TTCCGTTTTC CCCGTTCCGG CAGGCAGCCA AACCGAAATG
301 TCGACACGGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCGACCTT
351 GCAAGACCGT TTGGACTATC TGGAAGGCAA AATCGTCCGG CTGTCGAACG
401 AAGTGGAAAC CTTAAACGGC AAAGTCAAAG CACTGGAACA CGCAAAAACA
451 CATTCTTCCG GCAGGGCATA CGTCCAAAA CTCGACGACC GCAAGTTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACTGTCT
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TAAAGCGGCG
601 AAGTTTCTG CCGCTGCCTC CTTGTTGAAA GCGCGGACG GAGGCGACGG
651 CCGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGCAA CTGCGAATCC GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCTGAA GCCATGTTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTGCGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2324; ORF 695>:

```
m695.pep
1  LPQTRPSRRH HRHRQYFAER KGDARSGFRC AAQRHPQRF QSKPAERPAP
51  RPHHPARRRR LDPASEKIMK IKLPLFLIWL SVSASCASVS PVPAGSOTEM
101 STRENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVETLNG KVKALEHAKT
151 HSSGRAYVQK LDDRKLKEHY LNTGEGSASA HTVETAQNLY NQALKHYKSG
201 KFSAAAALLK GADGGDGGSI AQRSMYLLLO SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE AMFKIGECQY RLOOKDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 90.8% identity over a 305 aa overlap with a predicted ORF (ORF 695) from *N. gonorrhoeae*:

m695/g695 90.8% identity in 305 aa overlap

m695.pep	10	20	30	40	50	60
	LPQTRPSRRHHRQYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAPHRPHHPARRRR					
g695	10	20	30	40	50	60
	LPQTRPARRHHRQYFVERKGDARSGFCAAQCONSQRFSKPAERYADCPHHPARRRR					
m695.pep	70	80	90	100	110	120
	LDPASEKIMKIKLPLFIWLSVSASCASVSPVPAGSQTEMSTRENASDGIPYPVPTLQDR					
g695	70	80	90	100	110	120
	FDPASEKIMKTKLPLFIWLSVSASCASVLPVPEGSRTMPTQENASDGIYPVPTLQDR					
m695.pep	130	140	150	160	170	180
	LDYLEGKIVRLSNEVELNGKVKALEHAKTHSSGRAYVQKLDLDRKLKEHYLNTTEGGSASA					
g695	130	140	150	160	170	180
	LDYLEGKIVRLSNEVELNGKVKALEHTKIHPSGRTYVQKLDLDRKLKEHYLNTTEGGSASA					
m695.pep	190	200	210	220	230	240
	HTVETAQNLYNQALKHYKSGKFSAAASLLKGADGGDGGGSAQSRMYLLQLSRARMGNCS					
g695	190	200	210	220	230	240
	HTVETAQNLYNQALKHYQNGRFSAAAALLKGADGGDGGGSAQSRMYLLQLSRARMGNCS					
m695.pep	250	260	270	280	290	300
	VIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAARKRAA					
g695	250	260	270	280	290	300
	VIEIGGRYANRFKDSPTAPEVIFKIGECQYRLQKDIARATWRSLIQTYPGSPAARKRAA					
m695.pep	AVRKRX					
g695	AVRKRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2325>:

a695.seq

1	TTGCTCAAG	CTTGTCGGC	AAGCGGCGC	CATTGCCATC	GACAATATTT
51	TGTTGAACGG	AAGGGTGATG	CGCGAAGCGG	CTTCGGATGC	GCCGCCCAGC
101	GTCGGCATCC	TCAAAGATT	TAATCAAAC	CTGCCGAACG	ATACGCGGAT
151	TGTCCCATC	ACCCTGCCG	TCGGCGACGG	TTGACCCCTG	CTTCTGAATA
201	AATAATGAAG	ACCAAATTAC	CGCTTTTAT	CATTGGGCTG	TCCGTATCCG
251	CCGCTGTTC	TCCCTCTGT	TCCCGCAATA	TTCAGGATAT	GCGGCTCGAA
301	CCGCAGGCAG	AGGCAGGTAG	TTCGGACGCT	ATTCCCTATC	CCGTTCCAC
351	TCTGCAAGAC	CGTTTGGATT	ATCTGGAAGG	CACACTCGTC	CGCTGTCTGA
401	ACGAAGTGGA	AACCTTAAAC	GGCAAAGTCA	AAGCACTGGA	GCATGCGAAA
451	ACACACCCCT	CCAGCAGGCC	ATACGTCCAA	AACTCGACG	ACCGCAAGTT
501	GAAAGAGCAT	TACCTCAATA	CCGAACGCGG	CAGCGCATCC	GCACATACCG
551	TCGAAACCGC	ACAAAACCTC	TACAATCAGG	CACTCAAACA	CTATAAAAGC
601	GGCAGGTTT	CTGCCGCTGC	CTCCTGTGT	AAAGGCGCGG	ACGGAGGCGA
651	CGGCGGCAGC	ATCGCGCAAC	GCAGTATGTA	CCTGTGCTG	CAAAGCAGGG
701	CGCGTATGGG	CAACTGCGAA	TCCGTCATCG	AAATCGGAGG	GCGTTACGCC
751	AACCGTTTCA	AAGACAGCCC	AACCGCGCCT	GAAGCCATGT	TCAAATCGCG
801	CGAATGCCAA	TACAGGCTTC	AGCAAAAAGA	CATTGCAAGG	GCGACTTGCC
851	GCAGCCTGAT	ACAGACCTAT	CCCGGCAGCC	CGGCGGCAAA	ACGCGCCGCC
901	GCAGCCGTGC	GCAACGATA	G		

This corresponds to the amino acid sequence <SEQ ID 2326; ORF 695.a>:

a695.pep

1	LPQACPARRH	HCHRQYFVER	KGDARSGFRC	AAQRRHPQRF	*SKPAERYAD
51	CPHHPARRRR	FDPASEKIMK	TKLPLFIWLS	SVSAACSSPV	SRNIQDMRLE
101	PQAEAGSSDA	IPYPVPTLQD	RLDYLEGLTV	RLSNEVELTN	GKVKALEHAK
151	THPSSRAYVQ	KLDDRKLKEH	YLNTEGGSAS	AHTVETAQNL	YNQALKHYKS
201	GRFSAASLL	KGADGGDGGG	IAQRSMYLLL	QSRARMGNCE	SVIEIGGRYA
251	NRFKDSPTAP	EAMFKIGECQ	YRLQKDIAR	ATWRSLIQTY	PGSPAARKRAA
301	AAVRRR*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 695 shows 88.3% identity over a 308 aa overlap with a predicted ORF (ORF 695) from *N. meningitidis*:

m695/a695 88.3% identity in 308 aa overlap

m695.pep	10	20	30	40	50	60
a695	10	20	30	40	50	60
m695.pep	70	80	90	100	110	
a695	70	80	90	100	110	
m695.pep	120	130	140	150	160	170
a695	120	130	140	150	160	170
m695.pep	180	190	200	210	220	230
a695	180	190	200	210	220	230
m695.pep	240	250	260	270	280	290
a695	240	250	260	270	280	290
m695.pep	300					
a695	300					

The following partial DNA sequence was identified in *N. gonorrhoeae*
g696.seq: not found

This corresponds to the amino acid sequence < ORF 696.ng>:
g696.pep: not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2327>:

m696.seq

1	TTGGGTTGCC	GGCAGGCGGC	ATCCCATCAT	TTTGCCAAG	GCAACAAATT
51	ATTGGCGGC	ATCTTTCATT	TTGTCTGCCG	CTTCCTGAGT	CGCGTCGGCA
101	GCTTTGTCA	AAGTATCTTT	AGCTGCTTCA	GTTACAGCTT	CTTTGGCTTC
151	AGTTACAGCT	TCCTCGGCAC	TTGCCTTTGC	ATCAGCCGCA	GCATCTTTGA
201	CTTGGTCTTT	CGCTTCTTCG	ACGGCAGAAG	CGGCAGACTC	GGCGGCAGAA
251	GCCGAGTGT	CTTTAACATC	GGACTCAACG	GCTTGAACCG	CTTCCTTAAC
301	CTCCTGTTTG	GCTTCTTGCG	AACAAGCTGC	CAAGGCAGCC	GCCATCATTG
351	CGGCAATCAA	TAA			

This corresponds to the amino acid sequence <SEQ ID 2328; ORF 696>:

m696.pep

1	LGCROAASHH	FCQGNKLFEG	IFHEVCRFLS	RVGSFVQSIF	SCFSYSFFGF
51	SYSFLGTCLC	ISRSIFDLVF	RFFDGRSGRL	GGRSRSVFNI	GLNGLNRFLN
101	LLFGFLRTSC	QGSRRHCGNQ	*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2329>:
a696.seq

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```

1  TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAATT
51  ATTTGGCGGC ATCTTTTCATT TTGTCTGCCG CTTCTGAGT CGCGTCGGCA
101 GCTTTGTTC AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTGC ATCAGCCGCA GCATCTTGA
201 CTTGGTCTTT CGCTTCTCG ACGGCAGAAG CGGCAGACTC GCGCGCAGAA
251 GCGCAGTGT CTTTAACATC GGAACAACG GCTTGAACCG CTTCTTAAC
301 CTCCTGTTT GCTTCTTGGC AACAAGCTGC CAAGGCAGCC GCCATCATTG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2330; ORF 696.a>:

a696.pep

```

1  LGCRQAASHH FCQGNKLFGG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSFLGTCCLC ISRSIFDLVF RFFDGRSGRL GGRSRSVFNI GLNGLNRFLN
101 LLFGFLRTSC QGSRHHHCNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 696 shows 100.0% identity over a 120 aa overlap with a predicted ORF (ORF 696.a) from *N. meningitidis*:

m696/a696 100.0% identity in 120 aa overlap

```

          10      20      30      40      50      60
m696.pep  LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFYSFLGTCLC
          |||
a696      LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFYSFLGTCLC
          10      20      30      40      50      60

          70      80      90      100     110     120
m696.pep  ISRSIFDLVFRFFDGRSGRLGGRSRSVFNI GLNGLNRFLNLLFGFLRTSCQGSRHHHCNQ
          |||
a696      ISRSIFDLVFRFFDGRSGRLGGRSRSVFNI GLNGLNRFLNLLFGFLRTSCQGSRHHHCNQ
          70      80      90      100     110     120

```

```

m696.pep  X
          |
a696      X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2331>:

g700.seq

```

1  ATGAGCAGCC TGATGACGTT GTTTTCGGTA TTGGTACCGA TGTTTGCCGG
51  ATTTTTTATC CGTGTTCCCA AGCCTTACCT GCCCGCTTCG GACAAGGTGC
101 TGTCGGTTTT GGTGTATGCC GTGCTGCTGC TGATCGGCGT ATCGTTGTCTG
151 CGCGTGAGG ATTTGGGTTT CCGGTTGGGC GATATGGCGT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TAGGGGCGAA CCTGCTTGCC TTGGCAGTGT
251 TGGGAAAGTT GTCCCGTGG CGGATAGGGG GAAAAGGGAA GGGCGTTTCG
301 GTCGGCGTGT CGGGCAGTGT GAGGCAGCTC GGATGCGTAC TGCTCGGTTT
351 TGTGTCCGGC AAATTGATGT GCGATATTG GATGCCGTCT GAAAACGCGG
401 GTATGTACTG CCTGATGCTG CTGGTGTTCC TCATCGGCGT ACAGCTCAAA
451 AGTAGCGGCG TATCGTTGCG GCAGGTTTTG CTTAACCGGC GGGGCATCCG
501 GCTGTCGGTT TGGTTTATAT TGTCTCTCT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGATGGTGTG TCGTGACGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATTCCCT CTCGGGTTTG GTAATGACCG AGGCTTACGG
651 GCGGATATGG GGCAGCATCA TGCTGCTGAA CGATTGGCA CGAGAGCTGT
701 TTGACTGGC ATTTATPCCG CTGCTGATGA AGCGTTTTCC GGATGCGGCG
751 GTGGGGGTCC GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTAATTCA
801 GGGTGCGGCG GGTTTGGAAG TCGTGCCGGT AGCGGTGAGC TTCGCGGTGG
851 TGGTCAATAT CGCCGCCCGG TTTCTGATGG TGGTGTTTTC CACGCTGGGC
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2332; ORF 700>:

g700.pep

```

1  MSSMLTFLSV LVPMFAGFFI RVPKPYLPAS DKVLSVLVYA VLLLIGVSL
51  RVEDLGSRLG DMALTVLWLF VCTVGANLLA LAVLGKLSPW RIGGKGKGV
101 VGVSGSVRQL GCVLLGFVSG KLMCDIWMP ENAGMYCLML LVFLIGVQLK
151 SSGVSLRQVL LNRRGIRLSV WFILSSLSGG LLFAASADGV SWTKGLAMAS

```

201 GFGWYLSGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA
 251 VGVGGATSMD FTLPVIOGAG GLEVVPVAVS FGVVVNIAAP FLVVVFSTLC
 301 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2333>:

m700.seq

1 ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG
 51 ATTTTATC CGTGTGCCCA AGCCTTACCT GCCCGCTTG GATAAGGTGC
 101 TATCGGCTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTTGTCTG
 151 CGCGTGGAGG ATTTGGGTTC GCGTTGGAC GATATGGCGT TGACGGTTCT
 201 GTGGCTGTTT GTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
 251 TGGGAAAGTT ATTCCCGTGG CGGATAAAGG GGAAGGGAA GGGCGTTTCG
 301 GTCGGCGTGT CGGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT
 351 TGCATTCCGC AAACGATGC GCGATATTG GATGCCGTCT GAAAGCGCGG
 401 GCATGTATTG TCTGATGCTG CTGGTGTTC TCATCGGCGT ACAGCTCAA
 451 AGCAGCGCGG TATCGTTGCG GCAGGTTTGT GTCAACCGCA GGGGTATTCTG
 501 GTTGTGCGTC TGGTTTATGC TTTCATCTCT TTCGGGCGGG CTGCTCTTGT
 551 CCGCATCCGC AGACGGTGTG TCGTGGACGA AAGGTTTGGC GATGGCTTCC
 601 GGCTTCGGTT GGTATTCCCT CTCGGGTTTG GTCATGACCG AGCCTTACGG
 651 CGCGGTATGG GGCAGCATCA TGCTGCTGAA CGATTGGCA CGAGAGCTGT
 701 TTGCACTGGC ATTTATCCCG CTGCTGATGA AGCGTTTCC AGATGCGGCG
 751 GTGGGGTTG GCGGTGCGAC CAGTATGGAT TTTACATTGC CCGTGATTCA
 801 GGTGCGGGC GGTTTGGAAG TCGTGCCGT AGCGGTCAGC TTCGGCGTGG
 851 TGGTCAATAT CGCCGCCCGG TTTCTGATGG TGGTGTTCG CGCTTTGGGT
 901 TGA

This corresponds to the amino acid sequence <SEQ ID 2334; ORF 700>:

m700.pep

1 MDSLMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLIGVSL
 51 RVEDLGSRD DMALTVLWLF VCTVGANLLA LAVLGKLPW RIKGKKGVS
 101 VGVSGSVQGL GCVLLGFAGF KLMRDIWMP ESAGMYCLML LVFLIGVQLK
 151 SSGVSLRQVL VNRGIRLSV WFMLSSLSGG LLEFAASTDGV SWTKGLAMAS
 201 GFGWYLSGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA
 251 VGVGGATSMD FTLPVIOGAG GLEVVPVAVS FGVVVNIAAP FLVVVFSALG
 301 *

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with menB

ORF 700 shows 94.7% identity over a 300 aa overlap with a predicted ORF (ORF700.ng) from *N. gonorrhoeae*:

m700/g700

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLIGVSLSRVEDLGSRD					
g700	MSSLMTLFSVLVPMFAGFFIRVPKPYLPASDKVLSVLVYAVLLIGVSLSRVEDLGSRD					
	10	20	30	40	50	60
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLPWRIKGKKGVS VGVSGSVQGLGCVLLGFAGF					
g700	DMALTVLWLFVCTVGANLLALAVLGKLPWRIGGKKGVS VGVSGSVRQLGCVLLGFVSG					
	70	80	90	100	110	120
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRGIRLSVWFMLSSLSGG					
g700	KLMCDIWMPSENAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRGIRLSVWFILSSLSGG					
	130	140	150	160	170	180
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYLSGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
g700	LLFAASADGVSWTKGLAMASGFGWYLSGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
	190	200	210	220	230	240

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	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDA	AVGVGGAT	SMDFTLP	VIQAGGLE	VVPVAVS	FGVVVNIA
g700	LLMKRFPDA	AVGVGGAT	SMDFTLP	VIQAGGLE	VVPVAVS	FGVVVNIA
	250	260	270	280	290	300
	FLMVVFSALG					
m700.pep	x					
g700	x					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2335>:

```

a700.seq
1  ATGGACAGCC  TGATGACGTT  GCTTTCGGTA  TTGATACCGA  TGTTGCCGG
51  ATTTTATATC  CGTGTGCCCA  AGCCTTACCT  GCCCGCTTTG  GATAAGGTGC
101  TATCGGTCTT  GGTGTATGCT  GTGCTGCTGC  TGATCGGCGT  CTCGTTGTCG
151  CGCGTGGAGG  ATTTGGGTTT  GCGGTGGGAC  GATATGGCGT  TGACGGTTCT
201  GTGGCTGTTT  GTTGTACGG  TCGGGGCGAA  CTGCTTGCT  TTGGCAGTGT
251  TGGGAAAGTT  ATTCCCGTGG  CGGATAAAGG  GGAAAGGGAA  GGGCGTTTCG
301  GTCGGTGTGT  CGGGCAGTGT  GGGGCAGCTC  GGATGCGTGC  TGCTCGGATT
351  TGCATCCGGC  AAACCTGATC  GCGATATTTC  GATGCCGTCT  GAAAACGCGG
401  GTATGTATTG  TCTGATGCTG  CTGGTGCTCN  TCATCGGCGT  ACAGCTCAAA
451  AGCAGCGGCG  TATCGTTGCG  GCAGGTTTTC  GTCAACCGCA  GGGGTATTTC
501  GTTGTCGGTC  TGGTTTATGC  TTTCATCTCT  TTCAGGCGGG  CTGCTGTTTG
551  CCGCATCGGC  AGACGGTGTG  TCGTGGGTGA  AAGGTTTGGC  GATGGCTTCC
601  GGCTTCGGTT  GGTATTCCCT  CTCGGTTTTC  GTGATGACCG  AGGCTTACGG
651  CGCGGTATGG  GGCAGTATCG  CGCTTTTGAA  CGATTGGCA  CGAGAGCTGT
701  TCGCGTGGC  ATTTATTCCG  CTGCTGATGA  AGCGTTTTC  CGATGCGGCA
751  GTGGGGGTCG  GCGGCGCGAC  CAGTATGGAT  TTCACATTGC  CCGTGATTCG
801  GGGTCCGGC  GGCTTGAAG  CCGTACCGGT  AGCGGTCAGC  TTCGGCGTGG
851  TGGTCAATAT  CGCCGCTCCG  TTTCTGATGG  TGGTGTTTTC  CGCTTTGGGC
901  TGA

```

This corresponds to the amino acid sequence <SEQ ID 2336; ORF 700.a>:

```

a700.pep
1  MDSLMTLLSV  LIPMFAGFFI  RVPKPYLPAL  DKVLSVLVYA  VLLLIGVSL
51  RVEDLGSRLD  DMALTVLWLF  VCTVGANLLA  LAVLGKLFPW  RIKGRKGVS
101  VGVSGSVGQL  GCVLLGFASG  KLMRDIWMP  ENAGMYCLML  LVLXIGVQLK
151  SSGVSLRQVL  VNRRGIRLSV  WFMLSSLSGG  LLFAASADGV  SWVKGLAMAS
201  GFGWYSLSL  VMTEAYGAVW  GSIALNLNLA  RELFALAFIP  LLMKRFPDAA
251  VGVGGATSMD  FTLPVIRGAG  GLEAVPVAVS  FGVVVNIAAP  FLMVVFSALG
301  *

```

m700/a700 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRV	PKPYLPALDKVLSVLVYAVLL	LIGVSLSRVEDLGSRLD			
a700	MDSLMTLLSVLIPMFAGFFIRV	PKPYLPALDKVLSVLVYAVLL	LIGVSLSRVEDLGSRLD			
	10	20	30	40	50	60
m700.pep	DMALTVLWLFVCTVGANLLA	LAVLGKLFPWRIKGRKGVS	SGVSGSVGQLGCVLLGFAG			
a700	DMALTVLWLFVCTVGANLLA	LAVLGKLFPWRIKGRKGVS	SGVSGSVGQLGCVLLGFAG			
	70	80	90	100	110	120
m700.pep	KLMRDIWMPSESAGMYCLML	LVLIGVQLKSSGVSLRQVL	VNRRGIRLSVWFMLSSLSGG			
a700	KLMRDIWMPSENAGMYCLML	LVLXIGVQLKSSGVSLRQVL	VNRRGIRLSVWFMLSSLSGG			
	130	140	150	160	170	180

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	190	200	210	220	230	240
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYSLSGGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
a700	LLFAASADGVSWVKGLAMASGFGWYSLSGGLVMTEAYGAVWGSIALNDLARELFALAFIP					
	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDAAVGVGGATSMDFTLPIQGAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
a700	LLMKRFPDAAVGVGGATSMDFTLPIRGAGGLEAVPVAVSFGVVVNIAAPFLMVVFSALG					
	250	260	270	280	290	300
m700.pep	X					
a700	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2337>:

g701.seq

```

1  ATGTCTTGGC ACATATTCCA AGTGCAGGG ATACCGACCG CTCGATGGC
51  ACAATCTACG CCGTCTTCGC CGACGATGGC GAAACTTGT TTGGAGACGT
101 CGCCGGAAGC GGGGCTGATG GTATGGGTCG CGCCCACTC TTTCGCCGT
151 TTCAAACGGT TTTCGTCCAT ATCGCACACG ATAATGGCGG CAGGGCTATA
201 CAGTTGGGCG GTCAACAAGG CGGACATACC GACAGGGCCG GCACCTGCGA
251 TGAATACGGT ATCGCCGGGT TTCACATCGC CGTATTGCAC GCCGATTTCG
301 TGGGCGGTCT GTAAAGCGTC GCTCAACAGC AGGGCGATTT CTTCGTTGAC
351 GTTGTCTGTC GGCGGCACGA GGCTGTTGTC GGCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2338; ORF 701>:

g701.pep

```

1  MSWHIFQVAG IPTASMAQST PSSPTMAKTC LETSPEAGLM VWVAPNSFAG
51  FKRFSISHT IMAAGLYSWA VNKADIPTGP APAMNTVSPG FTSPYCTPIS
101 WAVGKASLNS RAISSLTLSC GGTRLLSA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2339>:

m701.seq

```

1  ATGTCTTGGC ACATATTCCA TGTAGCAGGG ATACCGACCG CTCGATGGC
51  GCAATCCACG CCGTCTTCGC CGACGATGGC AAAGACTTGT TTGGATACTT
101 CGCCGGAAGC AGGGTTAATG GTATGGGTCG CACCCAATTC TTTCGCCAGT
151 TTCAAACGGT TTTCGTCCAT ATCGCAAACG ATGATGGCGG CGGGACTGTA
201 CAGTTGGGCG GTCAACAGGG CGGACATACC GACAGGGCCT GCCCCAGCGA
251 TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTCG
301 TGGGCGGTCT GCAAAGCGTC GCTCAACAAC AGGGCGATTT CTTCGTTGAC
351 ATTATCGGGC AGCGGAACGA GGCTGTTGTC GGCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2340; ORF 701>:

m701.pep

```

1  MSWHIFHVAG IPTASMAQST PSSPTMAKTC LDTSPEAGLM VWVAPNSFAS
51  FKRFSISQT MMAAGLYSWA VNRADIPTGP APAMNTVSPG LTSPYCTPIS
101 WAVGKASLNN RAISSLTLSC SCTRLLSA*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with *menB*

ORF 701 shows 92.2% identity over a 128 aa overlap with a predicted ORF (ORF701.ng) from *N. gonorrhoeae*:

m701/g701

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTNAKTC	LDTSPEAGLMVWVAPNSFAS	FKRFSISQT			
g701	MSWHIFQVAGIPTASMAQSTPSSPTNAKTC	LETSPEAGLMVWVAPNSFAG	FKRFSISHT			

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	10	20	30	40	50	60
	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIPTGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISSLTLSG					
	: : : : : :					
g701	IMAAGLYSWAVNKADIPTGPAPAMNTVSPGFTSPYCTPISWAVGKASLNSRAISSLTLSG					
	70	80	90	100	110	120
	129					
m701.pep	SGTRLLSAX					
	:					
g701	GGTRLLSAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2341>:

```
a701.seq
1  ATGTCTTGGC ACATATTCCA AGTTGCAGGG ATACCGACGG CTTGATCGC
51  GCAGTCCACG CCGTCTTCGC CGACGATAGC GGCAACTTGC TTGCTTACAT
101 CGCCGGAAGC AGGGTTAATG GTATGGGTG CGCCCAACTC TTTCGCCAGT
151 TTCAAACGGT TTCGTCCAT ATCGCAAACA ATGATGGCGG CGGGGCTGTA
201 CAGTTGGGCG GTCGGCAAGG CGGACATACC GACAGGAGCG GCACCTGCGA
251 TGAATACGGT GTCGCCGGT TTGACATCGC CGTATTGCAC GCCGATTTCG
301 TGTGCGGTCG GCAAAGCGTC GCTCAACAAC AGGGCGACTT CTTGTTGAC
351 GTTGTCTGGC AGCGGCACGA GGCTGTTGTC GGCATAA
```

This corresponds to the amino acid sequence <SEQ ID 2342; ORF 701.a>:

```
a701.pep
1  MSWHIFQVAG IPTASIAQST PSSPTIAATC LLTSPEAGLM VWVAPNSFAS
51  FKRFSSISQT MMAAGLYSWA VGKADIPTGA APAMNTVSPG LTSPYCTPIS
101 CAVGKASLNN RATSSLTSLG SGTRLLSA*
```

m701/a701 92.2% identity in 128 aa overlap

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVWVAPNSFASFKRFSSISQT					
	: : : : :					
a701	MSWHIFQVAGIPTASIAQSTPSSPTIAATCLLTSPPEAGLMVWVAPNSFASFKRFSSISQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIPTGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISSLTLSG					
	: : : : :					
a701	MMAAGLYSWAVGKADIPTGAAPAMNTVSPGLTSPYCTPISCAVKGKASLNNRATSSLTSLG					
	70	80	90	100	110	120
	129					
m701.pep	SGTRLLSAX					
a701	SGTRLLSAX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2343>:

```
g702.seq
1  ATGCCGTGTT ccaAAGCCAG TTGGACTTCG CCCGGAGtgg cAACGCCGGG
51  AATCAGGGGA ATGCCGCTGT TGCGGCCGGC TCTGGCGAGG GATTCGTGCA
101 AACCCGGGCT GATGGCGAAA ACCGCGCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGAT TGGTTACCGT ACCTGCGCCG ATGATGGCGT TGGGCATTTC
201 TTTGGCAATC AGGCGGATGG CCTCGAGTCC GACGGGGGTG CGCAAGGTAA
251 TTTCCGAGGT GGGGATGCCG CCTTCGACAA GGGCGCGGGA CAAATCGACG
301 GCGGTGCTTA AGTCGTCAAt cgCCATCACA GGCACAAC TG CGCCGGCGGT
351 CAGGATTTCG cgggggggtca gttga
```

This corresponds to the amino acid sequence <SEQ ID 2344; ORF 702>:

g702.pep

1127

```

1  MPCSKASWTS PGVATPGIRG MPLLRFALAR DSCKPGLMAK TAPASSTALS
51  CSGLVTVPPAP MMALGISLAI RRMASPTGV RKVISRVGMP ESTRARDKST
101 AVLKSSIAIT GTTAPAVRIS RGSV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2345>:

```

m702.seq
1  ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCGGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCGGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTTCGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAACG CGCCGGCGGT
351 CAAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGGAA
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2346; ORF 702>:

```

m702.pep
1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  CSGLVTVPPAP TMLGTSLAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

ORF 702 shows 91.9% identity over a 124 aa overlap with a predicted ORF (ORF702.ng) from *N. gonorrhoeae*:

```

m702/g702
m702.pep      10      20      30      40      50      60
               MPCSKASWISPGVATPGIRGMPLLWPALARDSCSPGLMAKTAPASSTALSCEGLVTVPPAP
               |||||
g702           MPCSKASWISPGVATPGIRGMPLLWPALARDSCCKPGLMAKTAPASSTALSCEGLVTVPPAP
               10      20      30      40      50      60

m702.pep      70      80      90      100     110     120
               TMLGTSLAIRRMASRPTGVRVISRVGMPPSTRAWDKSMVLKSSIAITGTTAPAVKIS
               |||||
g702           MMALGISLAIRRMASPTGVRKVISRVGMPPSTRARDKSTAVLKSSIAITGTTAPAVRIS
               70      80      90      100     110     120

m702.pep      130     140
               RGVSLDISVLRVEWGILLRWDRXL
               ||||
g702           RGVSX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2347>:

```

a702.seq
1  ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCGGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCGGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TSGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CSCAGGGTGA
251 TTTTCGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAACG CGCCGGCGGT
351 CAAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGGAA
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2348; ORF 702.a>:

```

a702.pep
1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  CSGLVTVPPAP TMLGTSLAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

m702/a702 100.0% identity in 143 aa overlap

```

10      20      30      40      50      60

```


1128

```

m702.pep    MPCSKASWISPGVATPGIRGMPLLWPALARDSCSPGLMAKTAPASSTALSCSGLVTPVPAP
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a702         MPCSKASWISPGVATPGIRGMPLLWPALARDSCSPGLMAKTAPASSTALSCSGLVTPVPAP
             10      20      30      40      50      60

             70      80      90      100     110     120
m702.pep    TMALGTSLAIRRMASRPTGVRVRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a702         TMALGTSLAIRRMASRPTGVRVRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
             70      80      90      100     110     120

             130     140
m702.pep    RGVSLDISVLRVEWGILLRWDRLX
             ||||||||||||||||||
a702         RGVSLDISVLRVEWGILLRWDRLX
             130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2349>:

g703.seq

```

1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCG CTGCTTGCCT GTTCCGGCAG
51 CCTGTTTGCC CAAACGCTGG CAACCGTTAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAACG AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAGA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CACTGCATAT CGCCAAAACC CAACCGTTT
401 CCGAGCAGGA AGTAAAAGCC GTTTACGACA ATATCAGCGG TTTTATAAAA
451 GGCACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCGAAAAAA GCGGTTGCCG ATTTGAAGGC GAAAAAAGGT TTTGATGCCG
551 TTTTGAACA ATACTCGCTC AACGACCGCA CCAAACGGAC CGGCGCGCCG
601 GACGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGCGCA ATTTACGGCA ACGCCGCTGA
701 AAAACGGCGC TTTCTACGGC GTTTATTATG TCAACGACAG CCGcgaggTG
751 AAAGTGCTT CTTTGGACGA AATGAAAGGA CAGATTGCCG GCAACCTTCA
801 GCGGGAACGG ATTGACCGTG CCGTctgTGc gcTGTtggtt aaggCAAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2350; ORF 703>:

g703.pep

```

1  MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51 EDTPQLRQSL LENEVNTTVV AOEVKRLKLD RSAEFKDALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA VYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKRTGAP
201 DGYVPLKDLE QGVPPYQAI KDLKKGEFTA TPLKNGDFYV VYYVNSREV
251 KVPSFDEMKQ QIAGNLQAER IDRAVCALLG KANIKPAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2351>:

m703.seq

```

1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
51 CCTGTTTGCC CAAACGCTGG CAACCGTCAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAACG AAGTGGTCAA
201 TACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CATTGCATAT CGCCAAAACC CAACCGTTT
401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTTGATGCCG
551 TCTTGAACA ATATTCCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
601 TGCGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGCGCA ATTTACGGCA ACGCCGCTGA

```

1129

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
 751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
 801 GCGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTGGGC AAGGCAAACA
 851 TCAAACCTGC AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2352; ORF 703>:

m703.pep

1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSR
 51 EDTPQLRQSL LENEVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
 101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
 151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
 201 VGYVPLKDLE QGVPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSREV
 251 KVPFSDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

ORF 703 shows 98.3% identity over a 288 aa overlap with a predicted ORF (ORF703.ng) from *N. gonorrhoeae*:

m703/g703

m703.pep	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSR					
g703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSR					
m703.pep	70	80	90	100	110	120
	LENEVNTVVVAQEVKRLKLDRAEAFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
g703	LENEVNTVVVAQEVKRLKLDRAEAFKDALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
m703.pep	130	140	150	160	170	180
	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTQKEENAKKAVADLKAKKG					
g703	EAYALHIAKTQPVSEQEVKAVYDNISGFYKGTQEVQLGEILTQKEENAKKAVADLKAKKG					
m703.pep	190	200	210	220	230	240
	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPLYQAIKDLKKGEFTATPLKNGDFYG					
g703	FDAVLKQYSLNDRTKRTGAPDGYVPLKDLEQGVPLYQAIKDLKKGEFTATPLKNGDFYG					
m703.pep	250	260	270	280	289	
	VYYVNSREVKVPFSDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
g703	VYYVNSREVKVPFSDEMKGQIAGNLQAERIDRAVCALLGKANIKPAKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2353>:

a703.seq

1 ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
 51 CCTGTTTGCC CAAACGCTGG CAACCGTCAA CGGTCAGAAA ATCGACAGTT
 101 CCGTCATTGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
 151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAACGAG AAGTGGTCAA
 201 CACCGTGGTC GCACAGGAAG TGAACGCCT GAAACTCGAC CGGTCGGCAG
 251 AGTTTAAAAA TGCGTTGCC AAATGCGTG CCGAAGCGAA AAAGTCGGGC
 301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAAATATG
 351 CTTGAACGGC GAGGCATACG CGCTGCATAT CGCCAAAACC CAACCGGTTT
 401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
 451 GGTACGCAGG AAGTCCAGT GGGCGAAATC CTGACCGACA AGGAAGAAAA
 501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAGGT TTCGATGCCG
 551 TCTTGAAACA ATATCCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
 601 GTCGGATATG TGCCGCTGAA AGATTTGGAA CAGGGTGTTC CGCCGCTTTA
 651 TCAGGCAATT AAGGACTTGA AAAAAGCGCA ATTTACGGCA ACGCCGCTGA

1130

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
 751 AAAGTGCCTT CTTTGTGATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
 801 GGCGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAACA
 851 TCAAACCTGC AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2354; ORF 703.a>:

a703.pep
 1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
 51 EDTPQLRQSL LENEVVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
 101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
 151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
 201 VGYVPLKDL E QGVPPYQAI KDLKKGEFTA TPLKNGDFYG VYYVNDREV
 251 KVPSFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

m703/a703 100.0% identity in 288 aa overlap

	10	20	30	40	50	60
m703.pep	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
a703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m703.pep	LENEVVNTVVAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
a703	LENEVVNTVVAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m703.pep	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTQKEENAKKAVADLKAKKG					
a703	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTQKEENAKKAVADLKAKKG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m703.pep	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
a703	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240
	250	260	270	280	289	
m703.pep	VYYVNDREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
a703	VYYVNDREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2355>:

a704.seq
 1 ATGAAAAAAA CCTGTTTCCA CTGCGGGCTG GACGTTCCCG AAAACCTGCA
 51 TCTGACCGTC CGTTACGAAA ACGAAGACCG CGAAACCTGC TGCGCCGTT
 101 GTCAGGCAGT CGCACAAAGC ATTATTGACG CGGGCTTGGG CAGTTATTAC
 151 AAACAACGCA CCGCCGACGC GCAAAAAACC GAGCTGCCCG CCCAAGAAAT
 201 CCTCGACCAA ATCCGCCTGT ACGACCTGCC CGAAGTCCAG TCCGACTTTG
 251 TGGAAACCCA CGCGGGCAGC CGCGAGGCGG TTTTAAATGCT CGGCGGCATC
 301 ACCTGCGCCG CTGCGCTCTG GCTGATCGAA CAGCAGCTTT TGCCTACAGA
 351 CGGCATCGTC CGCATCGACC TCAATTACAG CACGCACCGC TGCCTGCTCG
 401 TCTGGGACGA CGGCAAAATC CGCCTTCCG ACATTCTGTT GAAAAATCAGG
 451 CAGATAGGCT ACACCGCCGC ACCCTATGAC GCGCAAAAAA TCGAAGCCCG
 501 CAACCAAAAA GAACGCAAAC AATACATCGT CCGCCTCGCC GTTGCCGGGC
 551 TGGGGATGAT GCAGACGATG ATGTTTCGCG TGCCGACCTA CCTTTACGGC
 601 GGCACATCG AACCCGATTT CCTGCAAATC CTCCATTGGG GCGGCTTTTT
 651 AATGGTGCTG CCCGTCGTAT TCTATTGCGC CGTCCGTTTT TATCAAGCGC
 701 CGCTGCGCGA CTTGAAAAAC CGCCGCGTCG GCATGGATAC GCCGATTACC
 751 GTCGCCATCA TCATGACCTT TATCGCCGGC GTTTACAGCC TTGCGACAAA

```

801 TGGCGGGCAG GGGATGTATT TCGAATCCAT CGCGATGCTG CTGTTTTC
851 TGCTGGGCGG ACGCTTTATG GAACACATTG CCCGCCGTAA GGCAGGCGAT
901 GCGCGCCGAGA GGCTGGTGAA GCTGATTCCT GCGTTTGGCC ATCATATGCC
951 CGATTACCCC GATACGCAGC AAACCTGCGA GGCAGCTGTC STCAAATTGA
1001 AGGCGGGCGA TATCGTGCTG GTCAAACCGG GCGAAACCAT CCCCCTTGAC
1051 GGCACGGTGC TGGAAGGAAG CAGTGCCGTC AACGAATCTA TGCTGACCGG
1101 CGAGAGCCTG CCCGTCGCCA AAATGCCGTC TGAAAAAGTA ACCGCCGGCA
1151 CACTCAACAC GCAAAGCCCC CTGATTATAC GCACCGACCG CACCGCGCGC
1201 GGCACGCGAC TGTCGCACAT CGTCCGCTG CTCGACCGCG CCTTAGCGCA
1251 AAAACCGCGC ACTGCCGAGT TGGCGGAACA ATACGCCTCG TCTTTCATAT
1301 TCGGGCAACT CCTGTGTGCC GTCCCGCTCT TCATCGGCTG GACGCTGTAC
1351 GCGGACGCGC ACACCGCATT GTGGATTACC GTCGCCCTGC TGGTCATTAC
1401 CGTCCCTTGC GCCTTATCGC TTGCCACGCC GACCGCGCTG GCAGCTTCTA
1451 CCGGTACGCT GCGCGCGCAA GGTATTTTAA TCGGCGGAAA GCAGGCAATC
1501 GAAACCCTCG CCCAAACCAC CGACATCATC TTCGACAAAA CCGGCACGCT
1551 GACCCAAGGC AAACCCGCGG TCCGCCGTAT CTCATTGTTG AGAGGCACAG
1601 ACGAAGCCTT TGTTCGCG GTGGCGCAGG CTTTAGAACA ACAGTCCGAA
1651 CATCCCTTGC CCCGCCCAT CCTCAACTGC CGCATTTCAG ACGGCAGCGT
1701 CCGGACATC GCTATTAAAC AACGCCTCAA CCGCATCGGC GAAGGCGTGG
1751 GCGCGCAACT GACCGTCAAC GCGGAAACAC AGGTTTGGGC ATTGGGCAGG
1801 GCATCCTATG TCGCCGAAAT TTCAGGTAAG GAACCGCAA CAGAAGGCGG
1851 CCGCAGCGCG GTTTACCTCG GCAGTCAAAG CGGTTTCAA GCCGTGTTCT
1901 ACCTGCAAGA CCCGCTCAA GACAGCGCGG CGGAGGCGGT GCGGCAGTTG
1951 GCAGGCAAAA ACCTGACGCT GCACATTCTC AGCGCGGACC GTGAAACCGC
2001 CGTTGCCGAA ACCGCACGCG CCCTGGGTGT CGCGCACTAC CGCGCCCAAG
2051 CCATGCCCGA GGACAAACTG GAATACGTCA AAGCCTTGCA AAAAGAAGGG
2101 AAAAAAGTGC TGATGATAGG CGACGGCATC AACGACGCGC CCGTTTGGC
2151 GCAGGCGAGC GTATCCGCGC CCGCAGCGGG CGGACGGAT ATTGCGAGGG
2201 ACGGCGCGGA CATTGTGTTA TTGAACGAAG ATTTGCGTAC CGTCGCCAC
2251 CTGCTCGATC AGGCGCGGCG CACCGCCAAT ATTATCGGC AAAACCTGAT
2301 ATGGGCGGGC GCGTACAATA TCATTGCCGT ACCGCTTGCC GTTTTGGGCT
2351 ATGTCCAACC GTGGATAGCC GCACTGGGTA TGAGCTTCAG TTCGCTGGCG
2401 GTTTTGGGCA ACGCCCTGCG CCTTCACAAA CGGGGAAAA TGCAGTCTGA
2451 AAAAATGCCG TCCGAACAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2356; ORF 703>:

```

a704.pep
1 MKKTCFHCGL DVPENLHLTV RYENEDRET CAGCQAVAS IIDAGLSYY
51 KQRTADAQKT ELPPQEILDQ IRLYDLPEVQ SDFVETHGGT REAVLMLGGI
101 TCAACVWLIE QLLRTDGI V RIDLNYSTHR CRVWDDGKI RLSDILLKIR
151 QIGYTAAPYD AQKIEAANQK ERKQYIVRLA VAGLGMMQTM MFALPTYLYG
201 GDIEPDLQI LHWGGFLMVL FVVFYCAVPF YQGAALRDLKN RRVGMDTPIT
251 VAIIMTFIAG VYSLATNAGQ GMYFESIAML LFFLLGGRFM EHIARRKAGD
301 AAERLVKLIP AFCHHMPDYP DTQETCEAAV VKLKAGDIVL VKPGETIPVD
351 GTVLEGSSAV NESMLTGESL FVAKMPSEKV TAGTLNTQSP LIIRTDRTGG
401 GTRLSHIVRL LDRALAQKPR TAELAEQYAS SFIFGELLIA VPVFIGWTLY
451 ADAHTALWIT VALLVITCPC ALSLATPTAL AASTGTLARE GILIGGKQAI
501 ETLAQTDDII FDKTGTLTQG KPAVRRISLL RGTDEAFVLA VAQALEQQSE
551 HPLARAILNC RISDGSVPDI AIKQRLNRIG EGVGAQLTVN GETQVWALGR
601 ASYVAEISGK EPQTEGGGSA VYLSQSGFQ AVFYLDPLK DSAAEAVRQL
651 AGKNLTLHLI SGDRETAVAE TARALGVAHY RAQAMPEDKL EYVKALQKEG
701 KKVLMIGDGI NDAPVLAQAD VSAAGAGTD IARDGADIVL LNEDLRTVAH
751 LLDQARRTRH IIRQNLIWAG AYNIIAVPLA VLGYPQWIA ALGMSFSSLA
801 VLGNALRLHK RGKMQSEKMP SEQ*

```

m704/a704 99.8% identity in 823 aa overlap

```

          10      20      30      40      50      60
m704.pep MKKTCFHCGLDVPENLHLTVRYENEDRETCCAGCQAVASIIDAGLSYYKQRTADAQKT
          |||
a704      MKKTCFHCGLDVPENLHLTVRYENEDRETCCAGCQAVASIIDAGLSYYKQRTADAQKT
          10      20      30      40      50      60

          70      80      90     100     110     120
m704.pep ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLIEQQLRTDGI
          |||
a704      ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLIEQQLRTDGI

```

1132

	70	80	90	100	110	120
m704.pep	130	140	150	160	170	180
a704	130	140	150	160	170	180
m704.pep	190	200	210	220	230	240
a704	190	200	210	220	230	240
m704.pep	250	260	270	280	290	300
a704	250	260	270	280	290	300
m704.pep	310	320	330	340	350	360
a704	310	320	330	340	350	360
m704.pep	370	380	390	400	410	420
a704	370	380	390	400	410	420
m704.pep	430	440	450	460	470	480
a704	430	440	450	460	470	480
m704.pep	490	500	510	520	530	540
a704	490	500	510	520	530	540
m704.pep	550	560	570	580	590	600
a704	550	560	570	580	590	600
m704.pep	610	620	630	640	650	660
a704	610	620	630	640	650	660
m704.pep	670	680	690	700	710	720
a704	670	680	690	700	710	720
m704.pep	730	740	750	760	770	780
a704	730	740	750	760	770	780
m704.pep	790	800	810	820		
a704	790	800	810	820		

RIDLNYSTHRCRVVWDDGKIRLS DILLKIRQIGYTAAPYDAQKIEAANQKERKQYIVRLA
|||||
RIDLNYSTHRCRVVWDDGKIRLS DILLKIRQIGYTAAPYDAQKIEAANQKERKQYIVRLA
|||||
VAGLGMMQTMFALPTYLYGGDIEPDFLQILHWGGFLMVLPPVVFYCAVPFYQGALRDLKN
|||||
VAGLGMMQTMFALPTYLYGGDIEPDFLQILHWGGFLMVLPPVVFYCAVPFYQGALRDLKN
|||||
RRVGMDTPITVAIIMTFIAGVYSLATNAGQGMFYFESIAMLLFFLLGGRFMEHIAARRKAGD
|||||
RRVGMDTPITVAIIMTFIAGVYSLATNAGQGMFYFESIAMLLFFLLGGRFMEHIAARRKAGD
|||||
AAERLVKLI PAFCHHMPDYPDTQETCEAAVVKLRAGDIVLKPGETIPVDGTVLEGSSAV
|||||
AAERLVKLI PAFCHHMPDYPDTQETCEAAVVKLRAGDIVLKPGETIPVDGTVLEGSSAV
|||||
NESMLTGESLPVAKMPSEKVTAGTLNTQSPLIIRTDRTGGGTRL SHIVRLLDRALAQKPR
|||||
NESMLTGESLPVAKMPSEKVTAGTLNTQSPLIIRTDRTGGGTRL SHIVRLLDRALAQKPR
|||||
TAE LAEQYASSFI FGELLAVPVFIGWTL YADAHTALWITVALLVITCPCALSLATPTAL
|||||
TAE LAEQYASSFI FGELLAVPVFIGWTL YADAHTALWITVALLVITCPCALSLATPTAL
|||||
AASGTGLAREGILIGGKQAIETLAQTTDII FDKTGTLTQGGKPAVRRISLLRGTD EAFVLA
|||||
AASGTGLAREGILIGGKQAIETLAQTTDII FDKTGTLTQGGKPAVRRISLLRGTD EAFVLA
|||||
VAQALEQQSEHPLARAILNCRISDGSVPDIAIKQRLNRIGEGVGAQLTVNGETQVWALGR
|||||
VAQALEQQSEHPLARAILNCRISDGSVPDIAIKQRLNRIGEGVGAQLTVNGETQVWALGR
|||||
ASYVAEISGKEPQTEGGGS AVYLGSGSQGFQAVFYLT DPLKDSAAEAVRQLAGKNLTLHIL
|||||
ASYVAEISGKEPQTEGGGS AVYLGSGSQGFQAVFYLT DPLKDSAAEAVRQLAGKNLTLHIL
|||||
SGDRETAVAETARALGV AHYRAQAMPEDKLEYVKALQKEGKKVLMIGDGINDAPVLAQAD
|||||
SGDRETAVAETARALGV AHYRAQAMPEDKLEYVKALQKEGKKVLMIGDGINDAPVLAQAD
|||||
VSAAAAGGTDIARDGADIVLLNEDLRTVAHLLDQARRTRHII RQNLIWAGAYNIIAVPLA
|||||
VSAAAAGGTDIARDGADIVLLNEDLRTVAHLLDQARRTRHII RQNLIWAGAYNIIAVPLA
|||||
VLGYVQPWIAALGMSFSSSLAVLGNALRLHKRGKMQSEKMPSEQX
|||||
VLGYVQPWIAALGMSFSSSLAVLGNALRLHKRGKMQSEKMPSEQX
|||||

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2357>:

```
g705.seq
1  GTGTTCAATA ATTCCTtgc CTCTCIGCCG TTTATGACGG AAACACGCGC
51  TGATATGCTC ATCAGCGCGT TTTGGCCCAT GGTAAAGCC GGCTTTACAG
101 TGCTCTtgcc TTTGGCGATC GCTTCITTCG TTATCGGCAT GATTATGCGC
151 GTAGCCGTTG CTTTGGTAAG AATCATGCCT TCCGGCGGTA TTTCCAAAA
201 ATGCTTGTtG AAGCTGGTGG AATTTTATAT TTCCGTCGTT CGCGGTACGC
251 CGCTGTtGGT TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC GTCCGTCGGC
301 ATCTATATCA ATCCGATTCC CGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGCGGCATAC GCTTCCGAAA CCATACGCGC GCGGATTTTG TCCGTGCCGA
401 AAGGGCAGTG GGAAGCAGGT TTCTCCATCG GTATGACCTA TATGCAGACG
451 TTCCGCCGCA TCGTCGCACC GCAGGCATTC CGCGTCGCCG TTCCGCCGTT
501 GAGCAACGAG TTTATCGGCT TGTCAAAAA CACCTCGCTT GCCGCCGTGG
551 TAACGGTAAC GGAGCTTTTC CGTGTCCGAC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCTGTCTA TATCGAAGCT GCATTGTTTT ATTGGTGTtT
651 CTGTAAGTG CTGTTTTTGA TTCAGGCGCG TTTGAAAAA CGTTTCGACC
701 GTTATGTCGC CAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2358; ORF 705>:

```
g705.pep
1  VFNNFLASLP FMTETRADML ISAFWPMVKA GFTVSLPLAI ASFVIGMIIA
51  VAVALVRIMP SGGIFQKCLL KLVEFYISVV RGTPLLVLV IVFYGLPSVG
101 IYINPIPAAI IGFSNLVGAY ASETIRAAIL SVPKGQWEAG FSIGMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTELF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCKV LFLIQARLEK RFDRYVAK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2359>:

```
m705.seq
1  GTGTTCAATA ATTCCTTGC TTGCTGCCG TTTATGACGG AAACACGCGC
51  CGATATGATT GTCAGCGCGT TTTTGCCATAT GGTCAAAGCC GGCTTCGCGG
101 TCTCTCTGCC TTTGGCGGCA GCTTCITTCG TTATCGGTAT GATGATTGCG
151 GTAGCCGTGG CTTTGGTGGC GATTATGCCG GCCGGCGGCA TCGTGCAGAA
201 AATCCTGCTG AAATTGGTGG AATTTTATAT TTCCGTCATT CGCGGTACGC
251 CGCTGTtGGT TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC TTCCGTCGGC
301 ATCTATATCG ACCCGATTCC TGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGCGGCATAC GCTTCCGAAA CCATACGCGC GGCAATTTTG TCCGTACCTA
401 AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
451 TTCCGCCGCA TTGTCGCGCC GCAGGCATTC CGCGTTGCCG TGCCGCCTTT
501 GAGCAACGAG TTTATCGGTT TGTTAAAAA CACCTCGCTC GCGGCAGTCG
551 TGACGGTAAC GGAATTATTC CGCGTCGCGC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCCGTCTA TATCGAAGCT GCTTTGTTT ACTGGTGTtT
651 TTGTAAGTG CTGTTCTTGA TTCAGGCGCG TTTGAAAAA CGTTTCGACC
701 GCTACGTCGC CAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2360; ORF 705>:

```
m705.pep
1  VFNNFLASLP FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGMMIA
51  VAVALVRIMP AGGIVRKILL KLVEFYISVI RGTPLLVLV IVFYGLPSVG
101 IYIDPIPAAI IGFSNLVGAY ASETIRAAIL SVPKGQWEAG FSIGMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTELF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCKV LFLIQARLEK RFDRYVAK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 705 shows 95.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. gonorrhoeae*:

```
m705/g705    95.0% identity in 238 aa overlap

          10      20      30      40      50      60
m705.pep    VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
              ::|||  |||||:|||||  |||||:|||||
g705         VFNNFLASLPFMTETRADMLISAFWPMVKAGFTVSLPLAIASFVIGMIIAVALVRIMP
              10      20      30      40      50      60

          70      80      90     100     110     120
m705.pep    AGGIVRKILLKLVEFYISVIRGTPLLVLVIVFYGLPSVGIYIDPIPAAIIGFSNLVGAY
              :|||  :|  |||||:|||||:|||||:|||||:|||||:|||||
```

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```

g705      SGGIFQKCLKLVEFYISVVRGTPLLVQLVVFYGLPSVGIYINPIAAIIGFSLNVGAY
           70      80      90      100     110     120

           130     140     150     160     170     180
m705.pep  ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           |||||
g705      ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130     140     150     160     170     180

           190     200     210     220     230     239
m705.pep  AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLIARLEKRFDRYVAKX
           |||||
g705      AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLIARLEKRFDRYVAKX
           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2361>:

```

a705.seq
1  GTGTTCATAA ATTCCTTGC TTCGCTGCCG TTTATGACGG AACACGCGC
51  CGATATGATT GTCAGCGCGT TTTTGCCTAT GGTCAAAGCC GGCTTCGCGG
101 TCTCTCTGCC TTTGGCGGCA GCTTCTTTCC TTATCGGTAT GATGATTGCG
151 GTAGCCGTGG CTTTGGTGCG GATTATGCCC GCCGGCGGCA TCGTGCGGAA
201 AATCCTGCTG AAATGGTGG AATTTTATAT TTCCGTCATT CGCGGTACGC
251 CGCTGTTGGT TCAGCTTGTG ATTGTGTTT ACGGGCTGCC TTCCGTCGCG
301 TTCCGCTCGC ACCCGATTCC TGCCGCCATC ATCGGCTTT CGCTCAATGT
351 CGGCGCATAT GCTTCCGAAA CCATACGCGC GGCAATTTG TCCGTACCGA
401 AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
451 TTCCGCCGCA TCGTCGCGCC GCAGGCATTT CGCGTTGCCG TGCCGCCTTT
501 GAGCAACGAG TTTATCGGTT TGTTTAAAAA CACCTCGCTC GCGGCAGTCG
551 TGACGGTAAC GGAATTATTC CGCGTCGCGC AGGAAACGCG AAACCGCACT
601 TATGACTTTT TGCCCGTCTA TATCGAAGCC GCTTTGGTTT ACTGGTGT
651 TTGTAAAGTG CTGTTCCTGA TTCAGGCGCG TTTGAAAAA CGTTTCGACC
701 GCTACGTCGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2362; ORF 705.a>:

```

a705.pep
1  VFNNFLASLP FMTETRADMI VSAFLPNVKA GFAVSLPLAA ASFVIGMMIA
51  VAVALVRMP AGGIVRKILL KLVEFYISVI RGTPLLVLV IVFYGLPSVG
101 IYIDPIAAI IGFSNLVGAY ASETIRAAIL SVPKQWEAG FSIGMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTELF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCVK LFLIARLEK RFDRYVAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 705 shows 100.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. meningitidis*:

a705/m705 100.0% identity in 238 aa overlap

```

           10      20      30      40      50      60
a705.pep  VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
           |||||
m705      VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
           10      20      30      40      50      60

           70      80      90      100     110     120
a705.pep  AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIAAIIGFSLNVGAY
           |||||
m705      AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIAAIIGFSLNVGAY
           70      80      90      100     110     120

           130     140     150     160     170     180
a705.pep  ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           |||||
m705      ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130     140     150     160     170     180

           190     200     210     220     230     239
a705.pep  AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLIARLEKRFDRYVAKX
           |||||
m705      AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLIARLEKRFDRYVAKX
           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2363>:

g706.seq

```

1 ATGAATCCTT CGCAACGCAA ACGCCTTTCC GgccGCTGGC TCAACTCCTA
51 CGAACGCTAc cGCCaccGCC GCCTCATACA TGCCGTGCGG CTCGGCggaa
101 cctgCCTGTT CGCCACCGCA CTCGCCCGgc tACTCCACCT CCAacacggc
151 gAATGGATAG GGatgaCCGT CTTGCTCGTC CTCGGCATGC TCCAGTTCCA
201 AGGCgcgatt tActccaacg cgggtgGAacg taTGctcggg acggtcatcg
251 ggcctgGGCGC GGGTTTGGgc gTTTTATGGC TGAACGAGCA TTAttccac
301 ggcaacCTcc tctttacact gaccatcggc acggcaacgc cactggccgg
351 ctGGGCGGCG GTCCGCAAAA acggctacgt cctatgctg GCGGGGctgA
401 CGATGTGCAT gctcatcggc gACAACGGCA GCGAATGGCT CGACAGCGGC
451 CTGATGCGCG CGATGAACGT CCTCATCGGC GCCGCCATCG CCATGCGCGC
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGTATGA CGCGCGAACG TTTGGAGCAG AATATGGTCA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCAG CCACCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC TCCATGATGG AAGCCATGCA GCACGCCAC
751 CGCAAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 CGAATCTCCC AAACTCAACG GCAGCGAAAT CCGGCTGCTC GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGCGCCCT CATCAACGGC
901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG
1101 CCTGCTTGA ACACGGGAAC ACGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2364; ORF 706.ng>:

g706.pep

```

1 MNSSQRKRLS GRWLSYERY RRRRLIHAVR LGGTVLFAFA LARLLHLQHG
51 EWIGMTVFVV LGMLQFQGA YSNAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWLD SG
151 LMRAMNVLIG AAIATAAKL LPLKSTLMWR FMLADNLADC SKMIAEISNG
201 RRMTRERLEQ NMVKMRQINA RMVKSRSILA ATSGESRISP SMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNGSEIRLL DRHFTLLQTD LQQTVALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
351 TRRWLDAHE RQHLRQSLLE TREHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2365>:

m706.seq

```

1 ATGAACACCT CGCAACGCAA CCGCCTCGTC AGCCGCTGGC TCAACTCCTA
51 CGAACGCTAC CGCTACCGCC GCCTCATCCA CGCCGTCCGG CTCGGCGGGG
101 CCGTCCTGTT CGCCACCGCC TCCGCCCGGC TGCTCCACCT CCAACACGGC
151 GAGTGGATAG GGATGACCGT CTTGCTCGTC CTCGGCATGC TCCAGTTTCA
201 AGGGGCGATT TACTCCAAGG CGGTGGAACG TATGCTCGGC ACGGTCATCG
251 GGCTGGGCGC GGGTTTGGGC GTTTTATGGC TGAACGAGCA TTATTTCCAC
301 GGCAACCTCC TCTTCTACCT CACCGTCGGC ACGGCAAGCG CACTGGCCGG
351 CTGGGCGGCG GTCCGCAAAA ACGGCTACGT CCCTATGCTG GCAGGGCTGA
401 CGATGTGTAT GCTCATCGGC GACAACGGCA GCGAATGGCT CGACAGCGGA
451 CTCATGCGCG CCATGAACGT CCTCATCGGC GCGGCCATCG CCATCGCCGC
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGCAACCTG GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGCATGA CCCGCGAACG CCTCGAGGAG AACATGGCGA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCAG CCATCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC GCCATGATGG AAGCCATGCA GCACGCCAC
751 CGTAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AAACTCAACG GCAGCGAAAT CCGGCTGCTT GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGTCGCCCT TATCAACGGC
901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG
1101 CCTGCTTGA ACACGGGAAC ACGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2366; ORF 706>:

m706.pep

```

1 MNTSQRNRLV SRWLSYERY RYRRLIHAVR LGGAFLFAFA SARLLHLQHG
51 EWIGMTVFVV LGMLQFQGA YSKAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWLD SG
151 LMRAMNVLIG AAIATAAKL LPLKSTLMWR FMLADNLADC SKMIAEISNG
201 RRMTRERLEE NMAKMRQINA RMVKSRSILA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNGSEIRLL DRHFTLLQTD LQQTVALING

```


301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMROE ISALVILLQR
 351 TRRKWLDAHE RQHLRQSLLE TREHG*

m706/g706 96.5% identity in 375 aa overlap

	10	20	30	40	50	60
m706.pep	MNTSQRNRLVSRWLN	SYERYRYRRLIHAVRL	GGAVLFATASARLLHL	QHGEWIGMTVFVV		
g706	MNSSQRKRLSGRWLN	SYERYRRLIHAVRL	GGTTLFATALARLLHL	QHGEWIGMTVFVV		
	10	20	30	40	50	60
	70	80	90	100	110	120
m706.pep	LGMLQFQGAISKAVER	MLGTVIGLGAGLVWLN	QHGFHGNLLFYLT	VTASALAGWAA		
g706	LGMLQFQGAISNAVER	MLGTVIGLGAGLVWLN	QHGFHGNLLFYLT	IGTASALAGWAA		
	70	80	90	100	110	120
	130	140	150	160	170	180
m706.pep	VGKNGYVPMLAGLTM	CMLIGDNGSEWLD	SGLMRAMNVLIGAA	IAIAAAKLLPLK	STLMWR	
g706	VGKNGYVPMLAGLTM	CMLIGDNGSEWLD	SGLMRAMNVLIGAA	IAIAAAKLLPLK	STLMWR	
	130	140	150	160	170	180
	190	200	210	220	230	240
m706.pep	FMLADNLADCSKMAE	ISNGRRMTRERLEEN	MAKMRQINARMVKS	RSRSLAATSGES	RISP	
g706	FMLADNLADCSKMAE	ISNGRRMTRERLEQ	NMVKMRQINARMVKS	RSRSLAATSGES	RISP	
	190	200	210	220	230	240
	250	260	270	280	290	300
m706.pep	AMMEAMQHAHRKIVN	TTELLTTAAKLQSP	KLNGSEIRLLDRH	FTLLQTDLOQT	VALING	
g706	SMMEAMQHAHRKIVN	TTELLTTAAKLQSP	KLNGSEIRLLDRH	FTLLQTDLOQT	AALING	
	250	260	270	280	290	300
	310	320	330	340	350	360
m706.pep	RHARRIRIDTAINPE	LEALAEHLHYQWQGF	LWLSTNMROEISAL	VILLQTRRKWLDA	HE	
g706	RHARRIRIDTAINPE	LEALAEHLHYQWQGF	LWLSTNMROEISAL	VILLQTRRKWLDA	HE	
	310	320	330	340	350	360
	370					
m706.pep	RQHLRQSLLETREHG	X				
g706	RQHLRQSLLETREHG	X				
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2367>:

a706.seq

1	ATGAACACCT	CGCAACGCAA	CGGCCTCGTC	AGCCGCTGGC	TCAACTCCTA
51	CGAACGCTAC	CGCTACCGCC	GCCTCATCCA	CGCCGTCCGG	CTCGGCGGGG
101	CCGTCCTGTT	CGCCACCGCC	TCCGCCCGGC	TGCTCCACCT	CCAACACGGC
151	GAGTGGATAG	GGATGACCGT	CTTCGTCGTC	CTCGGCATGC	TCCAGTTTCA
201	AGGGGCGATT	TACTCCAAGG	CGGTGGAACG	TATGCTCGGC	ACGGTCATCG
251	GGCTGGGCGC	GGTTTGCGC	GTTTTATGGC	TGAACCAGCA	TTATTTCCAC
301	GGCAACCTCC	TCTTCTACCT	CACCGTCGGC	ACGGCAAGCG	CACTGGCCGG
351	CTGGGCGGCG	GTCGGCAAAA	ACGGCTACGT	CCCTATGCTG	GCGGGGCTGA
401	CGATGTGCAT	GCTCATCGGC	GACAACGGCA	GCGAATGGTT	CGACAGCGGC
451	CTGATGCGCG	CGATGAACGT	CCTCATCGGC	GCGGCCATCG	CCATCGCCGC
501	CGCAAACTG	CTGCCGCTGA	AATCCACACT	GATGTGGCGT	TTCTGCTTG
551	CCGACAACCT	GACCGACTGC	AGCAAAATGA	TTGCCGAAAT	CAGCAACGGC
601	AGGCGCATGA	CCCGCGAACG	CCTCGAAGAG	AACATGGCGA	AAATGCGCCA
651	AATCAACGCA	CGCATGGTCA	AAAGCCGCG	CCACCTCGCC	GCCACATCGG
701	CGGAAAGCCG	CATCAGCCCC	GCCATGATGG	AAGCCATGCA	GCACGCCCAC
751	CGTAAAATTG	TCAACACCAC	CGAGTGCTC	CTGACCACCG	CCGCCAAGCT
801	GCAATCTCCC	AAACTCAACG	GCAGCGAAAT	CCGGCTGCTT	GACCGCCACT
851	TCACACTGCT	CCAAACCGAC	CTGCAACAAA	CCGTGCGCCT	TATCAACGGC

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```

901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAG
1101 CCTGCTGAA ACACGGGAAC ACAGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2368; ORF 706.a>:

```

a706.pep
1  MNTSQNRNLV SRWLSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
51 EWIGMTVFVV LGMLQFGAI YSKAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTVG TASALAGWAA VGKNGYVPM LAGLTMCMLIG DNGSEWFD SG
151 LMRAMNVLIG AAIAIAAAKL LPLKSTLMWR FMLADNLTDC SKMIAEISNG
201 RRMTRERLEE NMAKMRQINA RMVKSRS HLA ATSGESRISP AMMEAMQHAH
251 RKIVNTELL LTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTVALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
351 TRRKWLDAHE RQHLRQSLE TREHS*

```

a706/m706 99.5% identity in 374 aa overlap

a706.pep	10	20	30	40	50	60
m706	10	20	30	40	50	60
a706.pep	70	80	90	100	110	120
m706	70	80	90	100	110	120
a706.pep	130	140	150	160	170	180
m706	130	140	150	160	170	180
a706.pep	190	200	210	220	230	240
m706	190	200	210	220	230	240
a706.pep	250	260	270	280	290	300
m706	250	260	270	280	290	300
a706.pep	310	320	330	340	350	360
m706	310	320	330	340	350	360
a706.pep	370					
m706	370					

g707.seq not found

g707.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2369>:

1138

m707.seq

```

1  ATGGAAATTA TTAACGATGC AGAACTTATC CGTTCCATGC AGCGTCAGCA
51  GCACATAGAT GCTGAATTGT TAACTGATGC AAATGTCCGT TTCGAGCAAC
101 CATTTGGAGAA GAACAATTAT GTCTGAGTG AAGATGAAAC ACCGTGTACT
151 CGGGTAAATT ACATTAGTTT AGATGATAAG ACGGTGCGCA AATTTCTTT
201 TCTTCCTTCT GTGCTCATGA AAGAAACAGC TTTTAAAACT GGGATGTGTT
251 TAGGTTCCAA TAATTTGAGC AGGCTACAAA AAGCCGCGCA ACAGATACTG
301 ATCGTGCGTG GCTACCTCAC TTCCCAAGCT ATTATCCAAC CACAGAATAT
351 GGATTCGGGA ATTCTGAAAT TACGGGTATC AGCAGGCGAA ATAGGGGATA
401 TCCGCTATGA AGAAAAACGG GATGGGAAGT CTGCCGAGGG CAGTATTAGT
451 GCATTCAATA ACAAAATTCC CTTATATAGG AACAAAATTC TCAATCTTCG
501 CGATGTAGAG CAGGGCTTGG AAAACCTGCG TCGTTTGGCG AGTGTTAAAA
551 CAGATATTCA GATTATACCG TCCGAAGAAG AAGGCAAAAG CGATTTACAG
601 ATCAAATGGC AGCAGAATAA ACCCATACGG TTCAGTATCG GTATAGATGA
651 TGCGGGCGGC AAAACGACCG GCAATATCA AGGAAATGTC GCTTTATCGT
701 TCGATAACCC TTTGGGCTTA AGCGATTGT TTTATGTTTC ATATGGACGC
751 GGTTCGGCGC AAAAAACGGA CTTGACTGAT GCCACCGGTA CGGAAACTGA
801 AAGCGGATCC AGAAGTTACA GCGTGCATTA TTCGGTGCCC GTAAAAAAAT
851 GGCTGTTTTC TTTTAATCAC AATGGACATC GTTACCAGA AGCAACCGAA
901 GGCTATTCCG TCAATTACGA TTACAACGGC AAACAATATC AGAGCAGCCT
951 GGCGCCGAG CGCATGCTTT GCGGTAACAG ACTTCATAAA ACTTCAGTCG
1001 GAATGAAATT ATGGACACGC CAACCTATA AATACATCGA CGATGCCGAA
1051 ATCGAAGTAC AACGCCGCCG CTCGTCAGGC TGGGAAGCCG AATTGCGCCA
1101 CCGTGCTTAC CTCAACCGTT GGCAGCTTGA CGGCAAGTTG TCTTACAAAC
1151 CGGSGACCGG CATGCCCAA AGTATGCCTG CACCGGAAGA AAACGGCGGC
1201 GATATTCTTC CAGGTACATC TCGTATGAAA ATCATTACTG CCAGTTTGGG
1251 CGCAGCCGCC CCATTTATTT TAGGCAAAAC GCAGTTTTC TACGCAACCG
1301 CCATTCAAGC TCAATGGAAC AAAACGCCGT TGGTTGCCCA AGATAAATTG
1351 TCAATCGGCA GCCGCTACAC CGTTCGCGGA TTTGATGGGG AGCAGAGTCT
1401 TTTGGGAGAG CGAGGTTTCT ACTGGCAGAA TACTTTAACT TGGTATTTTC
1451 ATCCGAACCA TCAGTTCTAT CTCGGTGCGG ACTATGGCCG CGTATCTGGC
1501 GAAAGTGCAC AATATGTATC GGGCAAGCAG CTGATGGGTG CAGTGGTCGG
1551 CTTGAGAGGA GGGCATAAAG TAGGCGGTAT GTTTGCTTAT GATCTGTTTG
1601 CCGGCAAGCC GCTTCATAAA CCCAARGGCT TTCAGACGAC CAACACCGTT
1651 TACGGCTTCA ACTTGAATTA CAGTTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2370; ORF 707>:

m707.pep

```

1  MEIINDAELI RSMQRQOHID AELLTDANVR FEQPLEKNNY VLSEDETPCT
51  RVNYISLDDK TVRKFSFLPS VLMKETAFKT GMCLGSNNLS RLQKAAQQIL
101 IVRGYLTSQA IIQPNMDSG ILKLRVSAGE IGDRIYEER DGKSAEGSIS
151 AFNNKFPLYR NKILNLRDVE QGLENLRRLP SVKTDIQIIP SEEEGKSDLQ
201 IKWQONKPIR FSGIDDAGG KTTGKYQGNV ALSFDNPLGL SDFYVSYGR
251 GLAHKTDLTD ATGTETESGS RSYSVHYSVP VKKWLFSFNH NGRHYHEATE
301 GYSVNYDYNG KQYQSSLAEE RMLWRNRLHK TSVGMKLWTR QYKYIDDAE
351 IEVQRRRSAG WEAE LRHRAY LNRWQLDGKL SYKRGTMGRQ SMPAPEENG
401 DILPGTSRNK IITASLDAEA PFILGRQOFF YATAIQAOWN KTLPLVAQDKL
451 SIGSRYTVRG FDGEQSLFGE RGFYQWNTLT WYFHPNHOFY LGADYGRVSG
501 ESAQYVSGEQ LMGAVVGFRG GHKVGCMFAY DLFAGKPLHK PKGFQNTNTV
551 YGFNLNYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2371>:

a707.seq

```

1  NTGAAAGAAA CAGCTTTTAA AACTGGGATG TGTTTAGGTT CCAATAATTT
51  GAGCAGGCTA CAAAAAGCCG CGCAACAGAT ACTGATTGTG CGTGGCTACC
101 TCACTTCCCA AGCTATTATC CAACCACAGA ATATGGATTG GGAATTCTG
151 AAATTACGGG TATCAGCAGG CGAAATAGGN GATATCCGCT ATGAAGAAAA
201 ACGGGATGNG AAGTCTGCCG AGGGCAGTAT TAGTGCATTC AATAACAAAN
251 TTCCCTTATA TAGGAACAAA ATTCCTCAATC TTCGCGATGT AGAGCAGGGC
301 TTGGA AAAACC TGCGTCGTTT GCCGAGTGTT AAAACAGATA TTCAGATTAT
351 ACCGTCCGAA GAAGAAGGCA AAAGCGATT ACAGATCAAA TGGCAGCAGA
401 ATAAACCCAT ACGGTTTCA GTATCGGTATAG ATGATGCGGG CGGCAAAACG
451 ACCGGCAAAAT ATCAAGGAAA TGTCGCTTTA TCGTNCGATA ACCCTTTGGG
501 NNTAAGCGAT TNGTTTATG TTTTCATATGG ACGCGGTTTG GTGCACAAAA
551 CGGACTTGAC TGNTGCCACC GGTACGGAAA CTGAAAGCGG ATCCAGAAGT
601 TACAGCGTGC ATTATTCGGT GNNCGTAAAA AAATGGCTGT TTTCTTTTAA
651 TCACAAATGGA CATCGTTACC ACGAAGCAAC CGAAGGCTAT TCCGTCAATT
701 ACGATTACAA CGGCAACAAA TATCAGAGCA GCCTGGCCGC CGAGCGCATG

```

1139

```

751 CTTTGGNNNN NNAGNTTTCN TNAAACTTCA GTCNGAATGA AATTATGGAC
801 ACGCCAAACC TATAAATACA TCGACGATGC CGAAATCGAA GTGCAACGCC
851 GCGGCTCTGC AGGCTGGGAA GCCGAATTGC GCCACCGTGC TTACCTCNAC
901 CGTTGGCAGC TTGACGGCAA GTTGTCTTAC AAACGCGGGA CCGGCATGCG
951 CCAAAGTATG CCCGCACCTG AAGAAAACGG CGGCGGTACT ATTCCAGNCA
1001 NATCCCGTAT GAAAATCATA ACCGCCGGAT TGGATGCAGC GGCCCCGTNT
1051 ATGTTGGGCA AACAGCAGTT TTTCTACGCA ACCGCCATTG AAGCTCAATG
1101 GAACAAAACG CCTTTGGTTG CCCAAGACAA GTTGTCTATC GGCAGCCGCT
1151 ACACCGTTCG CGGATTGAT GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT
1201 TTCTACTGGC AGAATACTTT AACTTGGTAT TTTCATCCGA ACCATCAGTT
1251 CTATCTCGGT GCGGACTATG GCCGCGTATC TGGCGAAAGT GCACATATG
1301 TATCGGCGAA GCAGCTGATG GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT
1351 AAAGTAGGCG GTATGTTTGC TTATGATCTG TTTGCCGGCA AGCCGCTTCA
1401 TAAACCCAAA GGCTTTCAGA CGACCAACAC CGTTTACGGC TTCAACTTGA
1451 ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2372; ORF 707.a>:

```

a707.pep
1  XKETAFTKGM CLGSNNLSRL QKAAQQILIV RGYLTSQAI QPQNMDSGIL
51  KLRVSAGEIG DIRYEEKRDX KSAEGSISAF NNXPLYRNK ILNLRDVEQG
101 LENLRLPSV KTDIQUIPSE EEGKSDLQIK WQONKPIRFS IGIDDAGGKT
151 TGKYQGNVAL SXDNPLGLSD XFYVSYGRGL VHKTDLTXAT GTETESGSR
201 YSVHYSVXVK KWLFSFNHNG HRYHEATEGY SVNYDYNKQ YQSSLAER
251 LWXXXFXXTS VXMKLWTRQT YKYIDDAEIE VQRRRSAGWE AELRHAYLX
301 RWQLDGKLSY KRGTMQRQSM PAPEENGGGT IPXXSRMKII TAGLDAAAPX
351 MLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD GEQSLFGERG
401 FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM GAVVGFRGGH
451 KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

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a707/m707 95.3% identity in 486 aa overlap

```

a707.pep                                10      20      30
                                XKETAFTKGMCLGSNNLSRLQKAAQQILIVR
                                |||
m707      EDETPCTRVNYISLDDKTVRKFSFLPSVLMKETAFKTMCLGSNNLSRLQKAAQQILIVR
                                50      60      70      80      90     100

                                40      50      60      70      80      90
a707.pep      GYLTSQAIQPPQNMDSGILKLRVSAGEIGDIRYEEKRDXKSAEGSISAFNNKXPLYRNKI
                                |||
m707      GYLTSQAIQPPQNMDSGILKLRVSAGEIGDIRYEEKRDGKSAEGSISAFNNKXPLYRNKI
                                110     120     130     140     150     160

                                100     110     120     130     140     150
a707.pep      LNLRDVEQGLLENLRLPSVKTDIQUIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
                                |||
m707      LNLRDVEQGLLENLRLPSVKTDIQUIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
                                170     180     190     200     210     220

                                160     170     180     190     200     210
a707.pep      GKYYQGNVALSXDNPGLGLSDXFFYVSYGRGLVHKTDLTXATGTETESGSRYSVHYSVXVKK
                                |||
m707      GKYYQGNVALSFDNPGLGLSDLFYVSYGRGLAHTDLTCTGTETESGSRYSVHYSVPVKK
                                230     240     250     260     270     280

                                220     230     240     250     260     270
a707.pep      WLFSFNHNGHRYHEATEGYSVNYDYNKQYQSSLAERMLWXXXFXXTSVXMKLWTRQTY
                                |||
m707      WLFSFNHNGHRYHEATEGYSVNYDYNKQYQSSLAERMLWRNRLHKTSGVMKLWTRQTY
                                290     300     310     320     330     340

                                280     290     300     310     320     330
a707.pep      KYIDDAEIEVQRRRSAGWEAELRHAYLXRWQLDGKLSYKRGTMQRQSMPEENGGGTI
                                |||
m707      KYIDDAEIEVQRRRSAGWEAELRHAYLNRWQLDGKLSYKRGTMQRQSMPEENGGDIL
                                350     360     370     380     390     400

```

1140

```

          340      350      360      370      380      390
a707.pep  PXXSRMKIITAGLDAAAPXMLGKQOFFYATAIQAQWNKTPLVAQDKLSIGSRYTVRGFDG
m707      PGTSRMKIITASLDAAAPFILGKQOFFYATAIQAQWNKTPLVAQDKLSIGSRYTVRGFDG
          410      420      430      440      450      460

          400      410      420      430      440      450
a707.pep  EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRRGGHK
m707      EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRRGGHK
          470      480      490      500      510      520

          460      470      480
a707.pep  VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX
m707      VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX
          530      540      550      560

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2373>:

```

g708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TTCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCGA TGGAAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCAACGGC AAGTATTGAA GATGCCTTGA AATCGAACCC
201 TAAAAACGAA CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACCTAC GGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CTTGCCGAAT CTATGGCATA TTTCGACAAA GCTCTGGCCG
401 ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGTATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAACGTTT
501 CCTCGCGGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGTGCA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCAAAATTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ACCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2374; ORF 708.ng>:

```

g708.pep
1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQATASIE DALKSNEPNE LAWLVRAEIY QYLKVNDAQ ESFRQALSIK
101 PDSAEINNNY GWFLCGRLNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSIAA QPQFPFAFKE LARTKMLAGQ LGDADYYFKR
201 YQSRVEVLQA DDLGLGWKIA KALGNVQAAY EYEAQLQANF PYSEELQTVL
251 TGG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2375>:

```

m708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTCG TTCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCGACGGC AAGTATTGAA GACGCCCTGA AATCGGACCC
201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACCTAC GGTGGTTTCC TATGCGGCAG
351 GCTCAACCGC CTTGCCGAAT CTATGGCATA TTTCGACAAA GCTCTGGCCG
401 ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAACGTTT
501 CCTCGCGGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATCATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCGAAATTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ACCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2376; ORF 708>:

m708.pep

1141

```

1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQATASIE DALKSDPKNE LAWLVRAEIY QYLVNDKAQ ESFRQALSIK
101 PDSAEINNNY GWFLCGRILNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSIAA QPQFPAPFKE LARTKMLAGQ LGDADYFFKK
201 YQSRVEVLQA DDLLLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 TGQ*

```

m708/g708 99.2% identity in 253 aa overlap

```

              10      20      30      40      50      60
m708.pep      MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
g708           MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
              10      20      30      40      50      60

              70      80      90     100     110     120
m708.pep      DALKSDPKNELAWLVRAEIYQYLVNDKAQESFRQALSIKPDSAEINNNYGWFLCGRILNR
g708           DALKSNPKNELAWLVRAEIYQYLVNDKAQESFRQALSIKPDSAEINNNYGWFLCGRILNR
              70      80      90     100     110     120

              130     140     150     160     170     180
m708.pep      PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPQFPAPFKE
g708           PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPQFPAPFKE
              130     140     150     160     170     180

              190     200     210     220     230     240
m708.pep      LARTKMLAGQLGDADYFFKKYQSRVEVLQADDLLGWKIAKALGNAQAAYEYEAQLQANF
g708           LARTKMLAGQLGDADYFFKKYQSRVEVLQADDLLGWKIAKALGNVQAAYEYEAQLQANF
              190     200     210     220     230     240

              250
m708.pep      PYSEELQTVLTGQX
g708           PYSEELQTVLTGQX
              250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2377>:

```

a708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TCCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTCT GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAAATATAT GCGCGGTCAG
151 GACTACCGTC AGGNGACGGC AAGTATTGAA GACGCCTTGA AATCAGACCC
201 TAAAAACGAG CTGCGCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGNCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACACT NGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA GCCCTGGCCG
401 ACCCCACNTA CCCGANCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTC
501 CCTCGCCGCC CAGCCGCAGT TCCCACCGCG ATTTAAAGAA CTGGCGCGCA
551 CCAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTGTC TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCGAATTTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ATCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2378; ORF 708.a>:

```

a708.pep
1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQXTASIE DALKSDPKNE LAWLVRAEIY QYLVNDKAQ ESFRQXLSIK
101 PDSAEINNNY XWFLCGRILNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSIAA QPQFPAPFKE LARTKMLAGQ LGDADYFFKK
201 YQSRVEVLQA DDLLLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 IGQ*

```

a708/m708 98.0% identity in 253 aa overlap

1142

	10	20	30	40	50	60
a708.pep	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQXTASIE					
m708	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQXTASIE					
	10	20	30	40	50	60
a708.pep	DALKSDPKNELAWLVRAEIQYLKVNDKAQESFRQXLSIKPDSAEINNXYWFLCGRNLNR					
m708	DALKSDPKNELAWLVRAEIQYLKVNDKAQESFRQALSIPKPSAEINNXYWFLCGRNLNR					
	70	80	90	100	110	120
a708.pep	PAESMAYFDKALADPTYXPYPIANLNKIGICSAKQGQFGLAEAYLKRSALAAQPQFPFAFKE					
m708	PAESMAYFDKALADPTYTPYPIANLNKIGICSAKQGQFGLAEAYLKRSALAAQPQFPFAFKE					
	130	140	150	160	170	180
a708.pep	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
m708	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
	190	200	210	220	230	240
a708.pep	PYSEELQTVLIGQX					
m708	PYSEELQTVLTGQX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2379>:

g709.seq

```

1  ATGTTTGCTT TCAAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC
51  CGTCGTCGTC GCTCTGATTG CCGCAATGGG CTATACCATC ATTTCAATTGG
101 AGTGCGTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGG CAGGGATGAT
201 AGGCGCGTTG AATCAGGGTA TGGGCGCGGT TTACCTGTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGGCTGAT TTCCCCGACT TATTTTATTT TTTCCGCGCTT
351 CGCGCTGTGT TCCGTCATCG GCGTGTCCAT CCGCAGCAGC CTGACCGCCT
401 GCGCCACTGT CGGCGTTGCC TTTATGGGGA TGGCGCGGCG GTTTCAGGCC
451 GATATGGCCA TGACGgcggg cgcgattgTT tccggtGTGT TTTTCGGCGA
501 TAAATGTCCA CCGCTTTCCG ACACCACGGG CATTTCGCGC TCCATCGTCG
551 GTATCGACCT GTTTGAACAC ATCAAAAACA TGATGTACAC CACCATCCCT
601 CGGTGGCTTA TCAGCGCGGC ACTGATGCTT TGGCTTCTTC CCAGCGTCGC
651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACGGCTAT TCGCTGATTC CGTTTGCACT GTTGGTCGTT
751 TTGGCATTGA TCGCGGTCAA TGCCGTGGTC GCCATGCTCT TTACCGTCAT
801 TGCCGCCGTT GCCGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC
851 TCGGCGCGTG GTTTTATGGC GGCTACAAAC TCGAAGGCGA AGCGTTTAAA
901 GACATTGCCA AACTGATTTC GCGCGGCGGC TTGGAGAGTA TGTTCCTTAC
951 GCAGACCATC GTTATCCTCG GTATGAGTTT GGGCGGGCTG CTGTTTGCGC
1001 TCGGTGTGAT TCCTTCCTTG CTGGAGGCGG TCCGTACCTT CTTGACGAAT
1051 GCGCGACGCG CGACGTTTCA GCTTGCCATG ACTTCGGTCG GGGTCAATTT
1101 CCTGATTGGA GAGCAATATT TGAGCATCCT GCTTTCGGGA GAAACGTTCA
1151 AACCCTTTTA CGACAACTC GGCTGCATT CGTGCAACCT GTCGCGGACT
1201 CTGGAAGATG CGGGGACGGT GATTAAACCG CTCGTGCCGT GGAGCGTGTG
1251 CGGCGTATTT ATCAGCCACG CCCTTGCGGT ACCGTTTGGG GAATATCTGC
1301 CTTATGCGCT TTTCTGCTAT TTGAGTTTGG CTTTAACCTT GTTATTCGGC
1351 TGGACGGGGC TGACTTTGAG CAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2380; ORF 709.ng>:

g709.pep

```

1  MFAFKSLDDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMOAGMIGAL NOGMGAVYLF EFIGLMVSAL MMSGAIPTLM
101 YYGFLISPT YFYFSAFALC SVIGVSIGSS LTACATVGVA FMGMAAFQA
151 DMAMTAGAIV SGVFFGDKMS PLSDTTGISA SIVGIDLFEB IKNMHTTIP
201 AWLISAALML WLLPSVAAOD LNSVESFRSQ LEATGLVHGY SLIPFALLV
251 LALMRVNAVV ANLFTVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
301 DIAKLISRGG LESMEFTQTI VILGMSLGL LFLGLVPSL LEAVRTFLTN

```

1143

351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSCNLSRT
 401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLFLFG
 451 WTGLTLSKK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2381>:

m709.seq
 1 ATGTTTCGCTT TCAAATCCTT ACTCGATATG CCGCGCGGTG AGGCACCTTGC
 51 CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTTCATTGG
 101 AGTGGTTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG
 151 TACGGCTTGG CCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
 201 AGGCGCGTTG AATCAGGGTA TGGCGCGGAT TTACCTGTTT TTCTTCATCG
 251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
 301 TATTACGGTT TCGGACTGAT TTCCCGGACT TATTTTATTT TTTCCTCCTT
 351 CCGGCTGTGT TCCGTCATCG GCGTGTCCAT CGGCAGCAGC CTGACCACCT
 401 GCGCCACTGT CCGCGTTGCC TTTATGGGGA TGGCGGCGGC GTTTCAGGCC
 451 GATATGGCGA TGACGGCGGG CCGGATTGTT TCGGGCGCAT TTTTGGCGA
 501 CAAAATGTCC CCGCTTTCGG ATACGACGGG TATTTCCGCG TCCATCGTCG
 551 GCATCGACTT GTTTGAGCAC ATCAAAAATA TGATGTACAC CACCATCCCC
 601 GCGTGGCTCA TTAGTGCGGC ACTGATGCTT TGGCTTTTGC CGAATGTGCG
 651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
 701 CCGGATTGGT GCACGGCTAT TCGCTGATTC CGTTTGGCGT GTTGGTCATT
 751 TTGGCATTGA TCGCATCAA CGCCGTCGTC GCCATGCTCT TTACCGTCAT
 801 GGTTGCCGTT GCTGTAACGT ATCTGCACAG CACGCCGAT CTGCGTCAGC
 851 TCGGTGCGTG GTTTTACGGC GGCTACAAAC TCGAAGGCGA AGCGTTTAAA
 901 GATGTTGTCA AACTGATTTC GCGCGCGGTT TTGCAAAATA TGTTTTTCAC
 951 GCAAACCATC GTGATTCTCG GGATGAGTTT GGGCGGACTG TTGTTTGCAG
 1001 TCGGTGTGAT TCCTTCCCTG TTGGAGGCCA TCCGTACCTT CTTGACGAAT
 1051 GCCGGACGGC CGACGTTTCA CGTTGCCATG ACTTCGGTCG GGGTTAATTT
 1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTGCGGT GAAACGTTCA
 1151 AAGCCGTTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG
 1201 CTGGAAGATG CCGGGACGGT GATTAAACCG CTCGTACCGT GGAGCGTATG
 1251 CCGCGTGTTT ATCAGCCACG CGCTGGGCGT GCCGTTTGG GAATATCTGC
 1301 CGTATGCCCT TTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT
 1351 TGGACGGGCG TGACTTTGAG CAAAAAATA

This corresponds to the amino acid sequence <SEQ ID 2382; ORF 709>:

m709.pep
 1 MFAPKSLDDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL
 51 YGLARGLKYN DMQQGMIGAL NQGMGAIYLF FFIGLMVSAL MMSGAIPTLM
 101 YYFGFLISPT YFYFSSFALC SVIGVSIGSS LTTTCATVGA FMGMAAFQA
 151 DMAMTAGAIV SGAFFGDKMS PLSDTTGISA SIVGIDLFH IKNMMYTTIP
 201 AWLISAALML WLLPNVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVI
 251 IALMRINAVV AMLFTVMVAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
 301 DVVKLISRGG LESMFFTQTI VILGMSLGGI LFGALGVPSL LEAIRFTLTN
 351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSCNLSRT
 401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLFLFG
 451 WTGLTLSKK*

m709/g709 96.9% identity in 459 aa overlap

	10	20	30	40	50	60
m709.pep	MFAPKSLDDMPRGEALAVVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
g709	MFAPKSLDDMPRGEALAVVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
	10	20	30	40	50	60
m709.pep	DMQQGMIGALNQGMGAIYLFFFIGLMVSALMMSGAIPTLMYYGFGLISPTYFYFSSFALC					
g709	DMQAGMIGALNQGMGAVYLFFFIGLMVSALMMSGAIPTLMYYGFGLISPTYFYFSAFALC					
	70	80	90	100	110	120
m709.pep	SVIGVSIGSSLTTCATVGVAFMGMAAFQADMAMTAGAIVSGAFFGDKMSPLSDTTGISA					
g709	SVIGVSIGSSLTACATVGVAFMGMAAFQADMAMTAGAIVSGVFFGDKMSPLSDTTGISA					
	130	140	150	160	170	180
m709.pep	SIVGIDLFH IKNMMYTTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFH IKNMMYTTIPAWLISAALMLWLLPSVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240
m709.pep	SIVGIDLFH IKNMMYTTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFH IKNMMYTTIPAWLISAALMLWLLPSVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240

1144

	250	260	270	280	290	300
m709.pep	SLIPFALLVILALMRINAVVAMLF	TMVAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK				
g709	SLIPFALLVILALMRVNAVAMLF	TVIAAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK				
	250	260	270	280	290	300
	310	320	330	340	350	360
m709.pep	DVVKLISRGGLESMTFTQ	TIVILGMSLGGLLFALGVIPSLLEAIRFTLTNAGRATFSVAM				
g709	DIAKLISRGGLESMTFTQ	TIVILGMSLGGLLFALGVIPSLLEAVRTLTNAGRATFSVAM				
	310	320	330	340	350	360
	370	380	390	400	410	420
m709.pep	TSVGVNFLIGEYQYLSILLSGETFKPVYDKLGLHSRNL	SRTLEDAGTVINPLVPWSVCGVF				
g709	TSVGVNFLIGEYQYLSILLSGETFKPVYDKLGLHSCNLS	RTELEDAGTVINPLVPWSVCGVF				
	370	380	390	400	410	420
	430	440	450	460		
m709.pep	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLT	LSKKX				
g709	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLT	LSKKX				
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2383>:

```

a709.seq
1  ATGTTGCGCTT TCNAATCCTT ACTCGATATG CCGCGCGGTG AGGCNCTTGC
51  CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTNNTTGG
101 AGTGGCTGCC GCATATGTCC ATTATTGCCG CCATCGTNGT GCTGATTTTG
151 TACGGCTTGG CCGCGCGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
201 AGGCGCGTTG AATCAGGTA TGGGCGCGAT TTACCTNTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGACTGAT TTCCCGACT TATTTTATT TTTCCGCCTT
351 CCGCTGTGT TCCGTTCATG GCGTGTCCAT CGGCAGCAGC CTGACCACCT
401 GCGCCACTGT CCGCGTTGCC TTNATGGGTA TNNNGNCGGC GTTTCNGGCC
451 NANATGGNGN NGNNGNNGN CHNGATTGTN NNGNCGCAT TTTNGGCGN
501 CAAAATGTCN CCGCTTCCG ATACGNCGGG CATNTCCCGG TCCATTGTCG
551 GTATCGACCT GTTTGAACAC ATCAAAATA TGATGTACAC NACCATTCCC
601 GCGTGGCTCA TCAGTGNNNC ACTGATGCTG TNGCTTCTT CCAGCGTCGC
651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTGAAGCCA
701 CGGGATTGGT GCACTGCTAT TCGCTGATTC CGTTTGCGCT GTTGGTCGTT
751 TTGGCATTGA TCGCGTCAA TGCCGTGCTC GCTATGCTCT TTACCGTCAT
801 TGCCGCCGTT GCCGTAACGT ATCTGCACAG CACGCCGAT CTGCGTCAGC
851 TCGCGCGCTG GTTTACGGC GGCTACAAC TCGAAGCGA AGCGTNTANA
901 GACATTGCCA AACTCATTTT TCGCGGCGGT TTGGAAGTA TGTTTTTCAC
951 GCAGACCATC GTGATTCTTG GGATGAGCCT TGGCGGGCTG CTGTTTGCAC
1001 TGGGCGCGAT TCCTTCCCTG CTGGATGCCG TCCGCAGCTT TTTGACGAAT
1051 GCCGGGCGTN CCACATTCAG CGTTGCCATG ACTTCGGTCG GGGTTAATTT
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTCTNGG GAAACGTTCA
1151 AACCTGTTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG
1201 CTGGAAGATG CGGGGACCGT CATCAACCCG CTCGTACCGT GGAGCGTATG
1251 CGGCGTGTTT ATCANCCACG CGCTGGGCGT GCCGGTTTGG GAATATCTGC
1301 CGTATGCCCT TTTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT
1351 TGGACGGGCG TGACTTTGAG CAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2384; ORF 709.a>:

```

a709.pep
1  MFAFXSLDM PRGEALAVVV ALIAAMGYI IXLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMQQGMIGAL NQGMGAIYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFLISPT YFYSAFALC SVIGVSIGSS LTTCATVGVA XMGXXXAFXA
151 XMXXXXXXIV XXAXXGXKMS PLSDTXGXSA SIVGIDLFH IKNMMYTTIP
201 AWLISXXLML XLLESVAAQD LNSVESFRSQ LEATGLVECY SLIPFALLVV
251 LALMRVNAV AVAMLFVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAXX
301 DIAKLISRGG LESMTFTQTI VILGMSLGG L FALGAIPSL L DAVRSFLT N
351 AGRXTFSVAM TSVGVNFLIG EQYLSILLSG ETFFKPVYDKL GLHSRNLST

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401 LEDAGTVINP LVPWSVCGVF IXHALGVPVW EYLPYAFFCY LSLALTLLFG
 451 WTGLTLSKK*

a709/m709 91.1% identity in 459 aa overlap

a709.pep	MFAFXSLDMPRGEALAVVVALIAAMGYTIIIXLEWLPHMSIIAAIVVLILYGLARGLKYN
m709	MFAFXSLDMPRGEALAVVVALIAAMGYTIIISLEWLPHMSIIAAIVVLILYGLARGLKYN
a709.pep	DMQQGMIGALNQGMGAIYLFFFIGLMVSALMMSGAIPITLMIYGFGLISPTYFYFSAFALC
m709	DMQQGMIGALNQGMGAIYLFFFIGLMVSALMMSGAIPITLMIYGFGLISPTYFYFSSFALC
a709.pep	SVIGVSISSLTTCATVGVAXMGXXXAFXAXMXXXXXIVXXAXXGXKMSPLSDTXGXSA
m709	SVIGVSISSLTTCATVGVAFMGMAAAFOADMAMTAGAIVSGAFFGDKMSPLSDTTGISA
a709.pep	SIVGIDLFEHIKNMYYTIPAWLISXXLMLXLLPSVAAQDLNSVESFRSQLEATGLVHCY
m709	SIVGIDLFEHIKNMYYTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY
a709.pep	SLIPFALLVILALMRVNAVVAAMLFVIAAVAVTYLHSTPDLRQLGAWFGGYKLEGEAXX
m709	SLIPFALLVILALMRINAVVAAMLFVMVAVAVTYLHSTPDLRQLGAWFGGYKLEGEAFK
a709.pep	DIAKLISRGGLESMTFTQITVILGMSLGGLLFALGAIPSLDAVRSFLTNAGRXTFSVAM
m709	DVVKLISRGGLESMTFTQITVILGMSLGGLLFALGVIPSLLEAIRFTLTNAGRATFSVAM
a709.pep	TSVGVNFLIGEQLSILLSGETFKPVYDKLGLHSRNLSTLEDAGTVINPLVPWSVCGVF
m709	TSVGVNFLIGEQLSILLSGETFKPVYDKLGLHSRNLSTLEDAGTVINPLVPWSVCGVF
a709.pep	IXHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTLSKKX
m709	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTLSKKX

g710.seq not found

g710.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2385>:

m710.seq
 1 ATGGAAACCC ACGAAAAAT CCGCCTGATG CGCGAATTGA ATAAATGGTC
 51 CCAGGAGGAT ATGGCGGAAA AGCTGGCGAT GTCGGCAGGC GGGTATGCCA
 101 AAATCGAACG GGGCGAAACG CAGTTAAATA TCCCGGTTT GGAGCAGTTG
 151 GCTCAGATTT TCAAAATCGA TATGTGGGAC TTGCTCAAAT CGGGCGGTGG
 201 TGGGATGGTG TTTCAGATTA ATGAAGGTGA TAGTGGTGGC GATATTGCGT
 251 TGTATGCGTC GGGTGATGTT TCGATGAAA TAGAATTTT AAAAATGGAG

1146

301 TTGAAACACT GCAAAGAAAT GTTGAACAA AAAGACAAAG AAATCGAGCT
 351 GCTCCGCAAG CTGACCGAAA CCGTTTAA

This corresponds to the amino acid sequence <SEQ ID 2386; ORF 710>:

m710.pep
 1 METHEKIRLM RELNKWSQED MAEKLAMSAG GYAKIERGET QLNIPRLEQL
 51 AQIFKIDMWD LLKSGGGGMV FQINEGDSGG DIALYASGDV SMKIEFLKME
 101 LKHCKEMLEQ KDEIEILLRK LTETV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2387>:

a710.seq
 1 ATGGAACCC ACGAAAAAT CCGCCTGATG CGCGAATTGA ATAAATGGTC
 51 CCAGGAGGAT ATGGCGGAAA AGCTGGCGAT GTCGGCAGGC GGGTATGCCA
 101 AAATCGAACG AGGCGAAACG CAGTTGAATA TCCCGCGTTT GGAGCAGTTG
 151 GCGCAGATTT TCAAAATTGA TATGTGGGAC TTGCTCAAAT CGGGCGGCGG
 201 CGGGATGGTG TTGCAGATTA ACGATGTGGA TACCAACAGC GGGGAATTG
 251 CAATCTATAC CGCTCAGGAT GCATCNGGTA AAGCTGGATT TGTTAAATG
 301 GAATTAAAC ACTGTAAAGA AATGTTGGAA CACAAAGACA AAGAAATCGA
 351 GCTGCTCCGC AAGCTGACCG AAACCGTTTA A

This corresponds to the amino acid sequence <SEQ ID 2388; ORF 710.a>:

a710.pep
 1 METHEKIRLM RELNKWSQED MAEKLAMSAG GYAKIERGET QLNIPRLEQL
 51 AQIFKIDMWD LLKSGGGGMV LQINDVDTNS GEFAIYTAQD ASGKAGFVKM
 101 ELKHCKEMLE HKDKEIELLR KLTETV*

a710/m710 85.7% identity in 126 aa overlap

	10	20	30	40	50	60
a710.pep	METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLEQLAQIFKIDMWD					
m710	METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLEQLAQIFKIDMWD					
	10	20	30	40	50	60
a710.pep	LLKSGGGGMVQLINDVDTNSGEFAIYTAQDASGKAGFVKMELKHCKEMLEHKDKEIELLR					
m710	LLKSGGGGMVFQINEGDSG-GDIALYASGDVSMKIEFLKMEELKHCKEMLEQKDEIELLR					
	70	80	90	100	110	120
a710.pep	KLTETVX					
m710	KLTETVX					
	120					

g711.seq not found

g711.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2389>:

```
m711.seq
  1 ATGCCCCGCGC CTGATTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
 51 AATCGAGTGG CTGGAAGTA AAAAGGTTAC GCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACTTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GCGGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTCGCCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAT ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGCGCA TCCGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTACCC GCCCAACGGC TACAACTGCC
551 GCTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTTGGGC AAAGCACGGC GGACAATCTG GTCGAGACCC ATAAATCTA
651 CAACAAAAAA GCGGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAACCAGC TTTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
901 CCCGATAAAG AGCAGAAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AGGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAAACCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG
```

This corresponds to the amino acid sequence <SEQ ID 2390; ORF 711>:

```
m711.pep
  1 MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTASEIA KVYTIARMTD
 51 LDMLNDIKTS MVESAKSEQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTADNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFYDYNAGRM
251 NYRPDLDKYD RALAHQFAKA EMGGADFSTS FKQLEKEFYE VKQRLDIDGK
301 PDKEQKIKIR NALSRLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2391>:

```
a711.seq
  1 ATGCCCCGCGC CTGATTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
 51 AATCGAGTGG CTGGAAGTA AAAAGGTTAC GCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACTTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GCGGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTCGCCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAC ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGCGCA TCCGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTACCC GCCCAACGGC TACAACTGCC
551 GTTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTCGGGC AAAGCACGTC GGACAATCTT GTTGAGACCC ATAAATCTA
651 CAACAAAAAA GCGGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAACCAGC TTTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
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901 CCCGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AAGGGCAGAA TTTTCATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAAACCCGT AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2392; ORF 711.a>:

a711.pep

```

1  MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTASEIA KVYTIARMTD
51  LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTSDNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFYDYNAGRM
251 NYRPDLKDYD RALAHQFAKA EMGGADFCTS FKQLEKEFYE VKQRLLDIDGK
301 PDKEQKIKIR NALSRQLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*

```

a711/m711 99.8% identity in 431 aa overlap

a711.pep	10	20	30	40	50	60
	MPAPDLGFALSLLPPKKAIEWLESKKVTAESYRNLTASEIAKVYTIARMTDLDMLNDIKTS					
m711	MPAPDLGFALSLLPPKKAIEWLESKKVTAESYRNLTASEIAKVYTIARMTDLDMLNDIKTS					
	10	20	30	40	50	60
a711.pep	70	80	90	100	110	120
	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
m711	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
	70	80	90	100	110	120
a711.pep	130	140	150	160	170	180
	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG					
m711	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG					
	130	140	150	160	170	180
a711.pep	190	200	210	220	230	240
	YNCRCSVIALSERDVERQGRIVGQSTSDNLVETHKIYNKKGDTYLTLAYKAPDGSLYTTD					
m711	YNCRCSVIALSERDVERQGRIVGQSTADNLVETHKIYNKKGDTYLTLAYKAPDGSLYTTD					
	190	200	210	220	230	240
a711.pep	250	260	270	280	290	300
	RGFDYNAGRMNYRPDLKDYDRALAHQFAKAEMGGADFCTSFKQLEKEFYEVKQRLLDIDGK					
m711	RGFDYNAGRMNYRPDLKDYDRALAHQFAKAEMGGADFCTSFKQLEKEFYEVKQRLLDIDGK					
	250	260	270	280	290	300
a711.pep	310	320	330	340	350	360
	PDKEQKIKIRNALSRQLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
m711	PDKEQKIKIRNALSRQLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
	310	320	330	340	350	360
a711.pep	370	380	390	400	410	420
	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
m711	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
	370	380	390	400	410	420

430

a711.pep	AKFMAKKKVLKX
m711	AKFMAKKKVLKX
	430

g712.seq not found yet

g712.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2393>:

```

m712.seq
1  ATGATGCCCC ATATTGATTT TGACACGATT CCGGGCAGCA TCCGCGTGCC
51  CGGGCAGTAT ATTGAATTTA ACACCCGCAA TGCCGTACAA GGT'TTGCCGC
101 AAAATCCGCA AAAGGTATTG ATGGTTGCAC CCATGCTGAC CGCGGGCATA
151 CAGCCCGCCT TAGAGCCGGT GCAACTATTT AGCGATGCCG AGGCGGCCGA
201 TTTGTTCCGA CAAGGCTCGC TGGCGCATTT GATGGTGCGC CAAGCATTTG
251 CCAACAACCC TTATT'TGGAT TTGACCGTTA TCGGTATTGC CGACCACAGC
301 GCAGGCGTGC AGGCAACCGC AACCGTTACC CTTTCCGGCA CGGCCACCGC
351 GCCGGGCGTG GTGGAATCA CGATTGGCGG CAAGCAGGTA AGCACGGCCG
401 TTAACACCGG CGAGACCGCC GCCACAGTGG CAGACCGTCT GAAAACCGCC
451 ATCACTGCCG CCGATGTAAC CGTTACCGCA TCCGGCAGCG GCGCAGCCGT
501 TACGCTGACG GCCAAACACA AAGGCGAGAT CGGCAACGAG AGCGGCTTAA
551 CCGTGAGCAC CGGCAATACC GGCCTAACTT ATCAAGCCAA TGCCTTTACC
601 GGCGGTGCCA AAAATGCGGA CATTGCCACG GCCTTGTCCTA AAGTGGCGGG
651 CAAGCATTAT CACATTATTT GCAGCCCGTT TAGCGATGAC GCCAACGCCA
701 AAGCCTTGAG CAACCATATT ACCAACGTAT CCAACGCCAT CGAGCAGCGC
751 GGCTGTATCG GCGTATTGGG TATGAGTGCG GCCTTGAGCA CGGCCACCAC
801 CGCTACCGGC GAAATCAACG ACGGCCGCAT GACCTGTGCT TGGTACAAAG
851 GTGCGGTAGA GCCAAACGGC ATCATCGCCG CAGGTTATGC GCGCGTGTTG
901 GCCTTTGAAG AAGACCTGCG CAAGCCGCTG AACACGCTGG AAATCAAAGG
951 GCTGGCCGTT ACACCTGATG CGCAATGGCC GCTGTTTGCA GAATGCAACA
1001 ATGCGCTGTA CAACGGCTTG ACCCGGCTCA CAGTGGTCAA CAACCGCGTG
1051 CAGATTATGC GTGCCGTATC CACCTATACC AAGTCGGCCA ACAACACCGA
1101 CGACCCGGCA CTACTCGACA TTACCACCAT CCGCACGCTG GATTATGTGC
1151 GCCGCAGCGT TAAAGAGCGC ATTGCCCTGC GTTTTCCGCG CGACAAATTG
1201 AGCGACCGCC TGCTGCCCAA GGTTAAGAGC GAGATTTTGG ACGTGCTGAT
1251 TAAGCTCGAC CAAGCCGAAA TCATCGAAAA CGCCGAGGCC AACAAAGGCA
1301 AGCTGGTGGT GCGCGGTGCG CAAAACGACC CCAACCGTGT TAATGCCATT
1351 ATCCCGCCCG ATGTGGTCAA CGGCCTGCAC GTCTTTGCCG GCGCATTGA
1401 TTTGATTTTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2394; ORF 712>:

```

m712.pep
1  MMPHIDFDTI PGSIRVPGQY IEFNTRNAVQ GLPQNPKXVL MVAFMLTAGI
51  OPALEPVOLF SDAEAADLFG QGSLAHLMVR QAFANNPYLD LTVIGIADHS
101 AGVQATATVT LSGTATAPGV VEITIGGKQV STAVNTGETA ATVADRLKTA
151 ITAADVTVTA SGSGAAVTLT AKHKGEIGNE SGLTVSTGNT GLTYQANAFT
201 GGAKNADIAT ALSKVAGKHY HII CSPFSDD ANAKALSNHI TNVSNAIEQR
251 GCIGVLGMSA ALSTATTATG EINDGRMTCA WYKGAVEPNG IIAAGYAAVL
301 AFEEDPAKPL NTLEIKGLAV TPDQOWPLFA ECNNALYNGL TPLTVVNNRV
351 QIMRAVSTYT KSANNTDDPA LLDITTIRTL DYVRRSVKER IALRFPRDKL
401 SDRLLPKVKS EILDVLKLD QAEIENAEA NKGKLVVARA QNDPNRVNAI
451 IPADVNVGLH VFAGRIDLIL *

```

a712.seq not found yet

a712.pep not found yet

g713.seq not found yet

g713.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2395>:

```
m713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTGATTTT GTCATCGGCA GGTGGGACC GGAGGCGGCC
151 ATACCGGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAA AGCAAGGGCA
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 CCGAAAACAA CCCCCTTTG GGCAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTCGGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGCGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CTGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGCTTTT CCGAGGTTAC
651 TTTTTTGGCG CAATCGCACG GCCGCGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCTTAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTTGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACTCTC ACGATAACCG
851 TGGGCGGCCA TAAACCCGCG GACGGCGTAT TGTGGCAACC TGGCCTGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGCGCGCGG TTTATGCTAT CCCGATGGA TGGTACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
1101 CAAAAGGCGC GGCAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA
```

This corresponds to the amino acid sequence <SEQ ID 2396; ORF 713>:

```
m713.pep
1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDF VISRLGPEAA
51  IPDLSGESCE VVIDGQIVNT GIIGSQRHGK SKGSRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTVLDAAKKL AAPWPQIKAV VLKAENNPAL GKIDIEFGET
151 VWQALTHIAN SVGLHPWLEP DGTLVVGGAD YSSFPVATLC WSRTDSRCNI
201 ERMDIEWDTD NRFSEVTFLA QSHGRSGDSA KHDLKWVYKD PTMTLHRPKT
251 VVVSADADNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVLWQPGLR
301 VHVIDDEHGI DAVFFLMGRR FMLSMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGRK KGVSHKGKKG GKQAEAVF E*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2397>:

```
a713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTGATTTT GTCATCGGCA GGTGGGACC GGAGGCGGCC
151 ATACCGGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAA AGCAAGGGCG
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 TCGAAAACAA CCCCCTTTG GACAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTCGGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGTGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CCGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGCTTTT CTGAGGTTAC
651 TTTTTTGGCG CAATCGCACG GCCGCGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCTTAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTTGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACTCTC ACGATAACCG
851 TGGGCGGCCA TAAACCCGCG GACGGCGTAT TGTGGCAACC TGGCCAGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGCGCGCGG TTTATGCTAT CTCGATGGA TGGCACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
```


1101 CAAAAAAGGC GGCAAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA

This corresponds to the amino acid sequence <SEQ ID 2398; ORF 713.a>:

a713.pep
1 MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDF VIGRLGPEAA
51 IPDLSGESCE VVIDGQIVMT GIIGSQRHGK SKGGRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTVLDAAKKL AAPWPQIKAV VLKVENNPAL DKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLLVVGVD YSSPPVATLC WSRTDSRRNI
201 ERMIDIEWTD NRFSEVTF LA QSHGRSGDSA KHDLLKVVYKD PTMTLHRPKT
251 VVVSADNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVWLQPGQR
301 VHVIDDEHGI DAVFFLMGRR FMLSMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGR KGVSHKGGKG GKKQAETAVF E*

a713/m713 98.4% identity in 381 aa overlap

a713.pep	10	20	30	40	50	60
m713	10	20	30	40	50	60
a713.pep	70	80	90	100	110	120
m713	70	80	90	100	110	120
a713.pep	130	140	150	160	170	180
m713	130	140	150	160	170	180
a713.pep	190	200	210	220	230	240
m713	190	200	210	220	230	240
a713.pep	250	260	270	280	290	300
m713	250	260	270	280	290	300
a713.pep	310	320	330	340	350	360
m713	310	320	330	340	350	360
a713.pep	370	380				
m713	370	380				

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g714.seq not found yet

g714.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2399>:

```
m714.seq
1   ATGAGCTATC AAGACATCTT GCGGGGCTTG TTGCCCCCGG TGTCGTATGC
51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GGCGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 CGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGA
201 CGGTACGGGC AAAAACC GCCACCGTGT GTTGCCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAACCGC GCGGCGGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401 GGCACGTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCCGCGCC
451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGCTA A
```

This corresponds to the amino acid sequence <SEQ ID 2400; ORF 714>:

```
m714.pep
1   MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
51  RSAGQMLADW ERLGLDGTG KNRQHRVLAV MAKLNETGGL SIPYFVRLAE
101 AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFRA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2401>:

```
a714.seq
1   ATGAGCTATC AAGACATCTT GCGGGGCTTG TTGCCCCCGG TGTCGTATGC
51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GGCGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 AGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGA
201 CGGTACGGGC AAAAACC GCCACCGTGT GTTGCCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAACCGC GCGGCGGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401 GGCACGTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCCGCGCC
451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGATA A
```

This corresponds to the amino acid sequence <SEQ ID 2402; ORF 714.a>:

```
a714.pep
1   MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
51  SSAGQMLADW ERLGLDGTG KNRQRRVLAV MAKLNETGGL SIPYFVRLAE
101 AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFRA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
```

a714/m714 98.9% identity in 186 aa overlap

	10	20	30	40	50	60
a714.pep	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPSSAGQMLADW					
m714	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPSSAGQMLADW					
	10	20	30	40	50	60
a714.pep	ERVLGLDGTGKNRQRRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPQPFRAGVNR					
m714	ERVLGLDGTGKNRQHRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPQPFRAGVNR					
	70	80	90	100	110	120
a714.pep	ERVLGLDGTGKNRQRRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPQPFRAGVNR					
m714	ERVLGLDGTGKNRQHRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPQPFRAGVNR					
	70	80	90	100	110	120
a714.pep	AGDRLAPQEIIMWVWHVNVRGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA					
m714	AGDRLAPQEIIMWVWHVNVRGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA					

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m714 AGDRLAPQEIMVWVHVNRGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA
 130 140 150 160 170 180

a714.pep IRFTYRX
 |||||
 m714 IRFTYRX

g715.seq not found yet

g715.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2403>:

m715.seq
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
 151 CCGAAATGGG TTGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTG
 201 GGGTCGTCTG AAAGACAGTT TTTCACACT GTCAGACAAC GATACAGCCC
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG
 301 GCGGGGCGCA ACCGCAAAGT TCGGATCCG CAACGGGAAT TTTTGACGCT
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
 401 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2404; ORF 715>:

m715.pep
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
 51 PKWVGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM
 101 AGRNRKVRIP QREFLTITDD DKQALMDDVQ DYFSGGLIP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2405>:

a715.seq
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
 151 CCGAAATGGT TGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTG
 201 GGGTCGTCTG AAAGACAGTT TTTCACACT GTCAGACAAC GATACAGCCC
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG
 301 GCGGGGCGCA ACCGCAAAGT TCGGATCCG CAACGGGAAT TTTTGACGCT
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
 451 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2406; ORF 715.a>

a715.pep
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
 51 PKWVGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM
 101 AGRNRKVRIP QREFLTITDD DKQALMDDVQ DYFSGGLIP*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2407>:

g716.seq
 1 ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTAT CCCTGTCTCT
 51 GGCGCCCGCG GCGTGTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
 201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
 251 AAAAGCCCCA CAAACACACC AAGCATCTA AAGCCAAAGC CAAATCTGCC
 301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

This corresponds to the amino acid sequence <SEQ ID 2408; ORF 716.ng>:

g716.pep
 1 MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
 51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG AVKRAKHHT KASKAKAKSA

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101 EGKCGEGKCG SK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2409>:

```
m716.seq
1  ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51  GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2410; ORF 716>:

```
m716.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

m716/g716 86.6% identity in 112 aa overlap

	10	20	30	40	50	
m716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----					
g716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQSGCGASKSAEGSCGASKSAEG					
	10	20	30	40	50	60
	60	70	80	90	100	
m716.pep	---AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
g716	SCGAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2411>:

```
a716.seq
1  ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51  GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAATAA
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2412.a>:

```
a716.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

a716/m716 100.0% identity in 102 aa overlap

	10	20	30	40	50	60
a716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
m716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
	10	20	30	40	50	60
	70	80	90	100		
a716.pep	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
m716	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2413>:

```
g717.seq
1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
```

```

51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCcccgCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  ACTGACGGTG
151  TCGGTATTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CGCCGCCGAC  AAAGACACTT  TGTTCAAAAC  CCTGTTCTTG  CCGCCGCTGC
251  TGTTTTCGCG  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTTCGCT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTCG
401  GTATGGAAGG  GCGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAA
451  CTCGCCATTC  TGCTGCTGTT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  GCGGAAACACC  TCCGTCTGTA  CCGCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCTT  TTTGCTGTTT  CAAAACCGAT  GCCGCTGAA  GGCGTCCCG
601  CGCGCGCCGT  TTTGCCCGCG  CGTCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGCTCGCA  CTGAGCAGCC  TTGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTGTTCCT  GAAAAATAT  GCGGGCCTGG  AACAGCTCGG  CGTTATTTCG
751  ATGGGTATTT  CGTTCGGCGG  GCGGCGATTA  TTGCTCCAAA  GCATCTTTTC
801  AACGCTCTGG  ACACCGTATA  TTTCCGCTGC  AATCGAAGAA  AACGCCACGC
851  CCGCCCGCCT  CTCGGCAACG  GCAGAATCCG  CCGCCGCCCT  GCTTGCTTCC
901  GCCCTCTGCC  TGACCGGAAT  TTTCTCGCCC  CTCGCCCTCC  TCCTGCTGCC
951  GGAAAACTAC  GCCGCCGTCC  GGTTTACCGT  CGTATCGTGT  ATGCTGCCGC
1001  cgtctGTTTA  CACGCTGACC  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GTCCGATCGC  GCTTGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCGTCTGCTG  CTGGGGCTTG  CCGTACCGTC  CGGCGGCACG  CGCGGCGCGG
1151  CGGTTGCGCT  TGCCGCCTCA  TTCTGGTTGT  TTTTGTGTTT  CAAGACAGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAA  CGCTGCGCG  TTTATATGCA
1251  CACATTGTTT  TGCTGCGCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACAC
1301  CGCAAACTAC  CCGCCTGTTT  gccggtgtat  GCGCGGCATA  TCTGGCAGGC
1351  TGCATCTGCG  GCCACCGGAA  AAATTTGCAC  AAATGTTTC  ATTATTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2414; ORF 717.ng>:

```

g717.pep
1  MDTKEILGYA  AGSIGSAVLA  VIILPLLSWY  FPADDIGRIV  LMQTAAGLTV
51  SVLCLGLDQA  YVREYYAAAD  KDTLFKTLFL  PPLLFSAIA  ALLLSRPSLP
101  SEILFSLDDA  AAGIGLVLE  LSLFLPIRELL  LVLMEGRAL  AFSSAQLVPR
151  LAILLLLPLT  VGLLHFPANT  SVLTAVYALA  NLAAAFLLF  QNRCRLKAVR
201  RAFPSPAVLH  RGLRYGIPLA  LSSLAYWGLA  SADRLFLKKY  AGLEQLGVYS
251  MGSIFGGAAL  LLOSIFSTVW  TPYIFRAIEE  NATPARLSAT  AESAAALLAS
301  ALCLTGFISE  LASLLLPENY  AAVRFTVVSC  MLPLFYTLT  EISGIGLNVV
351  RKTRPIALAT  LGALANLLL  LGLAVPSGGT  RGAAVACAAS  FWLFFVFKTE
401  SSCRLWQPLK  RLPLYMHTLF  CLASSAAYTC  FGTANYPLF  AGVWAAVLAG
451  CILRHRKNLH  KLFHYLKKQG  FPL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2415>:

```

n717.seq
1  ATGGACACAA  AAGAAATCCT  CGGCTACGCG  GCAGGCTCGA  TCGGCAGCGC
51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCCCGCGCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  GCTGACGGTG
151  TCGGTATTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CACCGCCGAC  AAAGACACTT  TGTTCAAAAC  CCTGTTCTTG  CCGCCGCTGC
251  TGCTGCCGCG  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTCACT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTCG
401  GTATGGAAGG  ACGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAG
451  CTCGCCATCC  TGCTGCTGCT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  AGCGAACACC  GCCGTCTGTA  CCGCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCCGCCT  TTTGCTGTTT  CAAAACCGAT  GCCGCTGAA  GGCGTCCCG
601  CACGCACCGT  TTTGCCCGCG  CGTCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGATCGCA  CTGAGCAGCA  TCGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTGTTCCT  GAAAAATAT  GCGGGCCTGG  AACAGCTCGG  CGTTTATTTCG
751  ATGGGTATTT  CGTTCGGCGG  GCGGCGATTA  TTGTTCCAAA  GCATCTTTTC
801  AACGCTCTGG  ACACCGTATA  TTTCCGCGCG  AATCGAAGAA  AACGCCCGCG
851  CCGCCCGCCT  CTCGGCAACG  GCAGAATCCG  CCGCCGCCCT  GCTTGCTTCC
901  GCCCTCTGCC  TGACCGGCAT  TTTCTCGCCC  CTGCGCTCCC  TCCTGCTGCC
951  GGAAACTAC  GCCGCCGTCC  GGTTTATCGT  CGTATCGTGT  ATGCTGCCGC
1001  CGCTGTTTTC  CACGCTGGCG  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GCCGATCGC  GCTCGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCGTCTGCTG  CTGGGGCTTG  CCGTGCCGTC  CCGCGGCGCG  CGCGGCGCGG
1151  CGGTTGCCCT  TGCCGCCTCA  TTCTGGCTGT  TTTTGCCTT  CAAGACCGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAA  CGCTGCGCG  TTTATCTGCA
1251  CACATTGTTT  TGCTGACCT  CCTCGGCGCG  CTACACCTGC  TTCGGCACGC
1301  CGCAAACTA  TCCCTGTTT  GCGGCGTAT  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCTGCG  GCCACCGGAA  AGATTGTCAC  AAATGTTTC  ATTATTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2416; ORF 717>:

```

m717.pep
1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMOTAAGLTV
51  SVLCLGLDQA YVREYYATAD KDTLFKTLFL PPLLSAAAIA ALLSRPSLP
101 SEILFSLDDA AAGIGLVLE LSFLPIRFL LVLMEGRAL AFSSAQLVPK
151 LAIIIIIIIT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 HAPFSPAVLH RGLRYGPIA LSSIAWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGGAAL LFQSIFSTVW TPYIFRAIEE NAPPARLSAT AESAAALLAS
301 ALCLTGIFSP LASLLLPENY AAVRFIVVSC MLPLFCTLA EISGIGLNVV
351 RKTRPIALAT LGALAANLLL LGLAVPSGGA RGAAVACAAS FWLFFAFKTE
401 SSCRLWQPLK RLPLYLHTLF CLTSSAAYTC FGTFANYPLF AGVWAAYLAG
451 CILRHRKDLH KLFHYLKKQG FPL*

m717/g717 96.4% identity in 473 aa overlap

      10      20      30      40      50      60
m717.pep MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
g717     MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
      10      20      30      40      50      60

      70      80      90     100     110     120
m717.pep YVREYYATADKDTLFKTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE
g717     YVREYYAAADKDTLFKTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLE
      70      80      90     100     110     120

      130     140     150     160     170     180
m717.pep LSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAILLLPLTVGLLHFPANTAVLTAVYALA
g717     LSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAILLLPLTVGLLHFPANTSVLTVAVYALA
      130     140     150     160     170     180

      190     200     210     220     230     240
m717.pep NLAAAFLLFQNRCRLKAVRHAPFSPAVLHRLRYGPIALSSIAWGLASADRLFLKKY
g717     NLAAAFLLFQNRCRLKAVRRAPFSPAVLHRLRYGPIALSSIAWGLASADRLFLKKY
      190     200     210     220     230     240

      250     260     270     280     290     300
m717.pep AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS
g717     AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIEENATPARLSATAESAAALLAS
      250     260     270     280     290     300

      310     320     330     340     350     360
m717.pep ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLAETISGIGLNVVRKTRPIALAT
g717     ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFYTLTISGIGLNVVRKTRPIALAT
      310     320     330     340     350     360

      370     380     390     400     410     420
m717.pep LGALAANLLLGLAVPSGGARGAAVACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF
g717     LGALAANLLLGLAVPSGGTRCAAVACAASFWLFFVFKTESSCRLWQPLKRLPLYMHTLF
      370     380     390     400     410     420

      430     440     450     460     470
m717.pep CLTSSAAYTCFGTFANYPLFAGVWAAYLAGCILRHRKDLHKLPHYLKKQGFPLX
g717     CLASSAAYTCFGTFANYPLFAGVWAAYLAGCILRHRKDLHKLPHYLKKQGFPLX
      430     440     450     460     470

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2417>:

```

a717.seq
1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
51  GGT'TTTAGCC GTCATCATCC TGCCGCTGCT GTCGTGGTAT TTCCCTGCCG
101 ACGACATCGG ACGCATCGTG CTGATGCAGA CGGCGGCGCG GCTGACGGTG
151 TCGGTGTTGT GCCTCGGGCT GGATCAGGCA TACGTCCGCG AATACTATGC
201 CGCCGCCGAC AAAGACACTT TGTTCAAAC CCTGTTCTCTG CCGCCGCTGC

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1158

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251 TGTCTGCCGC CGCGATAGCC GCCCTGCTGC TTTCCCGCCC ATCCCTGCCG
301 TCTGAAATCC TGTTCGCT CGACGATGCC GCCGCCGCCA TCGGGCTGGT
351 GCTGTTTGA CTGAGCTTCC TGCCCATCCG CTTTCTCTTA CTGGTTTTCG
401 GTATGGAAGG ACGCGCCCTT GCCTTTTCGT CCGCGCAACT CGTGTCCAAG
451 CTCGCCATCC TGCTGCTGCT GCCGCTGACG GTCGGGCTGC TGCACCTTCC
501 GCGGAACACC GCCGTCCTGA CCGCCGTCTTA CCGCTGGCA AACCTTGCCG
551 CCGCCGCCTT TTTGCTGTTT CAAAACCGAT GCCGCTGAA GGCCGTCGGG
601 CCGCGACCGT TTTCATCC3C CGTCCTGCAT CCGCGCCTGC GCTACGGCAT
651 ACCGATCGCA CTAAGCAGCA TCGCCTATTG GGGGCTGGCA TCCGCCGACC
701 GTTTGTTTCT GAAAAAATAT GCGCGCTAG AACAGCTCGG CGTTTATTCG
751 ATGGGTATTT CGTTCGGCGG AGCGGCATTA TTGTTCCAAA GCATCTTTTC
801 AACGGTCTGG ACACCGTATA TTTTCGCGC AATCGAAGCA AACGCCCGC
851 CCGCCCGCCT CTCGGCAACG GCAGAATCCG CCGCCGCCCT GCTTGCTTCC
901 GCCCTCTGCC TGACCGGCAT TTTCTGCCC CTCGCCCTCC TCCTGCTGCC
951 GGAAACTAC GCCGCCGTCC GGTATTATCGT CGTATCGTGT ATGCTGCCTC
1001 CGCTGTTTTC CACGCTGGTA GAAATCAGCG GCATCGGTTT GAACGTCGTC
1051 CGAAAAACAC GCCCGATCGC GCTCGCCACC TTGGGCGCGC TGGCGGCAAA
1101 CCTGCTGCTG CTGGGCTTG COGTACCGTC CGGCGGCGCG CGCGGCGCGG
1151 CGTTTGCTG TGCCGCCCTCA TTTTGCTGT TTTTGTTTT CAAGACCGAA
1201 AGCTCCTGCC GCCTGTGGCA GCCGCTCAA CGCCTGCCG TTTATATGCA
1251 CACATTGTTT TGCCTGGCCT CCGCGCGCG CTACACCTGC TTCGGCACTC
1301 CGGCAAACTA CCCCCTGTTT GCCGGCGTAT GGGCGGTATA TCTGGCAGGC
1351 TGCATCTGCG GCCACCGGAA AGATTGCGAC AAAGTGTTC ATTATTGAA
1401 AAAACAAGGT TTCCATTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2418; ORF 717.a>:

```

a717.pep
1 MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51 SVLCLGLDQA YVREYYAAAD KDTLFKTLFL PPLLSAAAIA ALLLSRPSLP
101 SEILFSLDDA AAGIGLVLE LSFPIRFL LVLMEGRAL AFSSAQLVSK
151 LAILLPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 RAPFSSAVLH RGLRYGPIA LSSIAWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGAAL LFQSFSTVW TPYIFRAIEA NAPPARLSAT AESAAALLAS
301 ALCLTGIFSP LASLLPENY AAVRFIVVSC MLPLFCTLV EISGIGLNVV
351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAUVACAAS FWLFVFKTE
401 SSCRLWQPLK RPLYMHTLF CLASSAAYTC FGTPANYPLF AGVWAVYLAG
451 CILRHRKDLH KLFHYLKKQG FPL*

```

a717/m717 97.9% identity in 473 aa overlap

	10	20	30	40	50	60
a717.pep	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
m717	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a717.pep	YVREYYAAADKDTLFKTLFLPPLLSAAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLE					
m717	YVREYYATADKDTLFKTLFLPPLLSAAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a717.pep	LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAILLPLTVGLLHFPANTAVLTAVYALA					
m717	LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAILLPLTVGLLHFPANTAVLTAVYALA					
	130	140	150	160	170	180
	190	200	210	220	230	240
a717.pep	NLAAAFLLFQNRCRLKAVRRAPFSSAVLHRLRYGIPALSSIAWGLASADRLFLKKY					
m717	NLAAAFLLFQNRCRLKAVRHAPFSPAVLHRLRYGIPIALSSIAWGLASADRLFLKKY					
	190	200	210	220	230	240
	250	260	270	280	290	300
a717.pep	AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIEANAPARLSATAESAAALLAS					

1159

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|||||
m717  AGLEQLGVYSMGISFGGAALLFQSI FSTVWTPYIFRAIEENAPPARLSATAESAAALLAS
      250      260      270      280      290      300

      310      320      330      340      350      360
a717.ppep ALCLTGIFSPLASLLLPENYA AAVRFIVVSCMLPPLFCTLVEISGIGLNVVRKTRPIALAT
|||||
m717  ALCLTGIFSPLASLLLPENYA AAVRFIVVSCMLPPLFCTLA EISGIGLNVVRKTRPIALAT
      310      320      330      340      350      360

      370      380      390      400      410      420
a717.ppep LGALAANLLLGLAVPSGGARGA AVACAASFVWLFVFKTESSCRLWQPLKRLPLYMHTLF
|||||
m717  LGALAANLLLGLAVPSGGARGA AVACAASFVWLFVFKTESSCRLWQPLKRLPLYLHTLF
      370      380      390      400      410      420

      430      440      450      460      470
a717.ppep CLASSAAYTCFGTPANYPLFAGVWAVYLAGCILRHRKDLHKL FHYLKKQGFPLX
|||||
m717  CLTSSAAYTCFGTPANYPLFAGVWAA YLAGCILRHRKDLHKL FHYLKKQGFPLX
      430      440      450      460      470

```

g718.seq not found yet

g718.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2419>:

```

m718.seq
1   TCAGACGGCC TTTACGTACC CCGAAACTTT ATCCACCGCC CGCAAAGCTG
51  GTTCAAATGG GACAAAGACA ACGGCTGCT GCTGCGTACC CGCGAAAATC
101 CGGAAGGCGA AGCCTTGTGG CCGCTGGGCT GGGTCGTTCA TACCCAAAAA
151 TCGCGCAGCG TCCAGCAGGC GCGCAACGGG CTTTCCGCA CGCTTTCCTG
201 GCTGTATATG TTCAAACACT ACGCCGTCCA CGATTTTGCC GAGTTTGTGG
251 AGCTGTACGG CATGCCCATC CGTATCGGCA AATACGGCGC GGGCGCAACC
301 AAAGAGGAAA AAAACACCCT GCTTCGAGCG GTGGCGGAAA TCGGTCACAA
351 CGCGGCAGGC ATCATGCCAG AAGGTATGGA AATAGAGCTC CACAACGCGG
401 CAAACGGTAC GACGGCAACC AGCAATCCGT TTTTGCAGAT GGCCGACTGG
451 TGCGAAAAAT CGGCGGCGCG GCTGATTTTG GGGCAAACGC TGACCGCGG
501 TGCGGACGGA AAATCCAGCA CCAACGCGCT GGGCAATATC CACAACGAGG
551 TACGCGCGGA TTTGCTGGTG TCGGACGCAA AACAGGTGGC GCAAACCATC
601 ACAAGCCAAA TCATCGGACC GTTCTGCAA ATCAACTATC CCCATGCCGA
651 CCCAAACCGC GTGCCGAAAT TTGAATTTGA CACGCGCGAG CCGAAAGACA
701 TCGCGGTCTT TGCCGACGCT ATCCCGAAAC TGGTGGATGT CGSCGTACAA
751 ATCCCGGAAA GCTGGGTGCG CGACAACTG GTCATTCCAG ATSTGCAGGA
801 GGGTGAGGCT GTGTTGGTGC GGCAGGTACC GGACAATCCG GTAAACAGAA
851 CTGCATTGGC GGCTTTATCC GCCACACCG TACCATCTAA GGCTACGGGC
901 AGGCATCAGG AAATATTGGA CGGCGCGTTG GATGACGCGC TGSTTGAGCC
951 CGATTTCAT TCTCAGCTCA ACCCGATGGT GCGTCAGGCG GTTGCCGCAC
1001 TTAATGCTTG CAACAGCTAC GAGGAGGCAG ATGCCGCACT GAATGCGCTT
1051 TATCCGAATT TGGACAACGC GAAACTGCGT ACCTATATGC AGCAGGCCTT
1101 GTTTATCAGC GATATTTTGG GACAAGACCA TGCCGCGGCC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2420; ORF 718>:

```

m718.pep
1   SDGLYVPRNF IHRPQSWFKW DKDNGLLLR T RENPEGEALW PLGWVVHTQK
51  SRSVQQARNG LFRTL SWLYM FKHYAVH DFA EFLELYGMPI RIGKYGAGAT
101 KEEKNTLLRA VAEIGHNAAG IMPEGMEIEL HNAANGTTAT SNPFLLQMA DW
151 CEKSAARLIL GQTLTSGADG KSSTNALGNI HNEVRRDLLV SDAKQVAQTI
201 TSQIIGPFLQ INYPHADPNR VPKEFD TRE PKDIAVFADA IPKLVDVG VQ
251 IPESWVRDKL VIPDVQEGEA VLVROVPDNP VNRTALAALS AHTVPSKATG
301 RHQEILDGAL DDALVEPDFN SQLNPMVRQA VAAALNACNSY EEADAALNAL
351 YPNLDNAKLR TYMQQALFIS DILGQDHARA *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2421>:

1160

a718.seq

```

1  ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CCGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCCAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TCGGTACCCG CGAAAAATCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCACGCGGCT TTCCGCGACG CTTTCCTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCTGC TTCGAGCGGT GCGGGAATC GGTCAACAAC GGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCCGCCGG CAATCCGTTT TTGCAGATGG CCGACTGCTG CGAAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAA CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAAATTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACCTGCT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCGG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2422; ORF 718.a>:

a718.pep

```

1  MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHELFADI EERDSIDIAN MGTRKRALLT LNWRVAPPRN
101 ATPEEEEKLS QAYEMMDSL P TLEDLIMDL DAVGHGFSAL EWEVVFSDGL
151 YLPRNFIHRP QSWFKWDKDN GLLLRTRNP EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRISK YCAGATKEEK
251 NTLRAVAEI GHNAAGIMPE GMEIELHNA NGMTSAGNPF LQMADWCEKS
301 AARLILGQTL TSGADGKSS T NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VCVGVQIPES
401 WVRDKLVIPD VQEGEAVLYR QVPDNPVNR ALAALSHTV PSKATGRHOE
451 ILDGALDDAL VEPDFNSQLN PMVRQAAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

```

a718/m718 98.4% identity in 380 aa overlap

	120	130	140	150	160	170
a718.pep	DSLPTLEDLIMDLMDAVGHGFSALEVEVVFSDGLYLPRNFIHRPQSWFKWDKDNGLLLRT					
m718	: SDGLYVPRNFIHRPQSWFKWDKDNGLLLRT					
				10	20	30
	180	190	200	210	220	230
a718.pep	RENPEGEALWPLGWVVHTQKRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI					
m718	RENPEGEALWPLGWVVHTQKRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI					
	40	50	60	70	80	90
	240	250	260	270	280	290
a718.pep	RICKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLOMADW					
m718	RICKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFLQMAW					

1161

	100	110	120	130	140	150
a718.pep	300	310	320	330	340	350
	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGPFLQ					
m718	160	170	180	190	200	210
	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEVRRDLLVSDAKQVAQTITSQIIGPFLQ					
a718.pep	360	370	380	390	400	410
	INYPHADPNRVPKFEFDTREPKDIAVFADAI PKLV DVG VQIPESWVRDKLVIPDVQEGEA					
m718	220	230	240	250	260	270
	INYPHADPNRVPKFEFDTREPKDIAVFADAI PKLV DVG VQIPESWVRDKLVIPDVQEGEA					
a718.pep	420	430	440	450	460	470
	VLVRQVPDNPVNR TALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
m718	280	290	300	310	320	330
	VLVRQVPDNPVNR TALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
a718.pep	480	490	500	510	520	
	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718	340	350	360	370	380	
	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2423>:

m718-1.seq

```

1  ATGGAGCCGA TAATGGCAAA AAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACGGCG ACCGGTCGGG
101 TTATCGCCGA GCATCCGTCC AATTTTATTA CGCCGCAAAA GATGCGGGCC
151 CTCTTCGAGG ACGCAGAAAG CGCGCACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAA ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCTGCCT ACCCTCGAAG ACCTGATTAT GGATTTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAATGGGA
501 CAAAGACAAC GGGCTGCTGC TGCGTACCCG CGAAAATCCG GAAGGCGAAG
551 CGTTGTGCCC GCTGGGCTGG GTCGTTTATA CCCAAAATC GCGCAGCGTC
601 CAGCAGCGCG GCAACGGGCT TTTCCGCACG CTTTCTTGGC TGTATATGTT
651 CATTGCCAGAA GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCCTG TTCGAGCGGT GCGGGAATC GGTCAACAAC CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TAGAGCTCCA CAACGCGGCA AACGGTACGA
851 CGGCAACCA GCAATCCGTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 CGCGCGCGCG TGATTTTGGG GCAACGCTG ACCAGCGGTG CGGACGGAA
951 ATCCAGCAC AACGCGCTGG GCAATATCCA CAACGAGGTA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCCGACCGT TCCTGCAAA CAACTATCCC CATGCCGACC CAAACGCGCT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGCTTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACCTGG CATTCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCCG CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACCT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2424; ORF 718-1>:

m718-1.pep.

```

1  MEPIMAKKNN KTKIQKPEAA LOTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHFLFADI EERDS DIAAN MGRKRALLT LNRVAPPNRN
101 ATPPEEKLSQ QAYEMMDSLP TLEDLIMDLN DAVGHGFSAL EWEVWFSGL
151 YLPRNFIHRP QSWFKWDDKN GLLLRTRNP EGEALWPLGW VVHTQKSRV
201 QARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLRAVAEI GHNAAGIMPE GMEIELHNAA NGTTATSNPF LQADWCEKS
301 AARLILGQTL TSGADGKSST NALGNHNEV RRDLLVSDAK QVAQTITSQI

```

351 IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2425>:

a718.seq

```
1 ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAGGCC
51 CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGCTCGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCGTGCCT ACCCTCGAAG ACCTGATTAT GGATTGTATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TGCCTACCCG CGAAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCAAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTCCGACACG CTTTCCTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTTCGCA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGCGCGCG GCGCAACCAA AGAGGAAAAA
751 AACACCCCTG TTCGAGCGGT GCGGGAATC GGTCAACACG CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCGCGCGG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGCG TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACCGCTGG GCAATATCCA CAACGAGATA CGCGCGGATT
1001 TGCTCGGTGC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAT CAATATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAATG GTGGATGTCG GCGTACAAAT CCCCGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGGCG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGACG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCGAGT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCTTGTG TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A
```

This corresponds to the amino acid sequence <SEQ ID 2426; ORF 718-1.a>:

a718.pep

```
1 MEPIMAKNN KTKIQKEAA LOTDVAQITA TGRVIAEHPS NFITPQKMRA
51 LFEDAESGDI RAQHELFADI EERDSIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEKLSD QAYEMMDSLP TLEDLIMDLN DAVGHGFSAL EWEVVFSDGL
151 YLPNFIHRP QSWFKWDKDN GLLRLTREN EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRICK YGAGATKEEK
251 NTLRAVAEI GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQADWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEI RRDLVSDAK QVAQTITSQI
351 IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*
```

a718/m718-1 99.0% identity in 526 aa overlap

	10	20	30	40	50	60
a718.pep	MEPIMAKNNKTKIQKEAALQTDVAQITATGRVIAEHPSNFITPQKMRALFEDAESGDI					
m718-1	MEPIMAKNNKTKIQKEAALQTDVAQITATGRVIAEHPSNFITPQKMRALFEDAESGDI					
	10	20	30	40	50	60
	70	80	90	100	110	120
a718.pep	RAQHELFADIEERDSIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSDQAYEMMDSLP					
m718-1	RAQHELFADIEERDSIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSDQAYEMMDSLP					
	70	80	90	100	110	120
	130	140	150	160	170	180
a718.pep	TLEDLIMDLMDAVGHGFSALEVWVFSDGLYLFRNFIHRPQSWFKWDKNGLLRLTREN					
m718-1	TLEDLIMDLMDAVGHGFSALEVWVFSDGLYLFRNFIHRPQSWFKWDKNGLLRLTREN					
	130	140	150	160	170	180

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a718.pep	190	200	210	220	230	240
	ESEALWPLGWVHTQKSRVQQARNGLFRTLWLYMFKHYAVHDAEFLELYGMPIRIGK					
m718-1	ESEALWPLGWVHTQKSRVQQARNGLFRTLWLYMFKHYAVHDAEFLELYGMPIRIGK					
	190	200	210	220	230	240
a718.pep	250	260	270	280	290	300
	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFQMDADNCEKS					
m718-1	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFQMDADNCEKS					
	250	260	270	280	290	300
a718.pep	310	320	330	340	350	360
	AARLILGQTLTSGADGKSSSTNALGNIHNEIRDLVSDAKQVAQTITSQIIGPFLQINYP					
m718-1	AARLILGQTLTSGADGKSSSTNALGNIHNEVRRDLVSDAKQVAQTITSQIIGPFLQINYP					
	310	320	330	340	350	360
a718.pep	370	380	390	400	410	420
	HADPNRVPKFEFDTREPKDIAVFADAIPKLVDPGVQIPESWVRDKLVI PDVQEGEAVLVR					
m718-1	HADPNRVPKFEFDTREPKDIAVFADAIPKLVDPGVQIPESWVRDKLVI PDVQEGEAVLVR					
	370	380	390	400	410	420
a718.pep	430	440	450	460	470	480
	QVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAVAAAL					
m718-1	QVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAVAAAL					
	430	440	450	460	470	480
a718.pep	490	500	510	520		
	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718-1	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
	490	500	510	520		

g719.seq not found yet

g719.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2427>:

m719.seq

```

1  ATGGCAAACG GGAACATGAA ACTGTCGTTG GTGTTAACCG CCCGAGATGA
51  CGGAGCGAGA CGGCTACTGG CTGATACTCA ACGACAATTA GATCGTACCG
101 CGAAATCGCG GCGCAACTT GAACGGCAA GCCATACTTA TGCCTTGACC
151 GGCATCCGCT CAGAAAAACA GATTCAACGC GAAATCATGC TGACACAGGC
201 TGCCTTTAAC CGTTTGGCGC GCAGCGGCAA GGCATCACAA AATGATTTGG
251 CACGGGCGGC GGTGCTACG CGTAACCGAA TTCGCGAGCT GAACGCGGAA
301 CTGAAACAGG GCACGGGATT TCGGACAAG ATGGGAAAAA TCGGAAGATT
351 CGGTGCAGCT GCGGTGGCTG GTGGCGCGGC AGCGTATACG GTGCTTAAGC
401 CTGCTATGGA CAACAGAAAG CAGCTTGATG AGAACATCAA CCGCGTGTCC
451 AGACAGGCAT TTATTGAGGA TAACAGTAAA TCGGCGAGCT GGATTGCAAC
501 TGAAGGTGCG CAACAGATCA AGGATTGGC ACTTGAACCT GTCCGAAAAA
551 ATGGCGGGAC CCACGATAAG GCTTTGGATT TAATCAGCGG CATGATGACC
601 ACCGGTCTGA ATTTTGCCCA AACCAAGAAT GAAGCGCAGG CCGCATATGC
651 TTTTGCACTT GCCTCAGAAG GCAGTGGCGA GGATACGGCA AAACCTGATTA
701 AAACCTGAA AGATGGCGGC ATGAGCGGTA AAGACCTGCA ACTCGGGCTT
751 GAGCACGTCT TGCAATCGGG TTTAGACGGC ACTTTCGAGG TGCGGGATAT
801 GGTTCGGGAG CTGCCGAGCC TGCTCTCTGC CGCGCAACAG GCAGGGATGA
851 ATGGTGTCTG CGGTTTGGAC TACCTGCTCT CACTCTTACA ATCTGCGGCG
901 AATAAATCGG GCAGTCCTGC CGAAGCGGCG ACTAATGTGC AAAATCTTTT
951 GAGTAAACT CTGTCGCCTG ACACGATAGG TCGTCTGAAG AAGATGGCAA
1001 ATCCGAATGA CCCGAAGAAA GGTGTCGATT GGATAGGCTC GGTGTGCAA
1051 GGCAAGCAAA ACGGCGAAAA CGCAGTGCAG GTGTTGTCCC GTCTTGCCGA
1101 TGCCATGCTA GTAAAGGATA AGCAATACCA AGATTATAAG AAACGCGCGG
1151 CTGACGGCGA TAAGACGGCG GCGGAGCAGG CAAATATGCT TAAGGGCGCG
1201 CTTTGGCGC AACTGCTGCC TGATTGTCAG GCAAAACAAG GTTGTCTGGC
1251 TGCAACGGAT ATGACGCAAA TCCGTGAATA TATGGCTTCG TTGCTGGCG

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1301 TAACGTTGGA TAACGGAAAA ATTGCTAAGA ACAACGAGGC GCGAATGTTG
1351 TCGGCAGCGG CGCAACAAGA GCAACAGGAA TCGCTGGCAA TGTTGCGGGA
1401 AAGTCTGACG GGAACATTGG TGGATATGGA AACCTCGTTT AAAAAGCTGG
1451 CAGCGGAATA CCTAATGCC ACTCTAGCCC TGCAAGCATT GACGACGGCG
1501 GCAACAGCGG CGTCTGCCGC AATGTTATTA ACCGCCGGTG GCGGTAAAGG
1551 TGCAGGCTTT CTGAAAGATG TAGGTAGTAA AGCGTTGGGA TGGGGTAAGG
1601 CTTCCGCGAG CGGCGTGGCA GCAGGTGCCA CAGCGGCAGG CGGTAAGTTG
1651 CTGTCATGGG GAAATCTGC CGGTAGCGGG CTCATGAATA ATCCAGCGTT
1701 AGTTAAACGG GCGGGTTTGT TAGGTATGTT GCTGTATTCC GAGTCTTTGG
1751 GTGACGGCAC ATTGCCAAAG GGTTCGCGTG GTACCAAGAC AACTCCTGAA
1801 ATGATTAATC GTCTGAAAAA CAACGGTATC CGATTGGAAC CTGCGCCGAA
1851 GCGGGAACAG GCGCGGGGTG GTGTCCCTCA GTATTGGCT GCTCCGTCAG
1901 CGCAGCCTAC CGATAAGATG TTGTCTCCGT TGTTTTC AAC TCAGACGGCG
1951 GCGTATCAGG CAGCCATTCA GCAGCAGACG GCGGCGTATC AGGCAGCATT
2001 GCGCGCAGGAT ACGGCTGCAG TTACAACAGG TTTGGCACAA GTGCAAAAGT
2051 CGATGGCGTC GGCAAGTCAG ACCATCAATA CCAATGTGAG CCTGAATATC
2101 GACGGACGTG TTATCGCGAA TGAGGTATCG CGGTATCAAG TGGCCATGTT
2151 GCGCCGTGGA GCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2428; ORF 719>:

```

m719.pep
1  MANGNMKLSL VLTARDDGAR RLLADTQRQL DRTAKSRAQL ERQSHTYALT
51  GIRSEKQIQE EIMLTQAAFN RLARSGKASQ NDLARAATVAT RNRIRELNAE
101 LKQGTGFADK MGKIGRFGAA AVAGGAAAYT VLKPMADNRK QLDENINRVS
151 RQAFIEDNSK SAAWIATEGA QQIKDLALEL VEKNGGTHDK ALDLISGMMT
201 TGLNFAQTKN EAQAAAYAFAL ASEGSGEDTA KLIKTLKDDG MSGKDLQLGL
251 EHVLSQGLDG TFEVRDMVRE LPSLLSAAQQ AGMNGVGGLD YLLSLLQSA
301 NKSQSPAEAA TNVQNLLSKT LSPDTIGRLK KMANPNDPKK GVDWIGSVVQ
351 GKQGENAVQ VLSRLADAML VKDKQYQDYK KRAAAGDKTA AEQANMLKGA
401 LLAQLLPDLQ AKQGLLAATD MTQIREYMAS LAGVTLNNGK IAKNNEARML
451 SAAQQEQEQE SLAMLRRESLT GTLVDMETSF KKLAAEYPNA TLALQALTTA
501 ATAASAAMLL TAGGGKAGGF LKDVGSKALG WGKASAGGVA AGATAAGGKL
551 LSWGKSAGSG LMNNPALVKE AGLLGMLLYS ESLGDTLPK GLRGTKTTPE
601 MINRLKNGI RFEPAKREQ ARGVPOYLA APSAQPTDKM LSPLFSTQTA
651 AYQAAIQQQT AAYQAALAQD TAAVTTGLAQ VQSAMASASQ TINTNVSLNI
701 DGRVIANEVS RYQVAMFGRG AGQ*

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a719.seq not found yet

a719.pep not found yet

g720.seq not found yet

g720.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2429>:

```

m720.seq
1  ATGAGCGGAT GGCATACCTT ATTGCAGGAC GCATCTTACA AGGGCGTCCG
51  CTTTGATATT GAGGTGGTGG ACGAGAGCAA CGGCAAGGCA TTGGCCGAGC
101 ATGCGCGGCC GTTGTGTCAG GGTATCGACC TTGAAGACAT GGCATGACC
151 GGGCGGCAGG TGCAGATTAA TCGGTGTTT TGGGCAAGG GCTATGCAGG
201 CCGTCTGAAA AAGCTGCTGG ATGCGCTGGA GCAGCCGGGC GCGGCGTGC
251 TGCTGCACCC TGTTCGGGG CGGATGCACA ACATGATTGC GGCATCATGG
301 AGTTACCGAC ATGAGGCCGA TTATGTGGAT TATGCGGGCA TCGATATTAC
351 TTTCGCGAG GCGCCGAAG CGCAGGAAAT CTTGTTTTT GAAAACGCCT
401 TTTTGGTCGA GCTTGAGGCG TTGATTGCTA ATATCGACAC CTACCGCGAG
451 GCGGCTATCG GCTTGTGTTA TCGGTGTTG GCGGTGGATG CCGGCGTATC
501 AGCTTTATGG GGCAGCGCGC TGGGCATTG GAGTGCAGCA TCGGGTACGT
551 TTGGCGCGGT GCGCCGTTG TTTGATTGG ACAAAATTCG CTTTCCCGAT
601 CCGGGCGGAT ACAGTGCAGC GCGTTTTAAA AACGGCTCGG CCAAGCTGTT
651 TCGGATATA TCGGTCATGG TAGATACTGG CATACGCCGT GAGGCGGGTT
701 TGGCCGATAA TGCCATGCAC CATGCCGTT GGTGCGCGCG ACAGCGGTTT
751 GACGGGGCTG CGGCTGTTGC CGACCGCGCC GCGCTATCC CTGATAATTT
801 GCTGACCGGC CGCTTTTCAG ACGCCCTGCA AAACCGCTG AACCGGTTAA

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1165

```

851 CCGCCAAACA GGTGCAGCCG GTAGCGCAGG CGGTGCGCCT GTTATCCACG
901 TCATCGCTGT TGTCGGTGGC AACGGCATT ATCGAGGCGC ATGGCGAAGA
951 GATGACCGCG CCCGATTGA TTGAGGTAA CCGCGCCATG CGCCGCCGTA
1001 TGCAGGCCGA GATTGCCGCC TTGCGGGCGG TGCAGACGGC TGCTGCCGAG
1051 TCTGGTGGGC TGACGGCCAA CGCGTGAT ACCGAGGCTT ACCAAACGGC
1101 AGAATCCCTG CGCGGGCGG CAGGCCGTCT GAATGCGTTG GTTGCGGCGG
1151 TCATCAACCA AAAGCCGCCG CTGATTGTGC GCCAAGCCCC AATCGACGGT
1201 ACGATACACC AAATCGCCCA CGAGTTTAC GGCATATAG CCCGCGCAGC
1251 AGAGCTGGTG CGGCTCAATC CCCATATCCA CCACCCCGCG TTTATCAAGC
1301 GCGGCACTTT GGTCAACAGC TATGCAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2430; ORF 720>:

```

m720.pep
  1 MSGWHTLLQD ASYKGVGFDI EVVDESNGKA LAEHARPFVQ GIDLEDMGMT
 51 GRQVQINAVF WGKGYAGRLK KLLDALEQPG GGVLVHPVWG RMHNMIAASW
101 SYRHEADYVD YAGIDITFRE AEAQEIVFV ENAFLVELEA LIANIDTYRE
151 AAIGFVDAVL AVDAGVSALW GSALGIWSAA SGTFGAVRRL FDLDKIAFPD
201 RGGYSAAAFK NGSAKLFADI SVMVDTGIRR EAGLADNAMH HAGWSPRQRF
251 DGAAAVADRA AAPDNLLTG RFSGLQNLRL NRLTAKQVQP VAQAVRLLST
301 SLLSVATAL IEAHGEEMTA PDLIEVNRAM RRRMQAEIAA LRAVQTAAAE
351 SGGLTANAVY TEAYQTAESE RAAAGRLNAL VAAVINQKPP LIVRQAPIDG
401 TIHQIAHEFY GDIARAALV RLNPHIHHPA FIKRGTLVNS YAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2431>:

```

a720.seq (partial)
  1 GGCTGCAAA ACCGCCTGAA CCGTTAACC GCCAAACAGG TGCAGCCGGT
 51 AGCGCAGGCG GTGCGCCTGT TATCCACGTC ATCGCTGTTG TCGGTGGCAA
101 CGGCATTAAT CGAGGCGCAT GCGGAAGAGA TGACCGCGCC CGATTGATT
151 GAGGTTAACC CGCCATGCG CCGCGTATG CAGGCCGAGA TGGCCGCTT
201 ACGGGCGGTG CAGACGGCTG CTGCCGAGTC TGGTGGGCTG ACGGCCAACG
251 CCGTGTATAC CGAGGCTTAC CAAACGGCAG AATCCCTGCG CGCGGCCGCA
301 GGCGTCTGA ATGCGTTGGT TCGGGCGGTC ATCAACCAA AGCCGCCGCT
351 GATTGTGCGC CAAGCCCCAA TCGACGGTAC GATACACCAA ATCGCCACG
401 AGTTTTACGG CGATATAGCC CGCGCAGCAG AGCTGGTGGC GCTCAATCCC
451 CATATCCACC ACCCGCGGTT TATCAAGCGC GGCACTTTGG TCAACAGCTA
501 TGCAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2432; ORF 720.a>:

```

a720.pep (partial)
  1 GLQNLRLNLT AKQVQPVQA VRLSTSSLL SVATALIEAH GEEMTAPDLI
 51 EVNRRMRM QAEIAALRAV QTAASGGL TANAVYTEAY QTAESELR
101 RLNALVAAV INQKPLIVR QAPIDGTIHO IAHEFYGDIA RAAELVRLNP
151 HHHHPAFIKR GTLVNSYAK*

```

m720 / a720 100.0% identity in 169 aa overlap

```

m720.pep      250      260      270      280      290      300
SPRQRFDGAAVADRAAAIPDNLLTGRFSDGLQNLRLNRLTAKQVQPVQAQAVRLLSTSSLL
a720          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
          GLQNLRLNLTAKQVQPVQAQAVRLLSTSSLL
                    10          20          30

m720.pep      310      320      330      340      350      360
SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
a720          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
                    40          50          60          70          80          90

m720.pep      370      380      390      400      410      420
QTAESELRRAAGRLNALVAAVINQKPLIVRQAPIDGTIHQIAHEFYGDIAAAELVRLNP
a720          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QTAESELRRAAGRLNALVAAVINQKPLIVRQAPIDGTIHQIAHEFYGDIAAAELVRLNP
                    100          110          120          130          140          150

m720.pep      430      440
HHHHPAFIKRGTLVNSYAKX

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1166

a720
|||||
HIIHHPAFIKRGTLVNSYAKX
160 170

g721.seq not found

g721.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2433>:

m721.seq
1 ATGTCCAAAA ATGCACAAAA AACCTACTT GCCGTGTGCA GTTTCGAGGT
51 GCAGCCAAAA GACGGGCGAA TCCAACCTGCT GCCATATGGC GAATTTTCGCG
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
151 AACGGTCATG ATGTGCGGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT
201 TGTCGATTAT GAACACCAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAAA
351 AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCCGC GTTGGACGGT
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GACCTGCCTG
551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCCGCGCT CGTGGGAAGCC
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTTCGCGC AGCTGGCGGA
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
701 TGAATAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
751 GCCCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAG
851 AAGGCGTATT GAAACAGCCG GCGGCTTGG CATTTTTGAC CGGCTTTATT
901 GAAAACGCCC AGCCGGTCCG TGCACTGGCA GGCTCGCAAA CGGGCGGTA
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGAG
1001 CAAAATGCT GGGCATGTCC GCGAAGAAT TTGTAAAAAT CAAAGAAAGC
1051 GAAGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2434; ORF 721>:

m721.pep
1 MSKNAQKTL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
51 NGHVVALLAN SSRNQLVVDY EHQTLYKEKN GQPAPAAGWM RWLEFTRKGM
101 FAEVWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPETEON PMKELLQQLF DLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KEDLTXYAPI SVVQELQSKV
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWARGVLKQP GGLAFLTFGI
301 ENAQVVAALA GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351 EGK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2435>:

a721.seq
1 ATGTCCAAAA ATGCACAAAA AACCTACTT GCCGTGTGCA GTTTCGAGGT
51 GCAGCCAAAA GACGGGCGAA TCCAACCTGCT GCCATATGGC GAATTTTCGCG
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
151 AACGGTCATG ATGTGCGGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT
201 TGTCGATTAT GAACACTAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAAA
351 AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCCGC GTTGGACGGT
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GGTCTGCCTG
551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCCGCGCT CGTGGGAAGCC
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTTCGCGC AGCTGGCGGA
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
701 TGAATAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAG
851 AAGGCGTATT GAAACAGCCG GCGGCTTGG CATTTTTGAC CGGCTTTATT
901 GAAAACGCCC AGCCGGTCCG TGCACTGGCA GGCTCGCAAA CGGGCGGTAA
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGAG
1001 CAAAATGCT GGGCATGTCC GCGAAGAAT TTGTAAAAAT CAAAGAAAGC

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1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2436; ORF 721.a>:

```

a721.pep
  1 MSKNAQKTLL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
 51 NGHDVALLAN SSRNQLVVDY EH*TLYKEKN GQPAPAAGWM RWLEFTPKGM
101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPETEON PMKELLQQLF GLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTKYAPI SVVQELQSKV
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAEGVLKQP GGLAFLTGFI
301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351 EGK*

```

a721/m721 99.2% identity in 353 aa overlap

a721.pep	10	20	30	40	50	60
	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPAWYLTEENGHDVALLAN					
m721	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPAWYLTEENGHDVALLAN					
	10	20	30	40	50	60
a721.pep	70	80	90	100	110	120
	SSRNQLVVDYEHXTLYKEKNGQPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
m721	SSRNQLVVDYEHQTLYKEKNGQPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
	70	80	90	100	110	120
a721.pep	130	140	150	160	170	180
	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQQLF					
m721	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQQLF					
	130	140	150	160	170	180
a721.pep	190	200	210	220	230	240
	GLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
m721	DLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
	190	200	210	220	230	240
a721.pep	250	260	270	280	290	300
	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAKGVKQPGGLAFLTGFI					
m721	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAKGVKQPGGLAFLTGFI					
	250	260	270	280	290	300
a721.pep	310	320	330	340	350	
	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAKMLGMSGEEFVKIKESGKX					
m721	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAKMLGMSGEEFVKIKESGKX					
	310	320	330	340	350	

g722.seq not found yet

g722.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2437>:

```

m722.seq
  1 GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCCGCA
 51 TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCTT GATACGCGCG ACCGCGAGTA
201 TTTGGAGCGG CATGCCTCCA TGC GCGGCTT GAGCCGCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTCA
301 GACGACCTGC AAGTGCCTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGCA ATCGCCGACG

```


1168

```

401 AGCCGGGCGC GCGCGCCAAT GTGGGCGACG GCGAGGCGCA ACTGATGGCC
451 GCGCCCGCCG GTGTGGCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTG GAAATCATCC
551 GCGGACCGCC CGCAGGCGGC AACCGTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG TCGTCGGAAG
701 AAAGTGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GTATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTGACA CCCTGATCCC CGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCTGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCGCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2438; ORF 722>:

m722.pep

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLSRR NPTTASGTLT VSGIAQSMLS
101 DDLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VGDGEAQLMA
151 APAGVATECR LTVQGGTDRE SDASLLARLL EIIRRPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV SSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDRR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2439>:

a722.seq

```

1 GTGTTTGAAA CCGCGACATT TGAGCAAATC GCGAGGCGTA TCCTGCGCGA
51 TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCGGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTCCCT GATACCGCCG ACCGCGAGTA
201 TTGGAGCGG CATGCCTCCA TCGCGGCTT GCGCGCGCGC AATCCTACCA
251 CGGCCAGGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGGCCTGC AAGTGCCTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG
401 AGCCGGGCGC GGCCGCCAAT GTGCGCGACG GCGAGGCGCA ACTGATGGCC
451 GCGCCCGCCG GTGTGTCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTG GAAATCATCC
551 GCGGACCGCC CGCAGGCGGC AACCGTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG CCATCGGAAG
701 AAAGTGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GCATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTGACA CCCTGATCCC CGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCGGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCTCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2440; ORF 722.a>:

a722.pep

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLRRR NPTTASGTLT VSGIAQSMLS
101 DGLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VRDGEAQLMA
151 APAGVSTECR LTVQGGTDRE SDASLLARLL EIIRRPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV PSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDLR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

g723.seq not found yet

g723.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2441>:

```
m723.seq
1  ATGCGACCCA AGCCCCGTTT CAGACGGTCT GTTATCGCTT GCTCAATATC
51  AGTGATCACG CCCGAACACC TTATTTTAC CGTTTACAAA CACAATACCG
101 TCTTCGCCCG CGGCCACTTC TTCGCCGCTA TCATCCACGC CCAGCTGCAC
151 TTCGCCTTTG GCCATAGCAC GCAGCAGGTC GAGCACGTCG ATTTTGTAGC
201 GGTTCGGGAT TTCGTCGGTA ATCAACACGC CCTGAGCCGC CGTCAGACGG
251 TAGCGGGCAA TGTCGCAGCA AAGGCGCACC AAGATGGGCG GCAGATCCTC
301 AAAAGGTCGT CTGAACCGCC CCAGATACGC GTCGATTTCG GCAGTGGCGT
351 CCACCAGCGC GGTTCGTGCG ACCTCGCGGT CAATCAGCCC CTCGTTGTTG
401 CCGTCGGTGA GCTGCAAGAC TTCCAGCTCA CCGAAACGCG CAACCATATC
451 CTCAACCGTC GCGTATGCCA TTACTCGACC GCCTTGCCTT GCAGCATAGG
501 CTCGGCGCAG ATTGCCTTCC ACACCGCTTC GCCGACTTCG GCGCGCTTCA
551 CTTGCGGCCA GCCGCCGTCA AACAGCAGGC CGCCGCGCCA AAATTCTTTG
601 CCGTCTGCGC CGGTACTGAC GAGCATCACA TCGCGGCTGT CCGCCAAAGC
651 GTCGGCGGCA CGTTGCGTAT GCTGCACCTT GAGTTCGGCA AGTTCGGCGG
701 ACAGTGCCTT TTTGTCGTCT TCGGCTTTT CCAAGGCTGT GGTCAGCATT
751 TCGACATCGT TTCGGGCGGC GCGAAGCTCT GCCTGCACGG CGTCCAATTC
801 GGCTTTGATG TCTTCAAACG ACGGGGCGGC GGTTTCGGCG GTTTCTGGTT
851 TGTGTTGGT TTTTGCCATG ATGACTCCTT GTTTCAGACG GCGGCGGATT
901 CGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 2442; ORF 723>:

```
m723.pep
1  MRPKPRFRRS VIACISIVIT PEHLIFTVYK HNTVFARGHF FAAIHAQLH
51  FAFGHSTQQV EHVDFVAVAD FVGNQHALSR RQTVAGNVAA KAHQDGRQIL
101 KRSSEPPQIR VDFGSGVHOR GLCDLAVNQP LVVAVGELQD FOLTETRNHI
151 LNRRVCHYST ALRCSIGSAQ IAFHTASPTS ARFTSRQPPS NSRPPRQNSL
201 PSAFVLTSIT SRLSAKASAA RCVCCTLSSA SSADSAFLSS SAFSKAVVSI
251 STSFRAAASS ACTASNSALM SSNDGAAVSA VSGLLLVFAM MTPCFRRRRI
301 RI*
```

a723.seq not found yet

a723.pep not found yet

g724.seq not found yet

g724.pep not found yet

The following partial DNA sequence, shown with its encoded amino acid sequence, was identified in *N. meningitidis* <SEQ ID 2443>:

```
m724.map
ATGAGTTTGAGTAAATTGGCGAAAAAACGGCACAACTGCTAAAAATATCGGCGAAACC
1  -----+-----+-----+-----+-----+ 60
TACTCAAACCTCATTTAACCGCTTTTTTTGCCGTGTTTGACGATTTTATAGCCGCTTTGG
a  M S L S K L A K K T A Q T A K N I G E T -
CTGCGCGCGGCCTTTCGGGGAAAAATCACGCTGGTGGTGTCTCGTCCGAGCCGATACAGCGC
61  -----+-----+-----+-----+-----+ 120
GACGCGCGCCGAAAGCCCCTTTTAGTGCGACCAACACAGCAGGCTCGGCTATGTGCGG
a  L R A A F R G K I T L V V S S E P I Q R -
GTGCAGTTGAGCGGCTTGCCGACGAAACCCTGCAAGACCTTGAACATTTGCAGGAATAC
121 -----+-----+-----+-----+-----+ 180
CACGTCAACTCGCCGAACCGGCTGCTTTGGGACGTTCTGGAACCTGTAAACGTCCTTATG
a  V Q L S G L A D E T L Q D L E H L Q E Y -
GGCTTTGCCAGCCATCCGCCGACGGCAGCGAAGCGGTAGTGATACCGCTGGGCGGCAAT
181 -----+-----+-----+-----+-----+ 240
CCGAAACGGTCGGTAGGCGGGCTGCCGTGCTTCGCCATCACTATGGCGACCCGCGGTTA
a  G F A S H P P D G S E A V V I P L G G N -
```

1170

```

      ACTTCGCACGGTGTGATTGTGTGCAGCCAGCACGGCAGCTACCGCATCAAAAACCTTAAG
241  -----+-----+-----+-----+-----+ 300
      TGAAGCGTGCCCACTAACACACGTCGGTCGTGCCGTGCGTAGTGTGGAATTC
a    T S H G V I V C S Q H G S Y R I K N L K -

      CCCGGCGAGACGGCGATTTTAAATCATGAGGGTGCAAAAATCGTGATTAAGCAAGGCAAA
301  -----+-----+-----+-----+-----+ 360
      GGGCCGCTCTCCGCTAAAAATAGTACTCCCACGTTTTTAGCTAATTCGTTCCGTTT
a    P G E T A I F N H E G A K I V I K Q G K -

      ATCATTGAGGCCGATTGCGACGTGTACCGGGTAACTGCAACAATACGAGGTTAATGCG
361  -----+-----+-----+-----+-----+ 420
      TAGTAACTCCGGCTAACGCTGCACATGGCCCAATTGACGTTTGTATGCTCCAATTACGC
a    I I E A D C D V Y R V N C K Q Y E V N A -

      GCCACGGATGCCAAATTTAACGCTCCGTTGGTGGAGACCAGTGAGTGTGACGGCGCAA
421  -----+-----+-----+-----+-----+ 480
      CGGTGCCTACGGTTTAAATTGCGAGGCAACCACCTCTGGTCACGTCACAACTGCCGCGTT
a    A T D A K F N A P L V E T S A V L T A Q -

      GGCCAAATCAACGGCAACGGCGGCATGGCCGTCGAGGGCGGOGACGGAGCCACCTTTAGC
481  -----+-----+-----+-----+-----+ 540
      CCGGTTTAGTTGCCGTTGCCGCGTACCGGCAGCTCCCGCCGCTGCCTCGGTGGAATCG
a    G Q I N G N G G M A V E G G D G A T F S -

      GCGCATGTTAACCAAACGGCGGCAGCTTTAACACCGACGGCGACGTGGTGGCCGGCAAT
541  -----+-----+-----+-----+-----+ 600
      CCGCTACAATTGGTTTGCCCGCGTCGAAATTGTGGCTGCCGCTGCACCACCGCCGCTTA
a    G D V N Q T G G S F N T D G D V V A G N -

      ATATCGTTGCCGACGACCCGCATACCGACAGCATCGGCGGCAAAACCTTACCGCGGAA
601  -----+-----+-----+-----+-----+ 660
      TATAGCAACGCGGTCTGTTGGGCGTATGGCTGTCTAGCCGCGTTTGGAAATGGCCGCTT
a    I S L R Q H P H T D S I G G K T L P A E -

      CCGGCATAG
661  ----- 669
      GGCCGTATC
a    P A * -

```

Enzymes that do cut: NONE

Enzymes that do not cut: BamHI BglII EcoRI HindIII KpnI NdeI NheI PstI SacI
SalI SmaI SphI XbaI XhoI

This corresponds to the amino acid sequence <SEQ ID 2444; ORF 724>:

m724.pep

```

1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
51  LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKNLK
101 PGETAIFNHE GAKIVIKQ GK IIEADCDVYR VNCKQYEVNA ATDAKFNA PL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
201 ISLRQHPHTD SIGKTLPAE PA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2445>:

a724.seq

```

1  ATGAGTTTGA GTAAATTGGC GAAAAAACG GCACAACTG CTAAAAATAT
51  CGGCGAAACC CTGCGCGCGG CCTTCGGGG AAAAATCACG CTGGTGGTGT
101 CGTCCGAGCC GATACAGCGC GTGCAGTTGA GCGGCTTGGC CGACGAAACC
151 CTGCAAGACC TTGAACATTT GCAGGAATAC GGCTTTGCCA GCCATCCGCC
201 CGACGGCAGC GAAGCGGTAG TGATACCGCT GGGCGGCAAT ACTTCGCACG
251 GTGTGATTGT GTGCAGCCAG CACGGCAGCT ACCGCATCAA AAACCTTAAG
301 CCCGGCGAGA CGGCGATTTT TAATCATGAG GGTGCAAAAA TCSTGATTAA
351 GCAAGGCAAA ATCATTGAGG CCGATTGCCA CGTGTACCGG GTTAACTGCA
401 AACAAATACGA GGTAAATGCG GCCACGGATG CCAAATTTAA CGTCCGTTG
451 GTGGAGACCA GTGCAGTGTT GACGGCGCAA GGCCAAATCA ACGGCAACGG

```

1171

```

501  CGGCATGGCC  GTCGAGGGCG  GCGACGGAGC  CACCTTTAGC  GGCGATGTTA
551  ACCAAACGGG  CGGCAGCTTT  AACACCGACG  GCGACGTGGT  GGCCGCAAT
601  ATATCGTTGC  GCCAGCACCC  GCATACCGAC  AGCATCGGCG  GCAAAACCTT
651  ACCGGCGGAA  CCGGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 2446; ORF 724.a>:

a724.pep

```

1   MSLSKLAKKT  AQTAKNIGET  LRAAFRGKIT  LVVSSEPIQR  VQLSGLADET
51  LQDLEHLQEY  GFASHPPDGS  EAVVIPLGGN  TSHGVIVCSQ  HGSYRIKNLK
101 PGETAIFNHE  GAKIVIKQGK  IIEADCDVYR  VNCKQYEVNA  ATDAKFNAPL
151 VETSAVLTAQ  GQINGNGGMA  VEGGDGATFS  GDVNQTGGSF  NTDGDVVAGN
201 ISLRQHPHTD  SIGGKTLPAE  PA*

```

a724/m724 100.0% identity in 222 aa overlap

	10	20	30	40	50	60
a724.pep	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLDLEHLQEY					
m724	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLDLEHLQEY					
	10	20	30	40	50	60
a724.pep	GFASHPPDGSEAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQGK					
m724	GFASHPPDGSEAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQGK					
	70	80	90	100	110	120
a724.pep	GFASHPPDGSEAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQGK					
m724	GFASHPPDGSEAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQGK					
	70	80	90	100	110	120
a724.pep	IIEADCDVYRVNCKQYEVNAATDAKFNAPLVETSAVLTAQGQINGNGGMAVEGGDGATFS					
m724	IIEADCDVYRVNCKQYEVNAATDAKFNAPLVETSAVLTAQGQINGNGGMAVEGGDGATFS					
	130	140	150	160	170	180
a724.pep	IIEADCDVYRVNCKQYEVNAATDAKFNAPLVETSAVLTAQGQINGNGGMAVEGGDGATFS					
m724	IIEADCDVYRVNCKQYEVNAATDAKFNAPLVETSAVLTAQGQINGNGGMAVEGGDGATFS					
	130	140	150	160	170	180
a724.pep	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
m724	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
	190	200	210	220		
a724.pep	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
m724	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
	190	200	210	220		

g725.seq not found yet

g725.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2447>:

m725.seq

```

1   ATGGTGCGCA  CGGTTAAAAG  CTACAACGGC  GAGGCCGACG  ATTTGGCGGG
51  GCAAAATCCAT  ACGCTGCCCTG  CGGTTTGGGT  AACGTATGGC  GGCAGCAAAG
101 TTGAGCCTGC  CAGCACCGGC  GGCGTATGCG  GACGTTATCA  GGATACCGCC
151 GAATTTGTGG  TGATSGTGCC  GGCCCGCAAT  CTGCGCAACG  AGCAGGCGCA
201 GCGGCAAGGC  GGATCGACA  GCCGCGAAAT  CGGCAGCAAC  GATTTAATCC
251 GCGCTGTTGC  CCGCCTGCTT  GACGGCCAGC  GGCTCGGTTT  TGCCGATAGC
301 CGCGGCTTGG  TGCCCAAAGC  GGTGCGCGCG  ATTGCCAATC  ATGTGCTGGT
351 GCAAAACGCC  GCAGTAAGCA  TATATGCGGT  TGAGTATGCC  ATCCGCTTTA
401 ACACCTGCGG  GTTGGAAAAT  GACCGCTACC  CCGAACGCAC  CGACAATCCC
451 GACGACCCCA  ACCATATCTT  TACCAAGTAT  CAGGGTACAT  TGAGCGAGCC
501 GTGGCCTGAT  TTCGAGGGGT  TGGACGGCAA  AATTTACGAC  CCGCAATCCG
551 CCGATGAAAT  ACGTGTAAC  CTAACCCTTA  AGGATAAGCA  ATGA

```

This corresponds to the amino acid sequence <SEQ ID 2448; ORF 725>:

m725.pep

```

1   MVRTVKSUNG  EADDLAQIHL  TLPVWVTYGG  GSKVEPASTG  GVCGRYQDTA
51  EFVVMVAARN  LRNEQAQRQG  GIDSREIGSN  DLIRAVRRLL  DGQRLGFADS
101 RGLVPKAVRA  IANHVLVQNA  AVSIYAVEYA  IRFNTCGLEN  DRYPERTONP
151 DDENHIIFTKY  QGTLSEPWPD  FEGLDGKIYD  PQSADEIPVN  LTLKDKQ*

```

a725.seq not found yet

a725.pep not found yet

g726.seq not found yet

g726.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2449>:

```
m726.seq
1  ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACAT TGGGCGGCAT
51  CCCCGAAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101 CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151 GTTTTAACCC CGCCGCGCCC GTCCGATTAC CACGAATGGG ACGGCAAAAA
201 ATGGGAAATC AGCAAAGCCG CCGCCGCCGC CCGTTTCGCC AAACAAAAAA
251 CCGCCTTGGC ATTCCGCCTC GCGGAAAGG CCGACGAACT CAAAAACAGC
301 CTCTTGGCGG GCTATCCCA AGTGGAATC GACAGCTTTT ACAGGCAGGA
351 AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401 TGGCGCAAAT CGCCGCCGCA AGGGGCGTGG AATTGGACGT TTTGATTGAA
451 AAAGTTATCG AAAAATCCGC CCGCTGGCT GTTGCCGCCG GCGCGATTAT
501 CGGAAAGCGT CAGCAGCTCG AAGACAAAT GAACACCATC GAAACCGCGC
551 CCGGATTGGA CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
601 GGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2450; ORF 726>:

```
m726.pep
1  MTIYFKNGFY DDTLGGIPEG AVAVRAEYEA ALLAGQAQGG QIAADSDGRP
51  VLTPPRPSDY HEWDGKKWKI SKAAAAARFA KQKTALAFRL AEKADELKNS
101 LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDLVIE
151 KVIEKSARLA VAAGAIIGKR QLEDKLNLI ETAPGLDALE KEIEEWTLNI
201 G*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2451>:

```
a726.seq
1  ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACCT TGGGCAGCAT
51  CCCCGAAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101 CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151 GTTTTAACCC CGCCGCGCCC GTCCGAATAC CACGAATGGG ACGGCAAGAA
201 ATGGGAAATC GGCGAAGCCG CTGCCGCCGC CCGTTTCGCC GAACAAAAAA
251 CCGCCACGGC ATTCGCGCTC GCGGCAAGG CCGACGAACT CAAAAACAGC
301 CTCTTGGCGG GCTATCCCA AGTGGAATC GACAGCTTTT ACAGGCAGGA
351 AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401 TGGCGCAAAT CGCCGCCGCA AGGGGCGTGG AATTGGACGT TTTGATTGAA
451 AAAGTTGTCT AAAAATCCGC CCGCTGGCC GTTGCCGCCG GCGCGATTAT
501 CGGAAAGCGG CAGCAGCTCG AAGACAAAT GAACACCATC GAAACCGCGC
551 CAGGATTGGA CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
601 GGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2452; ORF 726.a>:

```
a726.pep
1  MTIYFKNGFY DDTLGSIEG AVAVRAEYEA ALLAGQAQGG QIAADSDGRP
51  VLTPPRPSEY HEWDGKKWEI GEAAAAARFA EQKTATAFRL AAKADELKNS
101 LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDLVIE
151 KVIEKSARLA VAAGAIIGKR QLEDKLNLI ETAPGLDALE KEIEEWTLNI
201 G*
```

a726/m726 95.5% identity in 201 aa overlap

	10	20	30	40	50	60
a726.pep	MTIYFKNGFYDDTLGSIPEGAVAVRAEYEAALLAGQAQGGQIAADSDGRPVLTTPPRPSEY					
m726	MTIYFKNGFYDDTLGSIPEGAVAVRAEYEAALLAGQAQGGQIAADSDGRPVLTTPPRPSDY					
	10	20	30	40	50	60

1173

	70	80	90	100	110	120
a726.pep	HEWDGKKWEIGAAAAARFAEQKTATAFRLAAKADELKNSLLAGYPQVEIDSFYRQEKEA					
	: : :					
m726	HEWDGKKWKISKAAAAARFAQKTALAFRLAEKADELKNSLLAGYPQVEIDSFYRQEKEA					
	70	80	90	100	110	120
	130	140	150	160	170	180
a726.pep	LARQADNNAPTMLAQIAAARGVELDVLIEKVVEKSARLAVAAGAIIGKRQCLEDKLNTI					
	: : : : :					
m726	LARQADNNAPTMLAQIAAARGVELDVLIEKVIEKSARLAVAAGAIIGKRQCLEDKLNTI					
	130	140	150	160	170	180
	190	200				
a726.pep	ETAPGLDALEKEIEEWTLNIGX					
m726	ETAPGLDALEKEIEEWTLNIGX					
	190	200				

g727.seq not found yet

g727.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2453>:

m727.seq

1	ATGAATCTCG	TGAAACTGCT	GGCGAATAAC	TGGCAACCGA	TGCCCATTAT
51	CGCGCTTGTC	GGCACGGGCT	TGGCTGTGTC	GCACCATCAA	GGCTACAAGT
101	CGGCATTGTC	GAAGCAGCAG	GCGGTCATCG	ACAAGATGGA	GCGCGACAAG
151	GCGCAAGCCC	TGCTGTTGTC	GGCTCAAAAC	TATGCGCGCG	AACTGGAACT
201	GGCACGCGCG	GAAGCTAAAA	AATATGAAGT	CAAGGCGCAC	GCTGTCGGCA
251	TGGCTTTGGC	GAAAAAACAG	GCGGAAGTCA	GCCGTCTGAA	AACGGAAAGA
301	GACCTTTGCA	AAATTCCTTT	CCCTCCCGAC	AGCCGAAACC	CAAACACAGG
351	TTTTCGGCTG	TTTTCGCCCC	AAATACCGCC	TAATTTTACC	CAAATACCCC
401	CTTAA				

This corresponds to the amino acid sequence <SEQ ID 2454; ORF 727>:

m727.pep

1	MNLVKLLANN	WOPIAIIALV	GTGLAVSHHQ	GYKSAFAKQQ	AVIDKMERDK
51	AQALLLSAQN	YARELELARA	EAKKYEVKAH	AVGMALAKKQ	AEVSRLKTER
101	DLCKIPFPD	SRNPNTGERL	FSPQIPPNFT	QIPP*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2455>:

a727.seq

1	ATGAATCTCG	TGAAACTGCT	GGCGAATAAC	TGGCAACCGA	TGCCATCAT
51	CGCGCTTGTC	GGCACGGGTT	TGGCGGTGTC	GCACCATCAA	GGCTACAAGT
101	CGGCTTTTGC	GAAGCAGCAG	GCGGTCATTG	AGAAAATGAA	GCGCGACAAG
151	GCGCAAGCCC	TGCTGTTGTC	GGCTCAAAAC	TACGCCCGCG	AACTGGAACA
201	GGCGCGTGCG	GAAGCTAAAA	AATATGAAGT	CAAGGCGCAC	GCCGTGCGCA
251	TGGCTTTGGC	GAAAAAACAG	GCGGAAGTCA	GCCGTCTGAA	AACGGAAAAT
301	AAAAAGGAAA	TCGAAAATGT	CCTTACTCAA	GACCGTAAAA	ATGCAGGCGG
351	CGGTTGTATT	GACGGCTTTG	GCCATCACGG	CTTGCAGCTC	TACAAGCGCG
401	CCCTCGGCTA	CGGAAATTAA			

This corresponds to the amino acid sequence <SEQ ID 2456; ORF 727.a>:

a727.pep

1	MNLVKLLANN	WOPIAIIALV	GTGLAVSHHQ	GYKSAFAKQQ	AVIEKMKRDK
51	AQALLLSAQN	YARELEQARA	EAKKYEVKAH	AVGMALAKKQ	AEVSRLKTEN
101	KKEIENVLTQ	DRKNAGGGCI	DGFGHHGLQL	YKRALGYGN*	

a727/m727 83.2% identity in 119 aa overlap

	10	20	30	40	50	60
a727.pep	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN					
	: : : : :					

1174

```

m727      MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMERDKAQALLLSAQN
           10      20      30      40      50      60
           70      80      90      100     110     119
a727.pep   YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENV-LTQDRKNAGGGC
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m727      YARELELARAEAKKYEVKAHAVGMALAKKQAEVSRLKTE--RDLCIIPFPDSRNPNTGF
           70      80      90      100     110
           120     130     140
a727.pep   IDGFGHHGLQLYKRALGYGNX
m727      RLFSPIPPNFTQIPPX
           120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2457>:

```

g728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGAGACT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTTCGCTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CGGGGAATAA TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTTCGG ATTTGATGCG GCGGGGCGCG GGAATATCGG GGAAGATGTT
601 TATGATGCGT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCGG GGGGATGAAG CGCAACAGTC TTGTGGTTCG
801 TATATGATCG GACGGTCTGC CGCAAAAAGT CTATTGAGAT TTCGACAATG
851 GAAAAAAGCG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901 ATTGCACAAT CTTGACGCGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTTGGAT GGCGGGCGGA
1001 TATCCGCGCA AGAGAAACAG GGAGACAGAC TGCTGATTTT TCCTTTGAAC
1051 TTGGAAGATT TGGAAAAAGA GGTGAGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG GCCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2458; ORF 728>:

```

g728.pep
1  MFKFKPVL L SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNFV
51  AKLARLFERNA DRVVIVKES MRTEESLAGA VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTAHGEN YETTGEYRVV WPDGVSFDA AGRGKIGEDV
201 YEHCLGQYQM AQVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFFYQN
251 MRELMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
301 IAQSSSTVALK ADGVTADMOT YHAQQTWYLD GGRIIREEKQ GDRLPDFPLN
351 LEDLEKEVSR YAEAAAARRSG GRRGLSH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2459>:

```

m728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACCG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAATCTT TGCCGGAACG GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTTCGCTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA

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1175

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501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGCCAACCAG
551 ACGGTTCCGT ATTTGATGCG GCGGGGCGCG GGAAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGT'TGGGAC TTCCGCAAAG
701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAA
751 ATGCGGGAAT TGATGCCCGG AGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTT
901 ATTGCACAAAT CTTGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGAGACC TATCATGCGC AACAGACGTG GTATTGGAT GCGGGCGGA
1001 TTGTCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATT TCCTTTGAAC
1051 TTGGAAAATT TGGAAAAAGA GGTGCGCCG TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGC ACCTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2460; ORF 728>:

m728.pep

```

1 MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPKNPNAFV
51 AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTVHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGICYM AQVYLAKYRD VANDEQKVWD FRKESNRIAS DSRNSVFYQN
251 MRELMPRGMK ANSLVVGIDA DGLPQKVYWS FDNGKKRQSF EYYLKNLNF
301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
351 LENLEKEVRR YAEAAARRSG GRRDLSH*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 728 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF728.a) from *N. gonorrhoeae*:

m728 / g728

m728.pep	10	20	30	40	50	60
	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA					
g728						
	10	20	30	40	50	60
m728.pep	70	80	90	100	110	120
	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV					
g728						
	70	80	90	100	110	120
m728.pep	130	140	150	160	170	180
	WLDYHIGEGGLVAVLSQRSPEAFVNAEYLYRNDRPFSNVYGGTVHGENYETTGEYRVV					
g728						
	130	140	150	160	170	180
m728.pep	190	200	210	220	230	240
	WQPDGSVFDAAGRGKIGEDVYEHCLGICYMAQVYLAKYRDVANDEQKVWDFRKNESNRIAS					
g728						
	190	200	210	220	230	240
m728.pep	250	260	270	280	290	300
	DSRNSVFYQNMRELMPRGMKANSLVVGIDADGLPQKVYWSFDNGKKRQSF EYYLKNLNF					
g728						
	250	260	270	280	290	300
m728.pep	310	320	330	340	350	360
	IAQSSTVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					

1176

g728 IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIIREEKQGDRLPDFPLNLEDLEKEVSR
 310 320 330 340 350 360

 370

m728.pep YAEAAARRSGGRRDLSHX
 |||||
 g728 YAEAAARRSGGRRGLSHX
 370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2461>:

a728.seq

1	ATGTTTAAAA	AATTCAAACC	GCTACTGTTG	TCATTTTTTG	CACTTGTATT
51	TGCCTTTTGG	CTGGGAACGG	GTATTGCCTA	TGAGATTAAT	CCGCGTTGGT
101	TTTTGAGCGA	TACGGCAACT	GAAAAACCGA	ATGCTTTTGT	GGCGAAACTT
151	GCCCGCCTGT	TCCGAAATGC	CGACAGGGCG	GTTGTATCG	TGAAGGAATC
201	GATGAGGACG	GAGGAAAGTC	TTGCCGGAGC	TGTGGATGAC	GGTCCGTTGC
251	AGTCGGAGAA	GGATTATCTT	GCACTCGCTG	TCCGGCTCAG	TCGTTTGAAA
301	GAAAAGGCGA	AATGGTTTCA	CGTAACGGAG	CAGGAACATG	GGGAAGAGGT
351	TTGGCTGGAT	TACTATATCG	GCGAGGGCGG	TTTGGTTGCG	GTTTCGCTTT
401	CGCAACGCTC	GCCGGAAGCG	TTTGTTAATG	CCGAATATCT	GTATCGGAAC
451	GATCGTCCGT	TTTCTGTAAA	TGTGTACGGC	GGAACGGTTC	ACGGGGAAAA
501	TTATGAACAC	ACAGGAGAAT	ATCGGGTTGT	TTGGCAACCG	GACGGTTCGG
551	TATTTGATGC	GTCGGGGCGC	GGGAAAATCG	GGGAAGATGT	TTATGAGCAT
601	TGCCTCGGGT	GTTATCAGAT	GGCCCAGGTA	TATTTGGCGA	AATATCGGGA
651	TGTCGCGAAT	GATGAGCAGA	AGGTTTGGGA	CTTCCGCGAA	GAGAGTAACC
701	GGATTGCGTC	GGACTCGCGC	GATTCTGTGT	TTTATCAGAA	TATGCGGGAA
751	TTGATGCCCC	GAGGGATGAA	GGCAAACAGT	CTTGTGGTCG	GCTATGATGC
801	GGACGGTCTG	CCGCAGAAAG	TCTATTGGAG	TTTCGACAAT	GGGAAAAAAC
851	GCCAGAGTTT	CGAATATTAT	TTGAAAAACG	GAAATCTTTT	TATTGCACAA
901	TCTTCGACGG	TAGCATTGAA	AGCGGATGGC	GTAACGGCGG	ATATGCAGAC
951	CTATCATGCG	CAACAGACGT	GGTATTTAGA	TGGCGGGCGG	ATTGTCCCGG
1001	AAGAGAAACA	GGGGGACAGA	CTGCCTGATT	TTCTTTTGAA	CTTGAAGAT
1051	TTGGAAAAAG	AGGTGAGCCG	TTATGCAGAG	GCTGCGGCGA	GACGTTCCGG
1101	CGGCAGGCGC	GACCTTTCTC	ACTGA		

This corresponds to the amino acid sequence <SEQ ID 2462; ORF 728.a>:

a728.pep

1	MFKKFKPVLL	SFFALVFAFW	LGTGIAYEIN	PRWFLSDTAT	ENPNAFVAKL
51	ARLFRNADRA	VVIVKESMRT	EESLAGAVDD	GPLQSEKDYL	ALAVRLSRLK
101	EKAKWFHVTE	QEHGEEVWLD	YYIGEGGLVA	VLSQRSPEA	FVNAEYLYRN
151	DRPFSVNVYG	GTVHGENYET	TGEYRVVWQP	DGSVFDASGR	GKIGEDVYEH
201	CLGQYQMAQV	YLAKYRDVAN	DEQKVWDFRE	ESNRIASDSR	DSVFYQNMRE
251	LMPRGMKANS	LVVGYDADGL	PQKVYWSFDN	GKKRQSF EY	LKNGNLFIAQ
301	SSTVALKADG	VTADMQTYHA	QQTWYLDGGR	IVREEKQDGR	LPDFPLNLED
351	LEKEVSRYAE	AAARRSGGRR	DLSH*		

a728 / m728 96.3% identity in 377 aa overlap

	10	20	30	40	50	
a728.pep	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATE---NPNAFVAKLARLFRNA					
m728	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA					
	10	20	30	40	50	60
a728.pep	DRAVVIVKESMRT EESLAGAVDDGPLQSEKDYLALAVRLSRLKEKAKWFHVTEQEHGEEV					
m728	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV					
	70	80	90	100	110	120
a728.pep	WLDYYIGEGGLVAVLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV					
m728	WLDYHIGEGGLVAVLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV					
	130	140	150	160	170	180

g729.seq

This corresponds to the amino acid sequence <SEQ ID 2464; ORF 729>:

g729.pap

1	MNTTLKTTTL	SVAAAFALSA	CTMIPQYEQP	KVEVAETFQN	DTSVSSIRAV
51	DLGWHDFAD	PRLQKLIDIA	LERNTSLRTA	VLNSEIYRKQ	YMIERNLLP
101	TLAANANGSR	QGSLSGGNVS	SSYNVGLGAA	SYELDLFGRV	RSNSEAALQG
151	YFASVANRDA	AHLILIATVA	KAYFNERYAE	KAMSLAQRVL	KTREETYKLS

m729.seq

1	ATGGATACTA	CATTGAAAC	CACCTTGACT	TCTGTTGCAG	CAGCCTTTGC
51	ATTGCTGTC	TGACCATGA	TTCGCCAATA	CGAGCAGCCC	AAAGTCGAAG
101	TATGCCGAAT	GTTCAAAAC	GATACCCGCG	ACAGCGGCAT	CCGCGCCGTC
151	GATTTAGGTT	GGCATGACTA	TTTTGCCGAC	CCGCGCCTGC	AAAGCTIGAT
201	CGACATCGCA	CTCGAGCGCA	ATACCAGTTT	GCGTATCCGC	GTATTGAAAC
251	GCGAAATCTA	CCGCAAAACA	TACATGATTG	AGCGCAACAA	CCTCCTGCCC
301	ACGCTTGCC	CCAATTGCGA	CGACTCGCGC	CAAGGCAGCT	TGAGCGCGCG
351	CAATGTAAGC	AGCAGCTACA	AAGTCGGACT	GGGTGCGGCA	CTTTACGAAC
401	TCGATGTGTT	CGGGCGTGTA	CGCAGCA3CA	CGCAGGCGGC	ACTGCAAGGC
451	TATTTCGCCA	GCACCGCCAA	CCGCGAT3CG	GCACATTGTA	GCCTGATTGC
501	CACCGTTGCC	AAAGCCTTAT	TCAACGAACG	TTACGCCCGTA	GAAGCGATGT
551	CTTTGGCGCA	ACGTGTTTTG	AAAACGCGCG	AGGAAACCTA	CAAGCTGTCC
601	GAATTACGTT	ACAAGGCAGG	CGTGATTTCC	CCCGTCGCCC	TACGTGACGA
651	GGAAGCCCTG	ATCGAATCTG	CCAAAGCCGA	TTATGCCCAT	GCCGCGCGCA
701	GCCGCGAACA	GGCGCGCAAT	GCCTTGCGAA	CCTTGATTAA	CCAACCGATA
751	CCCGAAGACC	TGCCTCGCGG	TTTGCCCGTG	GACAACAGAT	TTTTTGTTGA
801	AAAATGCGC	CGCGGTTTGA	GTTCGGAAGT	ATTGCTCGAC	CGTCCCGATA
851	TCCGTGCTGC	CGAACACGCG	CTCAAACAGG	CAAACGCCAA	TATCGGTGCG
901	GCACGCGCCG	CCTTTTTTCC	ATCCATTCCG	CTGACCCGAA	CCGTGCGTAC
951	GGGTTCGTCC	GAATTGGGTG	GGTTGTTCAA	AAGCGGCACG	GGCGTTTGGT
1001	CGTTCGCGCC	GCTATTATCC	TGCGCGATT	TTACCTGGGG	TACGAAACAAG
1051	GCGAACCTTG	ATGTAGCCAA	GCTGCGCCAA	CAGGTACAAA	TCGTTGCGCTA
1101	TGAATCCGCG	GTCCAATCCG	CATTTCAAGA	CGTGGCAAC	GCATTGCGCG
1151	CGCGCGAGCA	GCTGGATAAA	GCCTATGACG	CTTTAAGCAA	ACAAGAGCCG
1201	GCCCTCTAAG	AAGCTTTGCG	CTTGTCGCG	CTGCGTTTAC	AGCAGCGCGT
1251	ATCGGCGCGC	CTCGACTTGC	TCGATGCGGA	ACGACGACG	TATGCGCGCG
1301	AGGTGCGCGC	TTTGTGCGGA	CAACTGACCC	GCGCGGAAA	CCTTGCCGAT
1351	TTGTACAAGG	CACTCGGCGG	CGGATTGAAA	CGGGATACCC	AAACCGACAA
1401	ATAA				

m729.ppt

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1 MDTTLKTTLT SVAAAFALSA CTNIPOYEQP KVEVAETFKN DTADSGIRAV
51 DLGWHDFYAD PRLOKLIDIA LERNSTLRTA VLNSEIYRKQ YMIERNNLLP
101 TLAANANDSR QGSLSGGNVS SSVYKVLGAA SYELDLFGRV RSSEALQG
151 YFASTANRDA AHLSLIATVA KAFYNERAYE EAMSLAQRVL KTREETYKLS
201 ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN ALATINQPI
251 PEDLPAGLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LQANANIGA
301 ARAAFPSIR LTGTVGTGSA ELGLLFKSGT GVWSFAPSIT LPIFTWGTNK
351 ANLDVAKLRV QVQIVAYESA VQSAFQDVAN ALAAREQLDK AYDALSKQSR
401 ASKEALRLVG LRYKHGVSGA LDLLDAERSS YAAEGAALSA QLTRAENLAD
451 LYKALGGGLK RDTOTDK*

```

ORF 729 shows 95.7% identity over a 467 aa overlap with a predicted ORF (ORF729.a) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m729.pep	<u>MDTTLKTTLTSVAAAFALSACTMIPQYEQPKVEVAETFKNDDTADSGIRAVDLGWHDYFAD</u>					
	: :					
g729	<u>MNTTLKTTLTTSVAAAFALSACTMIPQYEQPKVEVAETFQNDSVSISRAVDLGWHDYFAD</u>					
	10	20	30	40	50	60

1179

	70	80	90	100	110	120
m729.pep	PRLOKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQGSLSGGNVS					
g729	PRLOKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANGSRQGSLSGGNVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m729.pep	SSYKVGGLGAASYELDLFGRVRSSEALQGYFASTANRDAHLSLIATVAKAYFNERVAE					
g729	SSYNVGLGAASYELDLFGRVRSNSEALQGYFASVANRDAHLILIATVAKAYFNERVAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m729.pep	EAMSLAQRLVLTREETYKLSELRYKAGVISAVALRQQEALIESAKADYAHAAARSREQARN					
g729	KAMSLAQRLVLTREETYKLSELRYKAGVISAVALRQQEALIESAKADYAHAAARSREQARN					
	190	200	210	220	230	240
	250	260	270	280	290	300
m729.pep	ALATLINRPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
g729	ALATLINRPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m729.pep	ARAAFFPSIRLTGTVTGSAELGGLFKSGTGVWSFAPSITLPIFTWGTNKANLDVAKLRQ					
g729	ARAAFFPSIRLTGSVGTGSVELGGLFKSGTGVWAFAPSITLPIFTWGTNKANLDVAKLRQ					
	310	320	330	340	350	360
	370	380	390	400	410	420
m729.pep	QVQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSGA					
g729	QAQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSGA					
	370	380	390	400	410	420
	430	440	450	460		
m729.pep	LDLLDAERSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX					
g729	LDLLDAERISYSAEGAALSAQLTRAENLADLYKALDGGGLKRDQTQGX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2467>:

a729.seq

1	ATGGATACTA	CATTGAAAAC	CACCTTGACT	TCTGTTGCAG	CAGCCTTCGC
51	ATTATCCGCC	TGCACCATGA	TTCCCAATA	CGAGCAGCCC	AAAGTCGAAG
101	TTGCCGAAAC	GTTCAAAAAC	GATACCGCCG	ACAGCGGCAT	CCGTGCGGTC
151	GATTTGGGTT	GGCATGACTA	TTTTGCCGAC	CCGCGCCTGC	AAAAGCTGAT
201	CGACATCGCA	CTCGAGCGCA	ATACCAGTTT	GCGTACCGCC	GTATTGAACA
251	GCGAAATCTA	CCGCAACAA	TACATGATTG	AGCGCAACAA	CCTCTGCCCC
301	ACGCTTGCCG	CCAATGCGAA	CGACTCGCGC	CAAGGCAGCT	TGAGCGGCGG
351	CAATGTAAGC	AGCAGCTACA	AAGTCGGACT	GGGTGCGGCA	TCTTACGAAC
401	TCGATCTGTT	CGGGCGTGTA	CGCAGCAGCA	GCGAGGCGGC	ACTGCAAGGC
451	TATTTGCGCA	GCACCGCCAA	CCGCGATGCG	GCACATTTGA	GCCTGATTGC
501	CACCGTTGCC	AAAGCCTATT	TCAACGAACG	TTATGCCGAA	GAAGCGATGT
551	CTTTGGGCGA	ACGTGTTTTG	AAAACGCGCG	AGGAAACCTA	CAAGCTGTCC
601	GAAATPACGTT	ACAAGGCAGG	CGTGATTTC	GCCGTCGCC	TACGTCAGCA
651	GGAAGCCCTA	ATCGAATCTG	CCAAAGCCGA	TTATGCCCAT	GCCGCGCGCA
701	GCCGCGAACA	GGCGCGCAAT	GCCTTGGCAA	CCCTGATTAA	CCAACCGATA
751	CCCGACGACC	TGCCCGCCGG	TTTGCCGTTG	GACAAGCAGT	TTTTTGTGTA
801	GAGCTGCGG	GCCGTTTGA	GTTCCGAAGT	ATTGCTCGAC	CGTCCCGATA
851	TCCGTGCTGC	CGAACACGCG	CTCAACAGG	CAAACGCCAA	TATCGGTGCG
901	GCACGCGCG	CCTTTTCCC	ATCCATCCGC	CTGACCGGAA	GCGTCGATAC
951	GCATTCTGCC	GAATTGGGCG	GGCTGTTCAA	AAGCGGCACC	GGCGTTTGGT
1001	TGTTCCGACC	TTCCATTACC	CTGCCGATT	TTACCTGGGG	TACGAACAAG

1180

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1051 GCGAACCTCG ATGTAGCCAA GCTGCGCCAA CAGGCACAAA TC GTTGCCTA
1101 TGAAGCCGCC GTCCAATCCG CATTTCAAGA CGTGGCAAAC GCATTGACCG
1151 CGCGCGAGCA GTTGGATAAA GCCTATGACG CTTTAAGCAA ACAAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG TTTGGTCGGT CTGCGTTACA AACACGGCGT
1251 ATCCGGCGCG CTCGACTTGC TCGATGCGGA ACGCAGCAGC TATTCGGCGG
1301 AAGGTGCGGC TTTGTGCGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CACTCGGCGG CGGATTGAAA CGGGATACCC AAACCGACAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2468; ORF 729.a>:

a729.pep

```

1 MD TTLK TLT SVAAAFALSA CTMI PQYE QP KVEVAETFKN DTADSGIRAV
51 DLGWHDFAD PRLQKLIDIA LERN TSLRTA VLNSEIYRKQ YMIERNNLLP
101 TLAANANDSR QGSLSGGNVS SSYK VGLGAA SYELDLFGRV RSSSEALQG
151 YFASTANRDA AHLSLIATVA KAYFNER YAE EAMSLAQRVL K TREETYKLS
201 ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN ALATLINQPI
251 PDDLPA GLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
301 ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK
351 ANLDVAKLRQ QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR
401 ASKEALRLVG LRYKHGVS CA LDLLDAERSS YSAEGAALSA QLTRAENLAD
451 LYKALGGGLK RDTQTDK*

```

a729 / m729 98.1% identity in 467 aa overlap

	10	20	30	40	50	60
a729.pep	MD TTLK TLT SVAAAFALSA CTMI PQYE QP KVEVAETFKN DTADSGIRAV DLGWHDFAD					
m729	MD TTLK TLT SVAAAFALSA CTMI PQYE QP KVEVAETFKN DTADSGIRAV DLGWHDFAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
a729.pep	PRLQKLIDIALERN TSLRTAVLNSEIYRKQYMIERNNLLPTLAANANDSRQGSLSGGNVS					
m729	PRLQKLIDIALERN TSLRTAVLNSEIYRKQYMIERNNLLPTLAANANDSRQGSLSGGNVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
a729.pep	SSYK VGLGAASYELDLFGRVRSSEALQGYFASTANRDA AHLSLIATVAKAYFNER YAE					
m729	SSYK VGLGAASYELDLFGRVRSSEALQGYFASTANRDA AHLSLIATVAKAYFNER YAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a729.pep	EAMSLAQRVLK TREETYK LSELRYKAGVIS AVALRQOEALIESAKADYAH AARSREQARN					
m729	EAMSLAQRVLK TREETYK LSELRYKAGVIS AVALRQOEALIESAKADYAH AARSREQARN					
	190	200	210	220	230	240
	250	260	270	280	290	300
a729.pep	ALATLINQPI PDDLPA GLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
m729	ALATLINQPI PDDLPA GLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
	250	260	270	280	290	300
	310	320	330	340	350	360
a729.pep	ARAAFFPSIRLTGSVDTHSAELGGLFKSGTGVWLFAPSITLPIFTWGTNKANLDVAKLRQ					
m729	ARAAFFPSIRLTGTGTGS AELGGLFKSGTGVWLFAPSITLPIFTWGTNKANLDVAKLRQ					
	310	320	330	340	350	360
	370	380	390	400	410	420
a729.pep	QAQIVAYEAAVQSAFQDVANALTAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVS GA					
m729	QVQIVAYESAVQSAFQDVANALAAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVS GA					
	370	380	390	400	410	420

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	430	440	450	460
a729.pep	LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX			
m729	LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX			
	430	440	450	460

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2469>:

g730.seq

```

1   GTGAAACCGC TGCCGAGACT GACAAACCTC CTTGCCGCCT GCGCCGTAGC
51  GCGCGTCGCA CTCATACAGC CCGCCCTCGC GCGCGACTTG GCGCAAGACC
101 CGTTCATTAC CGATAACACC CAACGGCAGC ACTACGAACC CCGCGGCAAA
151 TACCACCTCT TCGGCGaCCC GCGCGGAGC GTTTCGACG GCACCGGCAA
201 AATCAACGTC ATCCAAGACT ATACCCACCA GATGGGCAAC CTGCTCATCC
251 AACAGCGCGC AATCCAAGGC AATCTGGT ACACCGTCCG CTTTCCGGA
301 CACGGACACG AAGAACACGC CCCCTTCGAC AACCACGCCG CCGACAGCGC
351 AAGCGAAGAA AAAGGCAACG TTGACGACGG CTTTACCGTG TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCGCGCG ATGCCTACGA CGGCCGAAG
451 GCGCGCAATT ACCCCAAACC TACGGGCGCA CGAGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCCCGCA GTATCAAACT CAATCCGACC GACACCGCA
551 GCATTCGGCA ACGCATATTC GACAACTACA ACAACCTCGG CAGCAATTTC
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TGTCACCGC GTCGCCGCCG
701 GCGCGCTCAA CCCCTTTATC AGCGCGGCGG AAGCCTTGGG CATAGCGGAC
751 ATACTGTACG GAACCGGCTA TGCCATAGAC AAAGCCGCGA TCGCAACAT
801 CGCCCCCTTA CCCGCCGAGG GCAAATTCGC CGCCATCGGC GGCTTGGGCA
851 GCGCGGCGGG CTTTGAAAAA AATACGCGCG AAGCCGTTGA CCGGTGGATA
901 CAGGAAAACC CCAATGCCGC CGAAACCGTC GAAGCCCTGG TCAACGTCCT
951 GCCGTTTGCC AAAGTCAAAA ACCTGACAAA GGCGGCAAAA CCGGGGAAGG
1001 CTGCGGTTAG TGGGGATTTT TCTAAATCCT ACACCTGCTC CTTCCACGGC
1051 AGCACCTTGG TCAAACGGC AGACGGCTAC AAAGCCATTG CCCATATTCA
1101 AGCCGGAGAC CGGTCCTTT CCAAGGACGA GGCAAGCGGA GAAACGGGAT
1151 ACAACCCCGT TACCGCCGA TACGGCAATC CGTATCAAGA AACCGTTTAC
1201 ATTGAAGTTT CAGACGGCAT CGGCAACAGC CAAACCTGTA TTTCCAACCG
1251 CATCCACCCG TTTTATTCGG ACGCAAAATG GATTAAGGCG GAAGATTTAA
1301 AAGCGGGAAG CCGGCTGTTA TCCGAAAGCG GCAAACCCA AACCGTCCGC
1351 AACATCGTTG TCAAACCAA ACCGCTCAA GCCTACAA C TGACCGTTGC
1401 CGATTGGCAT ACCTACTTCG TCAAGGGTAA TCAGGCGGAA ACGGAAGGGG
1451 TTTGGGTTCA TAAATGATTGT CCGCTAAAC CAAACCAAC CAATCATGCC
1501 CAACAAAGAA AAGAAGAAGC TAAACACGAT TCTCATCGAA GTGTGGGAGA
1551 TTCCAATCGT GTCGTTCCGG AAGGAAAGCA ATATTTAGAT TCCGACACAG
1601 GAAACCATGT TTATGTAAAA GGAGATAAAG TGGTTATTCT AACTCCTGAT
1651 GGAAGACAGG TAACTCAATT TAAGAACTCG AAAGCCAATA CGTCAAAAAG
1701 GGTAAAAAAT GGGAAATGGA CACCAAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2470; ORF 730.ng>:

g730.pep

```

1   VKPLRLTNL LAACAVAAVA LIQPALAADL AODPFITDNT QRQHYEPGGK
51  YHLFGDPRGS VSDRTGKINV IQDYTHQMGN LLIQAAAIQG NLGYTVRFSG
101 HGHEEHAPFD NHAADSASEE KGNVDDGFTV YRLNWEGHEH HPADAYDGPK
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQRIF DNYNNLGSNF
201 SDRADANRK MFEHNAKLDR WGNMSEFVNG VAAGALNPFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPL PAEGKFAAIG GLGSAAGFEK NTREAVDRWI
301 QENPNAETV EALVNVLPFA KVKNLTKAAK PGKAAVSGDF SKSYTCSFHG
351 STLVKTADGY KAIAHIQAGD RVLKSKDEASG ETGYPVTAR YGNPYQETVY
401 IEVSDGIGNS QTLISNRIEP FYSDGKWIKA EDLKAGSRLI SESGKTQTVR
451 NIVVKPKPLK AYNLTVADWH TYFVKGNQAE TEGVWVHND C PPKPKPTNHA
501 QQRKEEAKND SHRSVGDSNR VVREGKQYLD SDTGNHVYVK GDKVVILTFD
551 GRQVTQFKNS KANTSKRVKN GKWTFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2471>:

m730.seq

```

1   GTGAAACCGC TGCCGAGACT GACAAACCTC CTTGCCGCCT GCGCCGTAGC
51  GCGCGCGCGA CTCATACAGC CCGCCCTCGC GCGCGACTTG GCGCAAGACC

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```

101 CGTTCATTAC CGATAACGCC CAACGGCAGC ACTACGAACC CGGCGGCAAA
151 TACCACCTCT TCGGCGACCC GCGCGGCAGC GTTTCGACC GCACCGGCAA
201 AATCAACGTC ATCCAAGACT ATACCCACCA GATGGGCAAC CTGCTCATCC
251 AACAGGCAAA CATCAACGGC ACAATCGGCT ACCACACCCG CTTTCCGGA
301 CACGGACACG AAGAACACGC CCCCTTCGAC AACCACGCCG CCGACAGCGC
351 GAGCGAAGAA AAAGGCAACG TTGACGAAGG CTTTACCGTA TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCCGCCG ATGCCTACGA CGSCCGAAG
451 GCGGGCAATT ACCCCAAACC TACGGGCGCA CGAGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCCCGCA GTATCAAACT CAATCCGACC GACACCGCA
551 GCATCCGGCA ACGCATATCC GACAATTACA GCAACCTCGG CAGCAATTTC
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TATCAACGGC GTCCCGCCCG
701 GCGCGCTCAA CCCCTTTATC AGCGCGGGCG AAGCCTTGGG CATAGGCGAC
751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCAA TGCGCAACAT
801 CGCCCCCTTG CCCGCCGAGG GCAAATTCGC CGTCATCGGC GGCTTGGGCA
851 GCGTGGCGGG CTTTGAAAAG AATACGCGCG AAGCCGTGTA CCGGTGGATA
901 CAGGAAAAAT CCAATGCCGC CGAAACCGTC GAAGCCGTCT TCAACGTTGC
951 CGCAGCAGCC AAAGTCGCGA AGTTGGCAA GCGGCAAAA CCAGGGAAGG
1001 CTGCGGTTAG CGGGGATTTT GCTGATTCTT ATAAAAAGAA ATTGGCTTTG
1051 TCTGATAGTG CGAGACAGTT ATATCAAAAT GCAAAGTATA GAGAAGCTCT
1101 AGATATACAT TATGAAGATT TAATTAGAAG AAAAAGTAT GGTTCATCAA
1151 AATTATTATA CGGCAGAGAA ATTGACGCTG TTACGAATGA TGCTTTAATA
1201 CAAGCCAAAA GAACAATTTC AGCAATAGAT AAACCTAAAA ATTTCTTAAA
1251 TCAAAAAAAT AGAAAGCAA TTAAGCAAC CATCGAAGCA GCAAACCAAC
1301 AGGGAACACG TGCAGAATT TGGTTTAAAT ACGGTGTTC TACACAAGTT
1351 AAGTCATATA TTGAATCAA AGGCGGCATT GTTAAACAG GTTTAGGAGA
1401 TTA

```

This corresponds to the amino acid sequence <SEQ ID 2472; ORF 730>:

```

m730.pep
1  VKPLRRLTNL LAACAVAAAA LIQPALAADL AQDPFITDNA QRQHYEPGGK
51  YHLFGDPRGS VSDRTGKINV IQDYTHQMGN LLIQANING TIGYHTRFSG
101 HGHEEHAPFD NHAADSASEE KGNVDEGFTV YRLNWEGHEH HPADAYDGPK
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQRIS DNYSNLGSNF
201 SDRADENRKM FEHNAKLDR WGNMSEFING VAAGALNPFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAFL PAEGKFVIG GLGSVAGFEK NTREAVDRWI
301 QENPNAETV EAVFNVAAPA KVALAKAAK PGKAAVSGDF ADSYKKKLAL
351 SDSARQLYQN AKYREALDIH YEDLIRKTD GSSKFINGRE IDAVTNDALI
401 QAKRTISAID KPNFLNQKN RKQIKATIEA ANQQGRAEF WFKYGVHSQV
451 KSYIESKGGI VKTGLGD*

```

g730 / m730 93.0% identity in 344 aa overlap

	10	20	30	40	50	60
g730.pep	VKPLRRLTNLLAACAVAAVALIQPALAADLAQDPFITDNTQRQHYEPGGKYHLFGDPRGS					
m730	VKPLRRLTNLLAACAVAAVALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
	10	20	30	40	50	60
g730.pep	VSDRTGKINV IQDYTHQMGNLLIQAAIQGNLGYTVRFSGHGHEEHAPFDNHAADSASEE					
m730	VSDRTGKINV IQDYTHQMGNLLIQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
	70	80	90	100	110	120
g730.pep	KGNVDDGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT					
	130	140	150	160	170	180
g730.pep	DTRSIRQRIFDNYNNLGSNFSADRAENRKMFEHNAKLDRWGNMSEFVNGVAAGALNPFI					
m730	DTRSIRQRISDNYSNLGSNFSADRAENRKMFEHNAKLDRWGNMSEFINGVAAGALNPFI					
	190	200	210	220	230	240
g730.pep	DTRSIRQRISDNYSNLGSNFSADRAENRKMFEHNAKLDRWGNMSEFINGVAAGALNPFI					
m730	DTRSIRQRISDNYSNLGSNFSADRAENRKMFEHNAKLDRWGNMSEFINGVAAGALNPFI					
	190	200	210	220	230	240

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	250	260	270	280	290	300
g730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAAIGGLGSAAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSAAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
g730.pep	QENPNAAETVEALVNLVLPFAKVKNLTAAKPGKAAVSGDFSYSYCSFHGSTLVKTADGY					
m730	QENPNAAETVEAVFNVAATAAKVAKLAKAAKPGKAAVSGDFADSYKKKLALSDSARQLYQN					
	310	320	330	340	350	360
	370	380	390	400	410	420
g730.pep	KALAHIQAGDRVLSKDEASGETGYKPVTRYGNPYQETVYIEVSDGIGNSQTLISNRHP					
m730	AKYREALDIHYEDLIRKTDGSSKFINGREIDAVTNDALIQAKRTISAIDKPKNFLNQKN					
	370	380	390	400	410	420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2473>:

```

a730.seq
1  GTGAAACCGC  TGCGAAGACT  CATCAAGCTC  CTTGCCGCCT  GTGCCGTAGC
51  GCGCGCCGCA  CTCATACAGC  CCGCCCTCGC  GCGGACTTGG  GCGCAAGACC
101 CGTTCATTAC  CGATAACGCC  CAACGGCAGC  ACTACGAACC  CGGAGGCAAA
151 TACCACCTCT  TCGCGGACCC  GCGCGGCAGC  GTCTCCGACC  GCACCGGTCA
201 AATCAACGTC  ATCCAAGACT  ATACCCACCG  GATGGGCAAC  CTGCTCATCC
251 AGCAGGCAAA  CATCAACGGC  ACAATCGGCT  ACCACACCCG  CTTTTCGGGA
301 CACGGATACG  AAGAACACGC  CCCCTTCGAC  AACCACGCCG  CCGACAGCGC
351 GAGCGAAGAA  AAAGGCAACG  TTGACGAAGG  CTTTACCGTA  TACCGGCTCA
401 ACTGGGAAGG  ACACGAACAT  CATCCCGCCG  ATGCCCTACG  CGGCCCGAAG
451 GCGGGCAATT  ACCCCAAACC  TACGGGTGCA  CGCGACGAAT  ACACCTATCA
501 CGTCAACGGC  ACAGCACGCA  GCATCAAAC  CAATCCGACC  GACACCCGCA
551 GCATCCGGCA  ACGCATATCC  GACAATTACA  GCAACCTCGG  CAGCAATTTT
601 TCCGACCGCG  CCGATGAAGC  CAACAGAAAA  ATGTTTCGAG  ACAATGCCAA
651 GCTCGACCGC  TGGGGCAACA  GCATGGAGTT  TATCAACGGC  GTCGCGCCG
701 GCGCGCTCAA  CCCCTTTATC  AGCGCGGGCG  AAGCCTTGGG  CATAGGCGAC
751 ATACTGTACG  GAACGCGCTA  TGCCATAGAC  AAAGCCGCAA  TGCGCAACAT
801 CGCCCCCTTG  CCGCCGAGG  GCAAATTCGC  CGTCATCGGC  GGCTTGGGCA
851 GCGTGGCGGG  CTTTGAAAAA  AATACGCGCG  AAGCCGTGTA  CCGGTGGATA
901 CAGGAAACC  CCAATGCCGC  CGAAACCGTC  GAAGCCCTGG  TCAACGTCCT
951 GCCGTTTGCC  AAAGTCAAAA  ACCTGACAAA  GCGCGCAAAA  CCGGGGAAGG
1001 CTGCGGTTAG  CGGGGATTTT  TCTGCTGCAT  ACAATACAAG  AACAAC TAGA
1051 AAAGTTACTA  CAGAAACAGA  GGGGTTAAAT  AGAATCAGAC  AGAACCAGAA
1101 AAATAGTAAT  ATACATGAGA  AAAATTATGG  AAGAGATAAT  CCTAATCATA
1151 TTAATGTTTT  ATCTGGAAAT  TCTATACAAC  ATATACTGTA  TGGAGATGAA
1201 GCAGGAGGTG  GGCATCTTTT  TCCTGGCAAA  CCTGGTAAGA  CAACATTTCC
1251 CCAACATTGG  TCAGCCAGTA  AAATAACTCA  TGAAATTAGT  GATATCGTTA
1301 CATCCCCAAA  AACGCAATGG  TATGCACAGA  CTGGAACAGG  CGGCAATAT
1351 ATTGCTAAAG  GAAGACCAGC  TAGGTGGGTA  TCATATGAAA  CGAGAGATGG
1401 AATTCGTATC  AGAACAGTTT  ATGAACCTGC  AACAGGAAAA  GTGGTAACTG
1451 CATTCCCCGA  TAGAACCTCT  AATCCCAAAT  ATAACCCTGT  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2474; ORF 730.a>:

```

a730.pep
1  VKPLRRLIKL  LAACAVAAAA  LIQPALAADL  AQDPFITDNA  QRQHYEPGGK
51  YHLFGDPRGS  VSDRTGQINV  IQDYTHRMGN  LLIQQANING  TIGYHTRFSG
101 HGYEEHAPFD  NHAADSASEE  KGNVDEGFTV  YRLNWEGHEH  HPADAYDGP
151 GGNYPKPTGA  RDEYTYHVNG  TARSIKLNPT  DTRSIRQRIS  DNYSNLGSNF
201 SDRADANRK  MFEHNAKLDR  WGNSEMFING  VAAGALNFFI  SAGEALGIGD
251 ILYGTRYAID  KAAMRNIAPL  PAEGKFAVIG  GLGSAAGFEK  NTREAVDRWI
301 QENPNAAETV  EALVNLVLPFA  KVKNLTKAAK  PGKAAVSGDF  SAAYNTRTTR
351 KVTTETEGLN  RIRNQKNSN  IHEKNYGRDN  PNHNVLSGN  SIQHILYGDE
401 AGGGHLFPGK  PGKTTFPQHW  SASKITHEIS  DIVTSPKTQW  YAQTGTGGKY
451 IAKGRPARW  SYETRDGIRI  RTVYEPATGK  VVTAFDPRTS  NPKYNPVK*

```


1184

a730 / m730 88.6% identity in 376 aa overlap

	10	20	30	40	50	60
a730.pep	VKPLRRLIKLLAACAVAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
		:				
m730	VKPLRRLTNLLAACAVAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a730.pep	VSDRTGQINVIQDYTHRMGNLLIQANINGTIGYHTRFSGHGYEEHAPFDNHAADSASEE					
		:				
m730	VSDRTGKINVIQDYTHQMGNLLIQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a730.pep	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGNYPKPTGARDEYTYHVNGTARSIKLNPT					
	130	140	150	160	170	180
	190	200	210	220	230	240
a730.pep	DTRSIQRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWNSMEFINGVAAGALNPFI					
m730	DTRSIQRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWNSMEFINGVAAGALNPFI					
	190	200	210	220	230	240
	250	260	270	280	290	300
a730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a730.pep	QENPNAAETVEALVNVLPFAKVKNLTAAKPGKAAVSGDFSAAYNTRTTTRKVTETEGLN					
m730	QENPNAAETVEAVFNVAATAAKVAKLAKAAGKPGKAAVSGDFADSY-----KKKLALSDSAR					
	310	320	330	340	350	
	370	380	390	400	410	420
a730.pep	RIRQNQKNSNIHEKNYGRDNPNHINVLSGNSIQHILYGDEAGGHLFFGKPGKTTFPQHW					
	::	:	:	:	:	:
m730	QLYQNAKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIKPKNF					
	360	370	380	390	400	410

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2475>:

```

g731.seq
1  gattttcgag cgttttcatG CGAGAACGGT TTGTCTGTGC GCGTCCGCAA
51  TTTGGACGGC GGCAAAATCG CGTTGCGGCT GGACGGCAGG CGTGCCGTCC
101 TCTCTTCCGA CGTTGCCGCA TCCGGCGAAC GCTATACCGC CGAACACGGT
151 TTGTTCCGAA ACGGAACCGA GTGGCACCAG AAAGGCGGCG AAGCCTTTT
201 CGGCTTTACC GATGCCTACG GCAATTCGGT CGAACTTCC TGCCGCGCCC
251 GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2476; ORF 731.ng>:

```

g731.pep
1  DFRAFSCENG LSVVRNLDG GKIALRLDGR RAVLSSDVAA SGERYTAEHG
51  LFGNGTEWHQ KGGEAFFGFT DAYGNSVETS CRAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2477>:

```

m731.seq
1  ATGAATATCA GGTTTTTCGC GCTGACCGTA CCGGTTTTGT CTTTGGCGGC
51  CTGTGCCGTG CCGGAGGCGT ATGATGACGG CGGACGCGGG CATATGCCGC
101 CCGTTCAGAA CCAAGCCGGC ACGGACGATT TTCGGGCGTT TTCCTCGGAG
151 AACGGTTTGT CTGTGCGCGT CCGCCATTG GACAGCGGCA AAGTCGCGTT
201 GCGGCTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG

```

1185

```

251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG
301 CACCAGAAAG GCGGCGAAGC CTTTTCGGC TTTACCGATG CCTACGGCAA
351 TTCGGTCGAA ACTTCTGCC GCGCCCGTTA A

```

This corresponds to the amino acid sequence <SEQ ID 2478; ORF 731>:

```

m731.pep
  1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TDDFRAFSCE
  51 NGLSVRVRHL DSGKVALRLD GRRAVLSSDV AASGERYTAE HGLFGNATEW
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

```

g731/m731 95.2% identity in 84 aa overlap

```

                                10      20      30
g731.pep                                DFRFSCENGLSVRVRNLDGGKIALRLDGR
                                |||:|||:|||:|||:|||:|||:|||
m731      LSLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCEGLSVRVRHLDSGKVALRLDGR
              20      30      40      50      60      70

              40      50      60      70      80
g731.pep      RAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVETSCRARX
              |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
m731      RAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVETSCRARX
              80      90      100     110     120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2479>:

```

a731.seq
  1 ATGAATATCA GGTTTTTCGC GCTGACCGTA CCGGTTTGT CTTGGCGGC
  51 CTGTGCCGTG CCGGAGGCGT ATGATGACGG CCGACGAGGG CATATGCCGC
 101 CCGTTCAAAA CCAAGCCGGC ACGGCAGATT TTCGGGCATT TTCTGCGAG
 151 AACGGTTTGT CTGTGCACGT CCGCCGTTTG GACGGCGGCA GAATCGCGTT
 201 GCGGTTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG
 251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGG AACCGAGTGG
 301 CATCAGAAAG GCGGCGAAGC CTTTTCGGC TTTACCGATG CCTACGGCAA
 351 TTCGGTCGAA ACCTCCTGCC GCGCCCGCTA A

```

This corresponds to the amino acid sequence <SEQ ID 2480; ORF 731.a>:

```

a731.pep
  1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TADFRAFSCE
  51 NGLSVHVRRL DGGRIALRLD GRRAVLSSDV AASGERYTAE HGLFGNGTEW
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

```

a731/m731 94.4% identity in 126 aa overlap

```

              10      20      30      40      50      60
a731.pep      MNIRFFALTVPVLSLAACAVPEAYDDGGRGHMPPVQNQAGTADFRFSCENGLSVHVRRL
              |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
m731      MNIRFFALTVPVLSLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCEGLSVRVRHL
              10      20      30      40      50      60

              70      80      90      100     110     120
a731.pep      DGGRIALRLDGRRAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVE
              |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
m731      DSGKVALRLDGRRAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVE
              70      80      90      100     110     120

a731.pep      TSCRARX
              |||:|||
m731      TSCRARX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2481>:

```

g732.seq
  1 ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
  51 CAGCGGCGTG GCCGTAAAGT TGGCGGTGCA GGGTTTGCC GCCGagaagg
 101 ACGGgcgGGA TAACGAagtc CTGCCGTGTC AATCCATCCG TACGATGGCG

```

```

151 GAGGTTTACG GTCAGATTAA GGCAAACTAC TATCATGACA AACCCGATGC
201 CGATTGTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCGGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGETTT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGCGGEAGG
401 TGAAAAGCGG CGATTTCATT GTGAAAATCG ATAATGTTTC GACGCGCGGT
451 ATGACGGTGA GCGAAGCGGT GAAAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACCTTGTCGC GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTGC CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGCG GCGACGACCC CGGCGGGCTT
751 TTGACCGGCG CGGTGCGCGT GTCGCGGCGG TTTCTGCCGT CTGAAGCGGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACGGCATG GTACTGAAAG
851 CCGTTCGCCA GGATTATGTG TACGGTATGG GCGCGACCC TTTGGCGGGT
901 ATTCCTGCCG AGTTGAAAAC GATTCCGATG ACgtaATTGG TcaaTTCCGG
951 TTCggcttCG GCGTCGGAGA TTGtgcCGG CGCATTGCAG GACCACAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GTAAAGGTTT GGTTCAGACT
1051 TTGATTCCCTT TGTCCAACGG CAGCGCGGTC AAGTTGACGA CCGCCCTGTA
1101 TTACACGCCG AACGACCGTT CCATTTCAGC ACAGGGGATT GTTCCCGATG
1151 TCgaaGTAAA AGATAAGGAA CGTACTTTTG AAAGCCGCGA GCGCGACCTG
1201 GTCGGACACA TCGGCAATCC CTTgggcGGC GAGGATGTGA ACAGTGAAAC
1251 CcttgcCGTA CCGCTTGAAG AAGATGCGGA TAAGCCCGCT GCAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTCAAGGCG GATTCCGAAC
1351 CCTGCGAAAG ACGATCAGTT GCGTAAGGCT TTGGATTGG TCAAGTCGCC
1401 CGAGCAGTGG CAGAACTCTT TGGGGCTGGC GGCGAAAAA CCGGTTTCAA
1451 ATAAAGATAA AAAAGATAAG AAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2482; ORF 732>:

```

g732 . pep
1  MSKPVFKKIA LYTLGAISGV AVSLAVQGF A EKDGRDNEV LPVQSIRTMA
51  EVYQGIKANY YHDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIEDTPAE RAEVKSGDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLRKNADKP IVVNLTRAIL KVKSVRHHLI
201 EPDYGYIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGDGDM VLKAVPEDYV YMGGDPLAG
301 IPAELKTIEM TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFKGSVQT
351 LIPLSNGSAV KLTALYYTP NDRSIQAQGI VPDVEVKDKE RTFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDADKPA AKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNNKDKDK K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2483>:

```

m732 . seq
1  ATGTCGAAC CTGTTTTTAA GAAATCGCA CTTTATACTT TGGGTGCAAT
51  CAGCGGCGTG GCCGTGAGTC TGGCGGTGCA GGGTTTTGCC GCCGAGAAGG
101 ACA3GCGGGA TAACGAAGTC CTGCCGGTGC AATCCATCCG CACAATGGCG
151 GAG3TTTACG GTCAAATCAA GGCAAACTAC TATCAGGACA AACCCGATGC
201 CGATTGTGTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCGGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCGGAA CGGGCGGGGG
401 TGAAAAGCGG CGATTTCATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGCGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTGCG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTGC CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGCG GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTGCGCGT GTCGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACCGCATG GTACTGAAAG
851 CATTTCCTGA AGATTATGTG TACGGGATGG GCGGCGATTG GTTGGCGGGC
901 ATTCCTGCGG AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC GCGTCGGAGA TTGTGCGAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCCTT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA

```

1187

```

1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTGT AAAGCCGCGA GCGCGATTGT
1201 GTCGGACACA TCGGCAATCC CTTGGGCGGC GAGGATGTGA ACGGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTCAAGGCG GATTCCTAAC
1351 CCTGCCAAG ACACCAGTT GCGGAAAGCT TTGGATTAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAA AAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2484; ORF 732>:

m732.pep

```

1 MSKPVFKKIA LYTLGAISGV AVSLAVQF AAEKDRRDNEV LPVQSIRTMA
51 EVYQGIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIEDTPAE RAGVKSGDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLRKNADKP IVNLTALII KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELYKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA AFLPSEAVVVS TKGRDGKDRM VLKAIPEYV YGMGGDSLGA
301 IPAEKTIPTM TVLVNNGSAS ASEIVAGALQ DHKRAVIVGT QSFSGKSVQT
351 LIPLSNGSAV KLTALYYP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNGETLAV PLEKADAKPA VKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNDKKKKD KDKK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 732 shows 98.2% identity over a 491 aa overlap with a predicted ORF (ORF732.a) from *N. gonorrhoeae*:

m732/g732 98.2% identity in 491 aa overlap

	10	20	30	40	50	60
m732.pep	MSKPVFKKIALYTLGAISGVAVSLAVQGF AAEKDRRDNEVLPVQSIRTMAEVYQGIKANY					
g732	MSKPVFKKIALYTLGAISGVAVSLAVQGF AAEKDRRDNEVLPVQSIRTMAEVYQGIKANY					
	10	20	30	40	50	60
m732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
g732	YHDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
m732.pep	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKFGTKITLTLSRKNADKP					
g732	VSPIEDTPAERAEVKSDFIVKIDNVSTRGMTVSEAVKKMRGKFGTKITLTLSRKNADKP					
	130	140	150	160	170	180
m732.pep	IVNLTALIIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGPLKGLV					
g732	IVNLTALIIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGPLKGLV					
	190	200	210	220	230	240
m732.pep	LDLRDDPGGLLTGAVGVSA AFLPSEAVVVS TKGRDGKDRMVLKAIPEYVYGMGGDSLGA					
g732	LDLRDDPGGLLTGAVGVSA AFLPSEAVVVS TKGRDGKDRMVLKAIPEYVYGMGGDSLGA					
	250	260	270	280	290	300
m732.pep	IPAEKTIPTMTVLVNNGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLSNGSAV					
g732	IPAEKTIPTMTVLVNNGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLSNGSAV					
	310	320	330	340	350	360

1188

```

          370      380      390      400      410      420
m732.pep  KLTITALYYPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNGETLAV
          |||||
g732       KLTITALYYPNDRSIQAQGIVPDVEVKDKERTFESREADLVGHIGNPLGGEDVNSETLAV
          370      380      390      400      410      420

          430      440      450      460      470      480
m732.pep  PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK
          |||||
g732       PLEKDADKPAAKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK
          430      440      450      460      470      480

          490
m732.pep  PVSNNKDKKDKKDKKX
          |||||
g732       PVSNNKDKKDKKX
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2485>:

```

a732.seq
1  ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51  CAGCGGCGTG GCCGTCAGTC TGGCGGTGCA GGGTTTTGCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGTGTC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAACTAC TATCAGGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGTAT GGTGGCCCGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCGA TTGAGGACAC GCCTGCGGAA CGGGCGGGGG
401 TGAAAGCGG CGATTTCATT GTGAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGCTCA GCGAAGCGGT GAAGAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTGCG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTCT CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAGGAA AATAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGCG GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTCGGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACCGCATG GACTGAAAG
851 CCGTTCCTGA AGATTATGTG TACGGGATGG GCGGCGATTC GTTGGCGGGC
901 ATTCCTGCCG AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC GCGTCGAGAG TTGTCGAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCCT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA
1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTTG AAAGCCGCGA GCGGATTGTT
1201 GTCGGACACA TCGGCAATCC TTTGGGCGGC GAGGATGTGA ACAGTGAAAC
1251 CTTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTGTG CTTCAAGGCG GATTCCCAAC
1351 CTGCCCCAAG ACGACCAAGT GCGGAAAGCT TTGGATTAGT TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GGCGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2486; ORF 732.a>:

```

a732.pep
1  MSKPVFKKIA LYTLGAISGV AVSLAVQGF A EKDRRDNEV LPVQSIRTMA
51  EVYGOIKANY YQDKPDADLF ECAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIEDTPAE RAGVKSDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TFSRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIVRSV QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDRM VLKAVPEDYV YMGGDLSLAG
301 IPAEKLTIPM TVLVNNGSAS ASEIVAGALQ DHKRAVIVGT QSFKGKSVQT
351 LIPLSNGSAV KLTITALYYP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDADKPA VKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNNKDKKDK KKK*

```

1189

a732/m732 99.6% identity in 494 aa overlap

a732.pep	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY
m732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY
a732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV
m732	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV
a732.pep	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP
m732	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP
a732.pep	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV
m732	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV
a732.pep	LDLRDDPGLLTGAVGVSA AFLPSEAVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSL
m732	LDLRDDPGLLTGAVGVSA AFLPSEAVVSTKGRDGKDRMVLKAI PEDYVYGMGGDSL
a732.pep	IPAEKTIPTMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFGKGSVQTLIPLSNGSAV
m732	IPAEKTIPTMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFGKGSVQTLIPLSNGSAV
a732.pep	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV
m732	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV
a732.pep	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK
m732	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK
a732.pep	PVSNKDKKDKKDKKX
m732	PVSNKDKKDKKDKKX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2487>:

g733.seq

```

1  ATGATGAATC CGAAAACCTT GGGCCGTTTG TCGCTGTGTG CGGCGGTCTT
51 GGCTCTGACC GCCTGCGCCG GCGGCGGGCA TAAAAACCTG TATTATTACG
101 GCGTTATCC  CGATACGTC  TATGAAGTT  TGAAAAACG  cgACACTTCG
151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGCGG AAGCCGCCAA
201 CAAAAAATG  AATGCCGCC  CGGGTGCGCA CGCCATTG  GGACTGCTGC

```

1190

251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAATT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGtaaAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2488; ORF 733>:

g733.pep

1 MMNPKTLGRL SLCAAVLALT ACAGGGHKNL YYYGGYPDTV YEGLKNDDTS
 51 LGKQTEKMEK YFAEAANKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
 101 KRLFPESGVF MDFLMKTGKG GKR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2489>:

m733.seq

1 ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
 201 CAAAAAATG AATGCCGCC CGGGTGC GCGCCATCTG GGACTGCTGC
 251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGTAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2490; ORF 733>:

m733.pep

1 MMNPKTL SRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDDTS
 51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
 101 KRLFPESGVF MDFLMKTGKG GKR*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 733 shows 94.3% identity over a 123 aa overlap with a predicted ORF (ORF733.a) from *N. gonorrhoeae*:

m733/g733

	10	20	30	40	50	60
m733.pep	MMNPKTL	SRLSLCAAVLALTACGGNGQKSL	YYYGGYPDTV	YEGLKNDDTS	LGKQTEKMEK	
g733	MMNPKTL	GLRSLCAAVLALTACAGGGHKNL	YYYGGYPDTV	YEGLKNDDTS	LGKQTEKMEK	
	10	20	30	40	50	60
	70	80	90	100	110	120
m733.pep	YFVEAGNKKM	NAAPGAHAHLGLLLSRSGDKEGA	FRQFEEKRLFPESGVFMDFLMKTGKG			
g733	YFAEAANKM	NAAPGAHAHLGLLLSRSGDKEGA	FRQFEEKRLFPESGVFMDFLMKTGKG			
	70	80	90	100	110	120
m733.pep	GKRX					
g733	GKRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2491>:

a733.seq

1 ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
 201 CAAAAAATG AATGCCGCC CGGGTGC GCGCCATCTG GGACTGCTGC
 251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGTAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2492; ORF 733.a>:

a733.pep

1191

```

1  MMNPKTLSRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLNDDTS
51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEE
101 KRLFPESGVF MDFLMKTGKG GKR*

```

a733/m733 100.0% identity in 123 aa overlap

```

          10      20      30      40      50      60
a733.pep  MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLNDDTSLGKQTEKMEK
          |||||
m733      MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLNDDTSLGKQTEKMEK
          10      20      30      40      50      60

          70      80      90     100     110     120
a733.pep  YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG
          |||||
m733      YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG
          70      80      90     100     110     120

a733.pep  GKRX
          |||
m733      GKRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2493>:

```

g734.seq
1  ATGATGAAAA AGATACTGGC AGTATCGGCA CTATGCCTGA TGA CTGCGGC
51  GGCACAGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
101 AGGATGCAAA CGATGTTTGG CAGGTTAAAA CCACAAAAGA AGATTCGGCG
151 AAAAGCGAAG CGTTTGCCGA GTTGGAAGCC TTTTGCAAAG GTCAGGACAC
201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCGTGT
251 CGCTGAACAA TACCTGTGTC TCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCCT CGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TCATCAGGTC GCACTCAACC AGTGCAATAA AAAATACGGC GCACAGGGAC
401 AATGCGGCTT GGAAACAGTG TATTGCACGT CATCTTCTTA TTACGGCGGG
451 GCTGTTTCGT CCTAATCCA ACACCTGAAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2494; ORF 734.ng>:

```

g734.pep
1  MMKKILAVSA LCLMTAAQA ADTYGYLAVW QNPQDANDVL QVKTTKEDSA
51  KSEAFAELEA FCKGQDTLAG IAEDEPTGCR SVVSLNNTCV SLAYPKALGA
101 MRVENAVVIT SPRFTSVHGV ALNQCIKKYG AQGQCGLQTV YCTSSSYGG
151 AVRSLIQHLK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2495>:

```

m734.seq (partial)
1  TCGGGCATTG CTGAAGACGA GCCGACCGGA TGCCGGTCGG TCGTGTGCGT
51  GAACAATACC TGTGTCGCGC TGGCATACCC GAAAGCCTTG GGCGCGCTGC
101 GTGTCGACAA CGCCGTCGTG ATTACTTCTC CGCGTTTAC GAGCGTTCAT
151 CAGGTCGCAC TCAACCACTG CATCAAAAAA TACGGCGTAC AGGGACAATG
201 CGGCTTGGAA ACAGTGTATT GCACATCTTC TTCTTATTAC GGCGGAACTG
251 TGCGCTCTTT GATTCAAAAT CTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2496; ORF 734>:

```

m734.pep (partial)
1  SGIAEDEPTG CRSVSVLNNT CVALAYPKAL GALRVONAVV ITS PRFTSVH
51  QVALNQCIKK YGVQGQGLE TVYCTSSSY GGTVRSLIQN LK*

```

m734/g734 92.4% identity in 92 aa overlap

```

          10      20      30
m734.pep  SGIAEDEPTGCRSVSVLNNTCVALAYPKAL
          :|||
g734      VLQVKTTKEDSAKSEAFAELEAFCKGQDTLAGIAEDEPTGCRSVSVLNNTCVSLAYPKAL

```


		40	50	60	70	80	90
m734.pep		40	50	60	70	80	90
		GALRVDNAVVITS PRFTSVHC VALNQCICKYGVQGCGCLETVYCTSSSYYG GT VRSLIQN					
g'734		GAMRVENAVVITS PRFTSVHC VALNQCICKYGAQGCGCLETVYCTSSSYYGGA VR SLIQH					
		100	110	120	130	140	150
m734.pep	LKX						
g734	LKX						
	160						

```
a734.seq
1  ATGATGAAAA AGATACTGGC CGTATCGGCA CTATGCCTGA TGACTGCGGC
51  GGCACGGGCT GCCGATACTT ACGGCTATCT CGCGGTTTGG CAGAATCCGC
101 AGAATGCAAA CGATGTTTTG CAGGTATAAA CCACAAAAGA AGATTCTGACG
151 AAAAGCGAAG CGTTTGCCGA GTTGGAAAGCT TCTGCAAAAG GTCAGGACAC
201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CTGATGCCGG TCGGTCTGTG
251 CGCTGAACAA TACCTGTGTC GCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT TGTGATTACT TCCTCGCGTT TTACGAGCGT
351 TTATCAGGTC GCATCAACC AGTGCACTCA AAAATACG3C GCACAGGGAC
401 AATGCGGCTT GGAACACAGT TATTGCACGT CTTCTTCTTA TTACGGGGGA
451 ACTGTGCGCT CTTTGATTCA AAATCTCAAA TAA
```

a734.pep

1	<u>MMKKILAVSA</u>	<u>LCLMTAAARA</u>	ADTYGYLAVW	QNPQNANDVL	QVKTTKEDST
51	KSEAFAELEA	FCKGQDTLAG	IAEDEPTGCR	SVVSLNNTCV	ALAYPKALGA
101	MRVENAVVIT	SPRFTSVYQV	ALNQCIKKYG	AQGQCGLETV	YCTSSSYGG
151	TVRSLIQNLK	*			

	10	20	30	40	50	60
a734.pep	MMKKILAVSALCLMTAAARAADTYGYLAVWQNPNQANDVLQVKTTKEDSTKSEAFAELEA					
g734	MMKKILAVSALCLMTAAQAADTYGYLAVWQNPDANDVLQVKTTKEDSAKSEAFAELEA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a734.pep	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVALAYPKALGAMRVENAVVITSPRFTSVYQV					
g734	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVITSPRFTSVHQV					
	70	80	90	100	110	120
	130	140	150	160		
a734.pep	ALNQCIKKYGAQGQCGLTIVYCTSSSYGGTVRSLIQNLKX					
g734	ALNQCIKKYGAQGQCGLTIVYCTSSSYGGAVRSLIQHLKX					
	130	140	150	160		

```
m735.seq
1  ATGAATCTCG  TGAAACTGCT  GGCGAATAAC  TGGAACCGCA  TGCCATTAT
51  CGCGCTTGTC  GGCACGGGCT  TGCGTGTGTC  GCACCATCAA  GGCTACAAGT
101 CGGCATTGCG  GAAGCAGCAG  GCGGTCTGTC  ACAAGATTGA  GCGCGACAAG
151 GCGCAAGCCC  TGCTGTTGTC  GGCTCAAAAC  TATGCGCGCG  AACTGGAACT
201 GGCACGCGCG  GAAGCTAAAA  AATATAGTCT  CAAGCGCGAC  GCTGTCGGCA
251 TGGCTTTGGC  GAAAAAACAG  CCGGAAGTCA  GCCGCTGTA  AACGAAAAAT
301 AAAAAGGAAA  TCGAAAAATG  CCTTACTCAA  ACCGCTAAAA  ATGCAAGCGG
```

1193

351 CGGTTGCATT GACGGCTTTG GCTCTCACGG CCTGCAGCTC TACAACCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2500; ORF 735>:

m735.pep
1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQO AVIDKMERDK
51 AQALLLSAQN YARELELARA EAKKYEYKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNASGGCI DFGSHGLQL YNRALGYGN*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2501>:

a735.seq
1 ATGAATCTCG TGAACTGCT GGC GAATAAC TGGCAACCGA TTGCCATCAT
51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
201 GCGCGGTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAT
301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2502; ORF 735.a>:

a735.pep
1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQO AVIEKMKRDK
51 AQALLLSAQN YARELEQARA EAKKYEYKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DFGHHGLQL YKRALGYGN*

a735/m735 95.7% identity in 139 aa overlap

	10	20	30	40	50	60
a735.pep	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQOAVIEKMKRDKAQALLLSAQN					
m735	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQOAVIDKMERDKAQALLLSAQN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a735.pep	YARELEQARAEAKKYEYKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNAGGGCI					
m735	YARELELARA EAKKYEYKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNASGGCI					
	70	80	90	100	110	120
	130	140				
a735.pep	DGFGHHGLQLYKRALGYGNX					
m735	DGFGSHGLQLYNRALGYGNX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2503>:

g736.seq
1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51 CTTCCGGCAGT ATCAGCTGT TTCTGCTGAA CATTTTGCG AAATCCGGCA
101 CGGCTTTTCG CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTG TCGGTATGGT
201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TCGCGAACT GGGTCCCGTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGACAGCT CGAAGCGATG AACGTGATGG
401 CGGTCAACCC CGTCGCCCCG GTGGTTGCCC CGCGTTTTG GCGGGGCGTG
451 TTTTCTATGC CGCTTTTGGC TTCGATTTTC AACGTCGCGG GCATTTTCGG
501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
551 GGCCGCAGAT GCAGAACAAAC ATTACGATAC ATTACGATGT AATCAACGGT

1194

601 TTGATCAAAAT CCGCCGCGTT CGGCGTGCGG GTAACGCTGA TIGCCGTGCA
 651 TCAGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CCGCCAGCA
 701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGCGGT CGATTTTATA
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2504; ORF 736>:

g736.pep

1 MNFIRSVGAK TLGLIQSFGS ITLFLLNILA KSGTAFARPR LSVRQVYFAG
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
 101 LAAILFASSA GGAMTSEIGL MKTTGQLEAM NVMVNPVAR VVAPRFWAGV
 151 FSMPLLASIF NVAGIFGAYL VGVSWLGLDS GIFWPQMNN ITIHYDVIING
 201 LIKSAAFGVA VTLIAVHQGF HCIPTSEGIL RASTRTVVSS ALTILAVDFI
 251 LTAWMFTD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2505>:

m736.seq

1 ATGAATTTTA TCCGTTCGGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
 51 CTTCCGCGAGT ATCACGCTGT TTCTGCTGAA CATTGTGGCG AAATCCGGCA
 101 CGGCTTTTCG CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
 151 GTGCTGTCCG TGCTGATTGT TGCCGTTTCG GGGCTGTTTC TCGGTATGGT
 201 TTTGGGTTTG CAGGCTATA CGCAGTTGTC GAAATTCAA TCCGCCGATA
 251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TGCGCGAACT GGGTCCCGTG
 301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGTGCGA TGACCAGCGA
 351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
 401 CGGTCAACCC CGTCGCCCGC GTGGTTGCC CGCGTTTTTG GCGGGCGTG
 451 TTTTCTATGC CGCTTTTGGC TTCGATTTTC AACGTCGCG GCATTTTCGG
 501 CGCGTATTTG GTCGCGGTGA GCTGGCTGGG TTTGGACAGC GGIATTTTCT
 551 GGCCGCAGAT GCAGAACAAC ATTACGATAC ATTACGATGT AATCAACGGT
 601 TTGATCAAAAT CCGCCGCGTT CGGCGTGCGG GTAACGCTGA TTGCCGTGCA
 651 TCAGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CCGCCAGCA
 701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGCGGT CGATTTTATA
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2506; ORF 736>:

m736.pep

1 MNFIRSVGAK TLGLIQSLGS ITLFLLNILA KSGTAFVRPR LSVRQVYFAG
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
 101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NVMVNPVAR VVAPRFWAGV
 151 FSMPLLASIF NVAGIFGAYL VGVTWLGLDS GIFWSQMNN ITIHYDVIING
 201 LIKSAAFGVA VTLIAVHQGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
 251 LTAWMFTD*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 736 shows 97.7% identity over a 258 aa overlap with a predicted ORF (ORF736.ng) from *N. gonorrhoeae*:

m736/g736

	10	20	30	40	50	60
m736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNLA KSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
g736	MNFIRSVGAKTLGLIQSFGSITLFLNLA KSGTAFARPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
g736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130 140 150 160 170 180					
m736.pep	MKTTEQLEAMNVMVNPVARVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTWLGLDS					
g736	MKTTGQLEAMNVMVNPVARVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					

1195

	130	140	150	160	170	180
	190	200	210	220	230	240
m736.pep	GIFWSQMNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTRTVVSS					
g736	GIFWPMQNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCPTSEGILRASTRTRTVVSS					
	190 200 210 220 230 240					
	250	259				
m736.pep	ALTILAVDFILTAWMFTDX					
g736	ALTILAVDFILTAWMFTDX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2507>:

```

a736.seq
1  ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51  TCTCGGCAGT ATCAGCGCTGT TTCTGCTGAA TATCTGGCG AAATCCGGTA
101 CGGCTTTCGT CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
151 GTGCTGTCGG TGTGATTGT TGCCGTTTCA GGGCTGTTG TCGGCATGGT
201 CTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAA TC CGCCGATA
251 TTTTGGGCTA TATGGTCGCG GCTTCGCTGT TCGCGAACT GGGTCCGGTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGTTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGAACAGCT CGAAGCGATG AACGTGATGG
401 CGGTAAACCC CGTCGCCCGA GTGGTTGCGC CGCGCTTTTG GCGGGGCGTG
451 TTTTCCATGC CGCTTTTGGC TTCGATTTC AACGTGGCGG GTATTTTCGG
501 CGCGTATTG GTCGGTGTAA CCTGGCTGGG CTTGGACAGC GGTATTTTCT
551 GGTGCGAAAT GCAGAACAC ATCAGGATAC ATTACGATG AATCAACGGT
601 CTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
651 TCAGGGCTTC CACTGCGTCC CGACCTCGGA AGGCATTTG CGGCCAGCA
701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTGGCGGT CGATTTTATA
751 TTGACCGCGT GGATGTTTAC AGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2508; ORF 736.a>:

```

a736.pep
1  MNFIRSVGAK TLGLIQSLGS ITLFLNILA KSGTAFVRPR LSVRQVYFAG
51  VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
101 LAAILPASSA GGAMTSEIGL MKTTEQLEAM NMAVNPVAR VVAPRFWAGV
151 FSPMLLASIF NVAGIFGAYL VGVTLGLDS GIFWSQMNN ITIHVDVING
201 LIKSAAFGVA VTLIAVHQGF HCVPTSEGIL RASTRTRTVVSS ALTILAVDFI
251 LTAWMFTD*

```

a736/m736 100.0% identity in 258 aa overlap

	10	20	30	40	50	60
a736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
m736	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
m736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a736.pep	MKTTEQLEAMNMAVNPVARVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTLGLDS					
m736	MKTTEQLEAMNMAVNPVARVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTLGLDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
a736.pep	GIFWSQMNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTRTVVSS					

1196

```

m736      GIFWSQMQNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS
           190      200      210      220      230      240

           250      259
a736.pep   ALTILAVDFILTAWMFTDX
           ||||||||||||||||
m736      ALTILAVDFILTAWMFTDX
           250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2509>:

g737.seq

```

1  atgaACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51 CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACC GA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTTCTT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2510; ORF 737>:

g737.pep

```

1  MNIKHLLLTA AATALLGISA PALAHDGHG DDDHGHAHQ HGKQDKIISR
51 AQAEKAARAR VGGKITDIDL EHDGRPHYD VEIVKNGQY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2511>:

m737.seq.

```

1  ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51 CATTTCCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGGCGGT GTCGGCGGCA AAATCACC GA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTTCTT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2512; ORF 737>:

m737.pep

```

1  MNIKHLLLTS AATALLSISA PALAHDGHG DDDHGHAHQ HNKQDKIISR
51 AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 737 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF737.a) from *N. gonorrhoeae*:

m737/g737

```

           10      20      30      40      50      60
m737.pep   MNIKHLLLTS AATALLSISA PALAHDGHG DDDHGHAHQ HNKQDKIISR AQAEKAALAR
           |||||||:|||||:|||||:|||||:|||||:|||||
g737       MNIKHLLLTA AATALLGISA PALAHDGHG DDDHGHAHQ HGKQDKIISR AQAEKAARAR
           10      20      30      40      50      60

           70      80      90      100     109
m737.pep   VGGKITDIDL EHDNGRPHYD VEIVKNGQY KVVVDARTGR VISSRRDDX
           |||||||:|||||:|||||:|||||:|||||:|||||
g737       VGGKITDIDL EHDNGRPHYD VEIVKNGQY KVVVDARTGR VISSRRDDX
           70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2513>:

1197

a737.seq

```

1 ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51 CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCCG
301 GTGATTCTCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2514; ORF 737.a>:

a737.pep

```

1 MNFKRLLLLTA AATALMGISA PALAHHDHGHG DDDHGHAHQ HSKQDKIISR
51 AQAEEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

a737/m737 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a737.pep	MNFKRLLLLTA	AATALMGISA	PALAHHDHGHG	DDDHGHAHQ	HSKQDKIISR	AQAEEKAALAR
m737	MNFKRLLLLTA	AATALMGISA	PALAHHDHGHG	DDDHGHAHQ	HSKQDKIISR	AQAEEKAALAR
	10	20	30	40	50	60
	70	80	90	100	109	
a737.pep	VGGKITDIDL	EHDNGRPHYD	VEIVKNGQEY	KVVVDARTGR	VISSRRDDX	
m737	VGGKITDIDL	EHDNGRPHYD	VEIVKNGQEY	KVVVDARTGR	VISSRRDDX	
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2515>:

g738.seq

```

1 ATGTCCGCTG AAACGACCGT ATCCGGCGCG CGCCCCGCGG CCAAACGCGC
51 GATTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCATC CCCTTTACCT
101 TCGCACTCAG GCTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCGCGC
151 GCGGCGCGCC TGATTGTCTT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAAA ATCCCCGCCA TCAGCTTCCT CCTGTTTGCA ATGGCGGCAT
251 TTTGGTGCTC TCAGGCACGC CTGATGAACC TGATTTATCC CGGAATGAAC
301 GACATCGCCT CTTGGGTTTT CATCTTGCTC GCCGTACGCG CGTGGGCTTG
351 CAAGAGTTTG GTCGCACACT ACGGACAAGA ACGCATcgtT ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTcgtCATC
451 CAGTTTGCGG GCTGGGAAAA CACCCCTCTG CTTCAAAACA TCATCGTTCA
501 CAGAGGGCAA GCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTGGCTCCG CCTACCTCAA CGGACAACGA
601 AAAATCCCGG CAGCCCTCGG CGCAATCTGC CTGATTATGC AGACCGCGT
651 TTTAGGTTTG GTCAATTCGC GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCTT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGACGG
751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC GCCATTCTGG AAACCTTTAC AGGCATCCGC TACGAACTG
851 CCGTCGAACG CGTCGCCAAC GGCGGTTTCA CAGACTTGCC GCGCCAAAGC
901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCGGA TATTCGGGCA
951 CGGCTGGAAC AGTTTGGCCC AACAAACCTT CCTGATCAAT GCCGAACAGC
1001 ACACCATACA CGACAACCTT CTCAGCACCT TGTTACCCCA TTCCCAAC
1051 ATCATCTCTC AACTCCTTGC AGAAATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCGGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCTCCCTGA
1151 CCCCCGCATC ACTTTCTCTG CTGTGCGCGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCTTTT GTGGTATGTC TATTTCTCTA TCCCTTCTGG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCGGC CATATTGCGA
1351 GGATTGTGTC ACTTGGACTG GACATACACC CGGCTGGTTA ACTCCTTTTC
1401 CCCCAGCGCT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAAC
1451 TCGCGTATAT TTCCGCAAAAC AGCCCGATGC TGTCTTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAG CACTAAATAA CCGCCCTTAC TCCGCCACCT

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1601 ACCGCATCGC CCTCTACTTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCAACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCACCGCTG CTGCCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CTCCCGGCCA TCCGGAAACA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2516; ORF 738>:

g738.pep

```

1  MSAETTVSGA RPAAKLPYYI LPCFLWIGII PFTFALRLKP SPDFYHDAAA
51  AAGLIVLLFL TAGKKLFDVK IPAISFLLFA MAAFWWLOAR LMNLIYPGMN
101 DIASWFVILL AVSAWACKSL VAHYGQERIV TLFWSLLIG SLLQSCIVVI
151 QFAGWENTPL LQNIIVHRGQ GVIGHIGQRN NLGHYLMWGI LASAYLNGQR
201 KIPAAALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPEW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN AILEFTTGIR YETAVERVAN GGFTDLPRQS
301 EWNKALAAFO SAPIFGHWN SFAQQTFLIN AEQHTIHDNF LSLFTHSHN
351 IILQLLAEMG ISGTLVAAT LLTGIAGLLK RSLTPASLFL LCALAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAASDG IAFKKAANLG ILTASAAIFA
451 GLHLHDWYTY RLVSNSFSPA DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALPEY PETQTWAEAA TLKALKYRPY SATYRIALYL MRQKVAEAK
551 QWMRATQSYV PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPET
601 KPCK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2517>:

m738.seq

```

1  ATGCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAAGTGCC
51  GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TCGCGCTCAA ACTGAAACCG TCGCCGACT TTTACCACGA TGCCGCGGCC
151 GCAGCCGGCC TGATTGTCTT GTTGTCTCTC ACGGCAGGAA AAAAAGTGT
201 TGATGTCAAA ATCCCGGCCA TCAGCTTCCT TCTGTTTGCA ATGGCGGCGT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTIT CATCTTGCTC GCCGTACGCG CGTGGGCGCTG
351 CCGGAGCTTG GTCGCACACT TCGGACAAGA ACGCATCGTG ACCCTGTTTG
401 CCTGTCGCTG GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAACA TCATCGTTTA
501 CAGCGGGCAA GGCCTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCGCGC CCTACCTCAA CGGACAACGA
601 AAAATCCCGG CCGCCCTCGG CGTAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAACTCGC GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCGGT CGGACAAATC CAACAGGCGG
751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCGAAT
801 TTCCATGCA ACCATTCTGG AAACCTTTAC TGGCATCCGC TACGAAACTG
851 CCGTCGAACG CGTCGCCAAC GCGGGTTTCA CAGACTTGCC GCGCCAAATC
901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCGCA TATTCGGGCA
951 CGGCTGGAAC AGTTTGTGCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATATA CGACAACCTC CTCAGCAACT TGTTCACCCA TTCCACAAC
1051 ATCGTCTCTC AACTCCTTGC AGAGATGGGA ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTTAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCTTA ATCTGCACGC TTGCCGTGAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCA TCCCTTTCTG
1251 ACTGATGCTC TTCCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTGCGA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACGCCTTTTC
1401 CCCGCGCACT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCGTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GCGCGCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2518; ORF 738>:

m738.pep

```

1  MPAETTVSGA HPAAKLPYYI LPCFLWIGIV PFTFALKLKP SPDFYHDAAA

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1199

```

51  AAGLIVLLFL TAGKKLFDVK IP AISFLLEFA MAAFWYLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHFGQERIV TFAWSLLIG SLQSCIVVI
151 QFAGWEDTFL FQNIIVYSGQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR
201 KIPAAALGVIC LIMQTAVLGL VNSRTILTYI AAIALILPEW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN TILETFTGIR YETAVERVAN GGFTDLPRQI
301 EWNKALAAFQ SAPIFGHGWN SFAQQTFLIN AEQHNIDNL LSNLFTHSHN
351 IVLQLLAEMG ISGTLVAAT LLTGIAGLLK RPLTPASLEL ICTLAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAASDG IAFKKAANLG ILTASAAIFA
451 GLLHLDWYTY RLVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALPEY PETQWAEAA TLKSLKYRPH SATYRIALYL MRQKVAEAK
551 QWMRATQSY YPYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
601 KPCK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 738 shows 95.0% identity over a 604 aa overlap with a predicted ORF (ORF738.a) from *N. gonorrhoeae*:

m738/g738

m738.pep	10	20	30	40	50	60
	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL					
g738	MSAETTVSGARPAAKLPIYILPCFLWIGIIPFTFALRLKPSPDFYHDAAGLIVLLFL					
	10	20	30	40	50	60
m738.pep	70	80	90	100	110	120
	TAGKKLFDVKIP AISFLLFAMA AFWYLQAR LMNLIYPGMNDIVSWIFILLAVSAWACRSL					
g738	TAGKKLFDVKIP AISFLLFAMA AFWWLQAR LMNLIYPGMNDIASVWFILLAVSAWACKSL					
	70	80	90	100	110	120
m738.pep	130	140	150	160	170	180
	VAHFGQERIVT LFAWSLLIGSLQSCIVVIQFAGWEDTFLFQNIIVYSGQG VIGHIGQRN					
g738	VAHYGQERIVT LFAWSLLIGSLQSCIVVIQFAGWENTPLLQNIIVHRGQGVIGHIGQRN					
	130	140	150	160	170	180
m738.pep	190	200	210	220	230	240
	NLGHYLMWGI LAAAYLNGQRKIP AALGVICLIMQTAVLGLVNSRTILTYIAAIALILPEW					
g738	NLGHYLMWGI LAAAYLNGQRKIP AALGAICLIMQTAVLGLVNSRTILTYIAAIALILPEW					
	190	200	210	220	230	240
m738.pep	250	260	270	280	290	300
	YFRSDKSNRR TMLGIAAAVF LTALFQFSMN TILETFTGIR YETAVERVANGGFTDLPRQI					
g738	YFRSDKSNRR TMLGIAAAVF LTALFQFSMN AILETFTGIR YETAVERVANGGFTDLPRQS					
	250	260	270	280	290	300
m738.pep	310	320	330	340	350	360
	EWNKALAAFQ SAPIFGHGWN SFAQQTFLINAEQHNIDNLLSNLFTHSHNIVLQLLAEMG					
g738	EWNKALAAFQ SAPIFGHGWN SFAQQTFLINAEQHTIHDNLFSTLFTHSHNIIQLLAEMG					
	310	320	330	340	350	360
m738.pep	370	380	390	400	410	420
	ISGTLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
g738	ISGTLVAATLLTGIAGLLKRSLTPASLFLCALAVSMCHSMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
m738.pep	430	440	450	460	470	480
	FLSPAASDGI AFKKAANLG ILTASAAIFAGLLHLDWYTYTRLVNAFSPATDDSAKTLNRK					
g738	FLSPAASDGI AFKKAANLG ILTASAAIFAGLLHLDWYTYTRLVNSFSPAADDSAKTLNRK					

1200

	430	440	450	460	470	480
	490	500	510	520	530	540
m738 . pep	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEATLKSLKYRPHSATYRIALYL					
g738	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEATLKALKYRPYSATYRIALYL					
	490	500	510	520	530	540
	550	560	570	580	590	600
m738 . pep	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
g738	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPET					
	550	560	570	580	590	600
m738 . pep	KPCKX					
g738	KPCKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2519>:

```

a738 . seq
1  ATGCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCGG CCAAACCTGCC
51  GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TTGCGCTCAG GCTGCAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCG
151 GCAGCCGCGC TGATTGTCTT GTTGTTCTCT ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAAA ATCCACCTA TCAGCTTCCT TCTGTTTGCA ATGGCGGCGT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTACTC GCCGTCAGCG CGTGGGCCTG
351 CCGGAGCTTG GTCGCACACT ACGGACAAGA ACGCATCGTT ACCCTGTTTG
401 CCTGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCTCTG TTTCAAAACA TCATTGTTTA
501 CAGCGGGCAA GCGTAATCG GACACATCG ACAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGCATA CTCGCCGCG CCTACCTCAA CGGACAACGA
601 AAAATCCCGC CCGCCTTGGG TGCAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAATTGCG GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCGGT CGGACAAAT CAACAGCGCG
751 ACGATACTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC CGGCATCCGC TACGAAACCG
851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACCTGCC GCGCAAATC
901 GAATGGCGCA AAGCCTCGC CGCCTCCAG TCCGCCCGA TATTCGGGCA
951 CGGCTGGAAC AGTTTGGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATACA CGACAACCTC CTCAGCAACT TGTTCACCCA TTCCCAAC
1051 ATCGTTCTCC AACTCCTTGC AGAGATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCTTG ATCTGCACAC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCCTCA TCCCCTTCGG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGCG ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTAACCG CCTCCGCCGC CATATTGCGA
1351 GGATTGCTGC ACTTGGAAGT GACATACACC CGGATGGTTA ACGCCTTTTC
1401 CCCC GCCACT GACGACAGT CAAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCGAAACCC AGACTTGGG
1551 GGAAGAAGCA ACCCTCAAAT CACTAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TSCCGTATG GCGCCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTGCCGCGCG CGCCCGGTCA TCCGGAAGCA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2520; ORF 738.a>:

```

a738 . pep
1  MPAETTVSGA HPAAKLPYIY LPCFLWIGIV PFTFALRLQP SPDFYHDA
51  AAGLIVLLFL TAGKKLFDVK IPPISFLLEA MAEFWYLOAR LMNLIYFGMN
101 DIVSWIFILL AVSAWACRSL VAHYQERIV TFAWSLLIG SLQSCIVVI
151 QFAGWEDTPL FQNIIVYSQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR

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1201

201 KIPPALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
 251 TILGIAAAVF LTALFQFSMN TLETFGTGIR YETAVERVAN GGFTDLPRQI
 301 EWRKALAAFO SAPIFGHGWN SFAQQTFLIN AEQHNHNDNL LSNLFTHSHN
 351 IVLQLLAEMG ISGTLLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
 401 SMLEYPLWYV YFLIPFGLML FLSPAASDG IAFKKAANLG ILTASAAIFA
 451 GLLHLDWYTT RMVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
 501 SLVNFALPEY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQGVAEAK
 551 QWMRATQSY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAEGHPEA
 601 KPCK*

a738/m738 98.3% identity in 604 aa overlap

	10	20	30	40	50	60
a738.pep	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALRLQSPDFYHDAAGLIVLLFL					
m738	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL					
	10	20	30	40	50	60
	70	80	90	100	110	120
a738.pep	TAGKKLFDVKIPISFLLFMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
m738	TAGKKLFDVKIPISFLLFMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a738.pep	VAHYQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
m738	VAHFGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
	130	140	150	160	170	180
	190	200	210	220	230	240
a738.pep	NLGHYLMWGILAAAYLNGQRKIPALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
m738	NLGHYLMWGILAAAYLNGQRKIPALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	190	200	210	220	230	240
	250	260	270	280	290	300
a738.pep	YFRSDKSNRRITILGIAAAVELTALFQFSMNTILETFTGIRYETAVERVANGGFTDLPRQI					
m738	YFRSDKSNRRITMLGIAAAVELTALFQFSMNTILETFTGIRYETAVERVANGGFTDLPRQI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a738.pep	EWRKALAAFO SAPIFGHGWN SFAQQTFLINAEQHNHNDNL LSNLFTHSHNIVLQLLAEMG					
m738	EWNKALAAFO SAPIFGHGWN SFAQQTFLINAEQHNHNDNL LSNLFTHSHNIVLQLLAEMG					
	310	320	330	340	350	360
	370	380	390	400	410	420
a738.pep	ISGTLLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
m738	ISGTLLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
	430	440	450	460	470	480
a738.pep	FLSPAASDGI AFKKAANLGILTASAAIFAGLLHLDWYTRMVNAFSPATDDSAKTLNRK					
m738	FLSPAASDGI AFKKAANLGILTASAAIFAGLLHLDWYTRLVNAFSPATDDSAKTLNRK					
	430	440	450	460	470	480
	490	500	510	520	530	540
a738.pep	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEATLKSLKYRPHSATYRIALYL					
m738	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEATLKSLKYRPHSATYRIALYL					
	490	500	510	520	530	540

1202

	550	560	570	580	590	600
a738 . pep	MRQ GK V A E A K Q W M R A T Q S Y Y P Y L M P R Y A D E I R K L P V W A P L L P E L L K D C K A F A A A P G H P E A					
m738	MRQ GK V A E A K Q W M R A T Q S Y Y P Y L M P R Y A D E I R K L P V W A P L L P E L L K D C K A F A A A P G H P E A					
	550	560	570	580	590	600
a738 . pep	K P C K K X					
m738	K P C K K X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2521>:

g739 . seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCAGCGC CATCGGCGCA TTGGCAGTAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG AAAAAACCTT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGCCGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGAAG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCAAGAA AAACCGGGTc AAACCGGCC CTTCGGATGC
351 GGCCCGGGCA GCCGATTCGT TAACCGGCAC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGCCCCCA TCCCGAACCC
451 CGAAAAGAAA CACCCGAAA ACAGGCGCAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAACA
551 CGCCGGCCAA ACCCCATAAA GAGATTCTCG ACAACCTCTT TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2522; ORF 739>:

g739 . pep

```

1  MAKKPNKPF R LTPKLLIRAV LLICITAIGA LAVGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGAVG QDAAQPEHHH AASSEPAQPD GTEESGSGLP
101 SPAAPKKNRV KERPSDAARA ADSLTGTGTQ AENTLKETPV LPTNAPHPEP
151 RKETPEKQAO PKETPKKET PKENHTKPD T PKNTPAKPHK EILDNLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2523>:

m739 . seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCGCCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG AAAAAACCTT TCAAGCCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAA ACAGGCGCAG CCCAAAGAAA CGCCCAAGA
501 AAACCATACC AAACCGGACA CCCCAGAAA CACGCCGCC AAACCCATA
551 AAGAAATTCT CGACAACTC TTC

```

This corresponds to the amino acid sequence <SEQ ID 2524; ORF 739>:

m739 . pep

```

1  MAKKPNKPF R LTPKLLIRAV LLICIAAIGA LAIGIVSTFN PNGDKTLQAE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH AASSEPAQPD GTDESGSGLP
101 SPAAPKKNRV KPQPADTAQT DRPDDAGTQ AENTLKETPV LPTNVPRPEP
151 RKETPEKQAO PKETPKENHT KPDTPKNTTP KPHKEILDKL F

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 739 shows 86.3% identity over a 197 aa overlap with a predicted ORF (ORF739.a) from *N. gonorrhoeae*:

m739/g739

1203

	10	20	30	40	50	60
m739.pep	MAKKPNKPFRLTPKLLIRAVLLICITAAIGALAIGIVSTFNPNGDKTLQAEPOHTDSPRET					
	: : : : : :					
g739	MAKKPNKPFRLTPKLLIRAVLLICITAAIGALAVGIVSTFNPNGDKTLQTEPOHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m739.pep	EFWLPGVVGQDAAQPEHHHAASSEPAQPDGTDESGSGLPSAAPKKNRVKQPADTAQT					
	: : : : : :					
g739	EFWLPGVVGQDAAQPEHHHAASSEPAQPDGTEESGSGLPSAAPKKNRVKPRPSDAARA					
	70	80	90	100	110	120
	130	140	150	160	170	
m739.pep	DRQPDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKE-----NHTKPD					
	:	:	:	:	:	:
g739	ADSLTGTGTQAENTLKETPVLPTNAPHPEPRKETPEKQAQPKETPKEKETPENHTKPD					
	130	140	150	160	170	180
	180	190				
m739.pep	PKNTPPKPKHEILDKLF					
	: :					
g739	PKNTPAKPKHEILDNLFX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2525>:

```

a739.seq
1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCTT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCTCCTCAT
251 CCGCACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAGCACA GCTGAAACAA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAA ACAGGCACAG CCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAAACA
551 CGCCGCCTAA ACCCATAAA GAAATTCTCG ACAACCTCTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2526; ORF 739.a>:

a739.pep	1	MAKKPNKPFRLTPKLLIRAV	LLICITAIGA	LAIGIVSTFN	PNGDKTLQTE
	51	POHTDSPRET	EFWLPGVVG	QDAAQPEHHH	ASSSAPAQPD
	101	SPAAPKKNRV	KQPADTAQT	DRQPDAGAQ	AENTLKETPV
	151	RKETPEKQAQ	PKETPKEKET	PKENHTKPD	PKNTPPKPKH
					EILDNLFX*

a739/m739 93.9% identity in 197 aa overlap

	10	20	30	40	50	60
a739.pep	MAKKPNKPFRLTPKLLIRAVLLICITAAIGALAIGIVSTFNPNGDKTLQTEPOHTDSPRET					
	: : : : : :					
m739	MAKKPNKPFRLTPKLLIRAVLLICITAAIGALAIGIVSTFNPNGDKTLQAEPOHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
a739.pep	EFWLPGVVGQDAAQPEHHHASSSAPAQPDGTDESGSGLPSAAPKKNRVKQPADTAQT					
	: : : : : :					
m739	EFWLPGVVGQDAAQPEHHHAASSEPAQPDGTDESGSGLPSAAPKKNRVKQPADTAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
a739.pep	DRQPDAGAQENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKEKETPENHTKPD					
	: : : : : :					
m739	DRQPDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPK-----ENHTKPD					
	130	140	150	160	170	

1204

```

                190
a739.pep      PKNTPPKPKHKEILDNLFX
                |||||
m739          PKNTPPKPKHKEILDKLF
                180    190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2527>:

```

g740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTC GCCGCTCTGCC TCATCCCCCTT
51 GgcgACGCTT GCCGTTTTCG CCGCCAATcc gcCCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTTAAa
151 ttcgtgctCT TTGAAACCAT CAAGCATCAT CTTAaacaag gGTTTGATT
201 GAAACgtcaa ACCATGTTTC TGTATTATCC GATTGTTTGG CTGTTGTGT
251 ATTTGTTCCA CTATTTCGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2528; ORF 740.ng>:

```

g740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KPQHLINGII LACEATFLFK
51 FVLFDTIKHH LKQGFDLKRQ TMLLFIPIVL LVVYLFHYFG AF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2529>:

```

m740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GCCGCTCTGCC TCATCCCCGTT
51 GCGGACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACCTCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTTAAA
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATT
201 GAAACGTCAA ACTATGTTGC TGTATTATCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2530; ORF 740>:

```

m740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KLOHLINGII LACEATFLFK
51 FVLFDTIKHH LKQEFDLKRO TMLLFIPIL LIVYLFHYFG AF*

```

m740/g740 93.5% identity in 92 aa overlap

```

                10      20      30      40      50      60
m740.pep      MSRNLLVRWLA VCLIPLATL AVFAANPPED KLOHLINGII LACEATFLFK FVLFDTIKHH
                |||||
g740           MSRNLLVRWLA VCLIPLATL AVFAANPPED KPQHLINGII LACEATFLFK FVLFDTIKHH
                10      20      30      40      50      60

                70      80      90
m740.pep      LKQEFDLKRQ TMLLFIPIL LIVYLFHYFG AF*
                |||
g740           LKQGFDLKRQ TMLLFIPIVL LVVYLFHYFG AF*
                70      80      90

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2531>:

```

a740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GTCGCTCTGCC TGATACCCCTT
51 GCGGACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACCCAGC
101 ATCTGATTAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTCAAA
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATT
201 GAAACGTCAA ACTATGTTGC TGTATTATCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2532; ORF 740.a>:

```

a740.pep
1  MSRNLLVRWL VVCLIPLATL AVFAANPPED KPQHLINGII LACEATFLFK
51 FVLFDTIKHH LKQEFDLKRQ TMLLFIPIL LIVYLFHYFG AF*

```

a740/m740 97.8% identity in 92 aa overlap

```

                10      20      30      40      50      60

```

1205

```

a740.pep  MSRNLLVRWLVLPLATLAVFAANPPEDKPOHLINGIILACEATFLFKFVLFDTIKHH
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m740      MSRNLLVRWLVLPLATLAVFAANPPEDKLOHLINGIILACEATFLFKFVLFDTIKHH
          10      20      30      40      50      60

          70      80      90
a740.pep  LKQEFDLKROTMLLFIPILLIVLYLFHYFGAFX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m740      LKQEFDLKROTMLLFIPILLIVLYLFHYFGAFX
          70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2533>:

```

g741.seq
1  GTGAACCGAA CTACCTTCTG CTGCCTTTCT TTGACCGCCG GCCCTGATTG
51  TGACCGCCTG CAGCAGCGGA GGGGCGGAGG CGGTGGTGTC GCCGCCGACA
101 TCGGCACGGG GCTTGCCGAT GCATTAACCG CGCCGCTCGA CCATAAAGAC
151 AAAGGTTTGA AATCCCTAAC ATTGGAAGCC TCCATTCCCC AAAACGGAAC
201 ACTGACCTTG TCGGCACAAG GTGCGGAAAA AACTTTCAAA GCCGGCGGCA
251 AAGACAACAG CCTCAACACG GGCAAACTGA AGAACGACAA AATCAGCCGC
301 TTCGACTTCG TGCAAAAAAT CGAAGTGGAC GGACAAACCA TCACACTGGC
351 AAGCGGCGAA TTTCAAATAT ACAAAACAGGA TCACTCCGcc gtcgtTgcCC
401 TacgGATTGA AAAAATCAAC AACCCCGACA AAATCGACAG CCGTATAAAC
451 CAACGCTCCF TCCTTGTCAG CGATTGGGCG GGAGAACATA CCGCCTTCAA
501 CCAACTGCCT GACGGCAAAG CCGAGTATCA CGGCAAAGCA TTCAGCTCCG
551 ACGATGCCGA CGGAAACTG ACCTATACCA TAGATTTGCG CGCCAAACAG
601 GGACACGGCA AAATCGAACA CCTGAAACA CCGAGCAGA ATGTTGAGCT
651 TGCTCCGCC GAACTCAAAG CAGATGAAAA ATCACACGCC GTCATTTTGG
701 GCGACACGGC CTACGGCGGC GAAGAGAAAG GCACTTACCG CCTCGCCCTT
751 TTCGGCGACC GCGCCCAAGA AATCGCTGGC TCGGCAACCG TGAAGATAGG
801 GGAAAAGGTT CACGAAATCG GCATCGCCGA CAAACAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2534; ORF 741.ng>:

```

g741.pep
1  VNRTTFCCLS LTAGPDSRL QRRGGGGGV AADIGTGLAD ALTAPLDHKD
51  KGLKSLTLEA SIPONGTTLT SAQGAEKTFK AGGKDNSLNT GKLNKDKISR
101 FDFVQKIEVD GQTITLASGE FQIYKQDHSV VALRIEKIN NPDKIDSLIN
151 QRSFLVSDLG GEHTAFNQLP DGKAEYHGKA FSSDDADGKL TYTIDFAAKQ
201 GHGKIEHLKT PEQNVELASA ELKADEKSHA VILGDTRYGG EEKGTYRLAL
251 FGDRAQEIAG SATVKIGKEV HEIGIADKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2535>:

```

m741.seq
1  GTGAATCGAA CTGCCTTCTG CTGCCTTTCT CTGACCACTG CCTGATTCT
51  GACCGCCTGC AGCAGCGGAG GGGGTGGTGT CGCCGCCGAC ATCGGTGCGG
101 GGCTTGCCGA TGCACTAACC GCACCGCTCG ACCATAAGA CAAAGGTTTG
151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAAACGAGA AACTGAAGCT
201 GCGGCACAAA GGTGCGGAAA AACTTATGG AAACGGTGAC AGCCTCAATA
251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GTTTCGACTT TATCCGCCAA
301 ATCGAAGTGG ACGGGCAGCT CATTACCTTG GAGAGTGGAG AGTTCCAAGT
351 ATACAAACAA AGCCATTCCG CCTTAACCGC CTTTCAGACC GAGCAAATAC
401 AAGATTCCGA GCATTCCGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
451 GCGACATAG CGGGCGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
501 CAGGGCGACA TATCGCGGGA CGGCGTTCGG TTCAGACGAT GCCGGCGGAA
551 AACTGACCTA CACCATAGAT TTCGCCGCA AGCAGGGAAA CGGCAAAATC
601 GAACATTGTA AATCGCCAGA ACTCAATGTC GACCTGGCCG CCGCCGATAT
651 CAAGCCGGAT GGAAGACGCC ATGCCGTGAT CAGCGGTTCC GTCCTTTACA
701 ACCAAGCCGA GAAAGGCAGT TACTCCCTCG GTATCTTTGG CGGAAAAGCC
751 CAGGAAGTTG CCGGCAGCGC GGAAGTGAAA ACCGTAAACG GCATACGCCA
801 TATCGGCCCTT GCCGCCAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2536; ORF 741>:

```

m741.pep
1  VNRTAFCCLS LTTALILTAC SSGGGGVAAD IGAGLADALT APLDHDKDKL
51  QSLTLDQSVR KNEKLKLAAG GAEKTYGNGD SLNTGKLKND KVSRLFDFIRQ
101 IEVDGQLITL ESGEFQVYKQ SHSALTAFQT EQIQDSEHSG KMVAKRQFRI

```

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151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD AGGKLTYYTID FAAKQNGKI
 201 EHLKSPELNV DLAAADIKPD GKRHAVISGS VLYNQAEGKS YSLGIFGGKA
 251 QEVAGSAEVK TVNGIRHIGL AAKQ*

m741/g741 61.4% identity in 280 aa overlap

	10	20	30	40	50
m741.pep	VNRTAFCCLSLTT---ALILTACSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQ				
	: :	:	:	:	:
g741	VNRTTFCCLSLTAGPDSRLQQRGGGGVAADIGTGLADALTAPLDHKDKGLKSLTLEA				
	10	20	30	40	50
	60	70	80	90	100
m741.pep	SVRKNEKLKLAQAQAEKTY---GNGDSLNTGKLNKNDKVSRLFDFIRQIEVDGQLITLESGE				
	: : :	:	:	:	:
g741	SIPQNGTLTSLAQAQAEKTFKAGGKDNSLNTGKLNKNDKISRDFVQKIEVDGQTITLASGE				
	70	80	90	100	110
	120	130	140	150	160
m741.pep	FQVYKQSHSALTAFQTEQIQDSEHSKGMVAKRQFRIGDIAGEHTSFDKLPEGGRATYRG				
	: :	: :	: :	: :	: :
g741	FQIYKQDHSAAVVALRIEKINFPDKIDSLINQRSFLVSDLGGEHTAFNQLPDG-KAEYHGK				
	130	140	150	160	170
	180	190	200	210	220
m741.pep	AFGSDDAGGKLTYYTIDFAAKQNGKIEHLKSPELNVDLAAADIKPDGKRHAVISGSVLYN				
	:			: :	: :
g741	AFSSDDADGKLTYYTIDFAAKQGHGKIEHLKTEQNVELASAEKKADEKSHAVILGDTRYG				
	180	190	200	210	220
	230	240	250	260	270
m741.pep	QAEKGSYSLGIFGGKAQEVAGSAEVKTVNGIRHIGLAQKX				
	:	: :	: :	: :	: :
g741	GEEKGTYYRLALFGDRAQEIAGSATVKIGEKVHEIGIADKQX				
	240	250	260	270	280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2537>:

a741.seq

1	GTGAACCGAA	CTGCCTTCTG	CTGCCTTTCT	TTGACCGCCG	CCCTGATTCT
51	GACCGCCTGC	AGCAGCGGAG	GCGGCGGTGT	CGCGCGCGAC	ATCGGCGCGG
101	TGCTTGCCGA	TGCACTAACC	GCACCGCTCG	ACCATAAAGA	CAAAAGTTTG
151	CAGTCTTTGA	CGCTGGATCA	GTCCGTCAGG	AAAAACGAGA	AACTGAAGCT
201	GGCGGCACAA	GGTGCGGAAA	AAACTTATGG	AAACGCGGAC	AGCCTCAATA
251	CGGGCAAATT	GAAGAACGAC	AAGGTCAGCC	GCTTCGACTT	TATCCGTCAA
301	ATCGAAGTGG	ACGGGCAGCT	CATTACCTTG	GAGAGCGGAG	AGTTCCAAGT
351	GTACAAACAA	AGCCATTCCG	CCTTAACCGC	CCTTCAGACC	GAGCAAGTAC
401	AAGATTGCGA	GCATTCAGGG	AAGATGTTG	CGAAACGCCA	GTTCAGAATC
451	GGCGATATAG	CGSGTGAACA	TACATCTTTT	GACAAGCTTC	CCGAAGGCGG
501	CAGGGCGACA	TATCGCGGGA	CGGCATTCCG	TTCAGACGAT	GCCAGTGGAA
551	AACTGACCTA	CACCATAGAT	TTCGCGGCCA	AGCAGGGACA	CGGCAAAATC
601	GAACATTGGA	AATCGCCAGA	ACTCAATGTT	GACCTGGCCG	CCTCCGATAT
651	CAAGCCGGAT	AAAAAACGCC	ATGCCGTCAT	CAGCGGTTCC	GTCCTTTACA
701	ACCAAGCCGA	GAAAGGCAGT	TACTCTCTAG	GCATCTTTGG	CGGGCAAGCC
751	CAGGAAGTTG	CCGGCAGCGC	AGAAGTGGAA	ACCGCAAACG	GCATACGCCA
801	TATCGGTCTT	GCCGCCAAGC	AGTAA		

This corresponds to the amino acid sequence <SEQ ID 2538; ORF 741.a>:

a741.pep

1	VNRTAFCCLS	LTAALILTAC	SSGGGGVAAD	IGAVLADALT	APLDHKDKSL
51	QSLTLDQSVR	KNEKLKLAQ	GAEKTYGNGD	SLNTGKLNKND	KVSRLFDFIRQ
101	IEVDGQLITL	ESGEFQVYKQ	SHSALTALQT	EQVQDSEHSK	KMVAKRQFRI
151	GDIAGEHTSF	DKLPEGGRAT	YRGTAFGSDD	ASGKLTYYTID	FAAKQGHGKI
201	EHLKSPELNV	DLAASDIKPD	KKRHAVISGS	VLYNQAEGKS	YSLGIFGGQA
251	QEVAGSAEVE	TANGIRHIGL	AAKQ*		

a741/m741 95.6% identity in 274 aa overlap

1207

	10	20	30	40	50	60
a741.pep	VNRTAFCCISLTAALILTACSSGGGGVAADIGAVLADALTAPLDHDKSLQSLTLDQSVR					
m741	VNRTAFCCISLTTALILTACSSGGGGVAADIGAGLADALTAFLDHDKGLQSLTLDQSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
a741.pep	KNEKLKLAQAQAEKTYGNGDSLNTGKLNKDKVSRFD FIRQIEVDGQLITLESGEFQVYKQ					
m741	KNEKLKLAQAQAEKTYGNGDSLNTGKLNKDKVSRFD FIRQIEVDGQLITLESGEFQVYKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
a741.pep	SHSALTALQTEQVQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSDDD					
m741	SHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSDDD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a741.pep	ASGKLTYYTIDFAAQOGHGKIEHLKSPENVDLAASDIKPKKRHAVISGSVLYNQAEKGS					
m741	AGGKLTYYTIDFAAQOGNGKIEHLKSPENVDLAADIKPDGKRHAVISGSVLYNQAEKGS					
	190	200	210	220	230	240
	250	260	270			
a741.pep	YSLGIFGGQAQEVAGSAEVETANGIRHIGLAAKQX					
m741	YSLGIFGGKAQEVAGSAEVKTVNGIRHIGLAAKQX					
	250	260	270			

g742.seq not found yet

g742.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2539>:

m742.seq

```

1  ATGGTTACG GCATTGCCGA AGCCGATGCG GGCACAGCA GTGIGCTTAC
51  TTTGGGCGGC ATGTATCAGA AGAGTAGGGA GGTTCCTGAT TTTCGGGGCA
101 TTATTTTGCC CTGTGAAAAT CAGAAAAC TG CCGGTTT CAG TTCAACGCCT
151 GCCTGCAACC GGCCTTTGCA ACTGCCGCGC AACACTTATT TGGGGGAGGA
201 TTGGTCGCGG TTAAGTGCCG ACAATAACAA CCTTTTCTCA GGATTCAAAC
251 ATGTGTTTGA CAACGGTTGG CAGCTCAATG CCGAAGTGTC TTATACCAAG
301 AATGAATCCG ATGCGAAGGT GGGGCAAGTT TTTCTGAAAA ACGAATATGC
351 GCGGGGTTTG TCGGGTGAGG ATGCGGTAGG CTTTTTGA CT GAAAAAACG
401 AAGTCATCCC GTTCGAGCCG AAAGATAAGG CATGGAGAA ACTGAAAGCA
451 TATCGTGATG AAACCGCCAA GGAATACCGG GAGCGCAAAG ACGATTTTGT
501 TAAAAACCGT TTCGATAATA CTGCTTTTGA ACAGTATCGC AGCCGCCGTG
551 CCGCAGAACG CAAAGCCGGT TTTGACAAGT GTATGAGTGA CCCTTTCGCG
601 CTGGACTTTA TCTGTCAAGG TTCTTGGGGG GATCCGGGCG ITGATGCCGA
651 CAAGGCGGAA TTTGTCGATA AAGCCCTTGC GAAGGAGGGC ATCTTTAATA
701 ATGCGGCACA ACGTTTTC CA AACAGCCTGT ATGACTCTTC CTTTAATCGG
751 AAGGCTACCG CCAACCGACG ATACAGTTAT ATGCCGTTGC GGCATACCAA
801 AGACGACCGC CAATGGGGAA TTAACTTGA CCTGACCGGC ACATATGGGC
851 TGTTGCGGCG GGAGCATGAT TTCTTTGTCG GCTATGCC TA CGGTGATGAA
901 AAGATACGTT CGGAATATCT AGAAATCTAC GAACGCCGCT ACAGAGTACG
951 TCCGAATACG GGGGCAACGC ACGGCGTGTA TCGGGGAAGT TGTCAAGGAG
1001 AGCCGGACCG CGATTGTGCG TCTCCTTTGG TCAGGGGGCA TAAAGAACCC
1051 GATTGCGAGG CGTACGATGA AAAAGGCAAC CGTACCGTTT ATGCCGAAGA
1101 ATGCAGGAAC GCCAAGAAAA TAAAAACCGA GCCCAAGCTC GATGCCGAAG
1151 GCAAGCAGGT GTATTACTAT GACGAATACA GCGGCAAGCG GACACCGGTA
1201 TATGTCGATG TATATGAGCT GSACGAAAAA GGCAACAAGA TTCAGGAGAC
1251 CAATCCCGAC GGCACGCCTG CTTTACCGG TTTTCCGGT ACGGTGCCGG
1301 TTTGAAAAAC CGTCAAAGTG GCAGACGACC ATGTTCCCTG CTTGTATAAC
1351 TACGCCAAAT ACCTCAACAC CAACAAAACC CATTCGCTGA CTGCCAGCAC
1401 GCGTTTCAAC GTAACCGGCC GACTGCACCT TTTGGGCGG CTGCACTACA

```



```

1451 CGCGCTATGA GACTTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAGGGCGG ATCAGGACCA
1551 TTACACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCTATGACTT GACACGCAA CAGAGTATTT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCGGC ACAAACTATG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTC GCATTGTTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTCGTCG ATTTCCGCTA TGTTCCCGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTTCGAGT GTCCGGTGAG TTGAACGAAG ATTGGAAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAC GCCGCCGAAG TCAACGCCGA
2001 ACGCCTTGCC AAAAATTCCTA GTGCAGACCC GTACAACTTC AGCAATTTCA
2051 CACCCGTGCA CATATTCCGT TCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGGCGG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCC AAATTGAGCC TCATCGGTAC GAACCTIAAAC
2251 GGACGCACCT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAAAACA
2301 CTTCTACGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA

```

This corresponds to the amino acid sequence <SEQ ID 2540; ORF 742>:

```

m742.pep
1  M V Y G I A E A D A G D S S V L T L G G M Y Q K S R E V P D F S G I I L P C E N Q K T A P F S S T P
51  A C N R P L Q L P R N T Y L G E D W S R L S A D K Y N L F S G F K H V F D N G W Q L N A E V S Y T K
101 N E S D A K V G Q F F L K N E Y A A G L S G E D A V G F L T E K N E V I P F E P K D K A L E K L K A
151 Y R D E T A K E Y R E R K D D F V K N R F D N T A F E Q Y R S R R A A E R K A G F D K C M S D P F A
201 L D F I C Q G S W G D P G V D A D K A E F V D K A L A K E G I F N N A A Q R F P N S L Y D S S F N R
251 K A T A N R R Y S Y M P L R H T K D D R Q W G I K L D L T G T Y G L F G R E H D F F V G Y A Y G D E
301 K I R S E Y L E I Y E R R Y R V R P N T G A T H G V Y A G S C Q E E P D G D L S P L V R G H K E P
351 D W Q A Y D E K G N R T V Y A E E C R N A K K I K T E P K L D A E G K Q V Y Y Y D E Y S G S R T P V
401 Y V D V Y E L D E K G N K I Q E T N P D G T P A F T G F S G T V P V W K T V K V A D D H V P A L Y N
451 Y A K Y L N T N K T H S L T A S T R F N V T G R L H L L G G L H Y T R Y E T S Q T K D M P V R Y G Q
501 P A S D F Q T A S S I R A D Q D H Y T A K M Q G H K L T P Y A G I T Y D L T P Q Q S I Y G S Y T K I
551 F K Q Q D N V D V S A K T V L P P L V G T N Y E V G W K G A F L Q G R L N A S F A L F Y L E Q K N R
601 T V V D F G Y V P G A G G K Q G S F Q T V A K P I G K V V S R G A E F E L S G E L N E D W K V F A G
651 Y T Y N K S R Y K N A A E V N A E R L A K N S S A D P Y N F S N E T P V H I F R F G T S F H I P N T
701 G L T V G G G V S A Q S G T S S L Y N I R Q G G Y G L I D G F V R Y E L G K H A K L S L I G T N L N
751 G R T Y F E N N Y N R T R G A N N F Y G E P R T V S M K L D W Q F *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2541>:

```

a742.seq
1  A T G G T T T A C G G C A T T G C C G A A G C C G A T G C G G G C G A C A G C A G T G T G C T T A C
51  T T T G G G C G G C A T G T A T C A G A A G A T A G G A G G T T C C T G A T T T T C G G G C A
101 T T A T T T T G T C T G T G A A A A T C A G A A A A C T G C C C G T T C A G T T C A A C G C C T
151 C C C T G C A A C C G G C C T T T G C A A C T G C C G C G C A A C A C T T A T T G G G G G A G G A
201 T T G G T C G C G G T T G A G T G C T G A C A A A T A C A A C C T T T T C T C A G G T T C A A A C
251 A T G T G T T T G A C A A C G G T T G G C A G C T C A A T G C C G A A G T G T C T T A C C A A G
301 A A T G A A T C C G A T G C G A A G G T G G G C A G T T T T T C T G A A A A A C G A A C A T G C
351 G C C G G G T T T G T C A G A T G A G A T G C G G T A G G C T T T T T G A C C G A A A A A A C G
401 A A G T C A T C C C G T T C G A G C C G A A A G A T A A G G C A T T G G A G A A A C T G A A A G C A
451 T A T C G T G A C G A A A C C G C C A A G G A T A C C G T G A G C G C A A A G A C G A T T T T G T
501 T A A A A A C C G T T T C G A T A A T A C T G C T T T C G A G C A G T A C C G C A G C C G C G T G
551 C C G C A G A A C G C A A A G C C G G T T T T G A C G A G T G A T G A G T G C C C T T T T G C G
601 C T G G A C T T T A T C T G T C A A G G T T C T T G G G G G A T C C G G G T G T T G A T G C C G A
651 C A A G T C G G A A T T T G T C G A T A A G C C C T T G C G A A G G A A S G C A T C T T T A A T A
701 A T G C G G C A C A A C G T T T T C C A A A C A G C C T G T A T G A C T C T T C C T T A A T C G G
751 A A G G T A C C G C C A A C C G A C G A T A C A G T T A T A T G C C G T T G C G G C A T A C C A A
801 A G A C G A C C G C C A A T G G G G A A T T A A A C T T G A C C T G A C C G C G C A C A T A T G G G C
851 T G T T C G G G C G G A G C A T G A T T T C T T T G T C G G C T A T G C C T A C G G C A T G A A
901 A A G A T A C G T T C C G A A T A C T G G A A T C T A C G A A C G C C G C A C A G A G T A C G
951 T C C G A A T A C A G G G C A A C G C A C G C G T G T A T G C G G G A A G T G T C A G G G G G
1001 A C C C G A C G G T G A T T T G T C T T C C T T T G G T C A G G G G G C A T A A G A A C C C
1051 G A T T G G C A G G C G T A C G A T G A A A A G G C A A C C G T A C C G T T T A T G C C G A A G A
1101 A T G C A G G A A T G C C A A G A A A T A A A A C C G A G C C A A G C T C G A T G C C G A A G
1151 G C A A G C A G G T G A T T A C T A T G A C G A A T A C A C G G C A G C C G G A C G C C A G T A

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1209

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1201 TATGTCGATG TATATGAACT GGATGAAAAA GGCAATAAGA TTCAGGAGAC
1251 CAATCCCGAC GGCACGCCTG CCTTTACCGG TTTTTCGGT ACGGTGCCGG
1301 TTTGGAAAAC CGTCAAAGTG GCCGACGACC ATGTTCTCTG GCTGTATAAC
1351 TACGCCAAAT ACCTCAACAC CAACAAAACC CATTGCTGTA CTGCCGGCAC
1401 ACGTTTCAAC GTAACCGGCC GACTGCATCT TTTGGGCGGG CTGCACTACA
1451 CGCGCTATGA AACCTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAAGGCGG ATCAGGACCA
1551 TTATACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCTATGATTT GACACCGCAA CAGAGTATTT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCCGG ACAAACTATG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTT GCATTGTTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTCGTCG ATTTTGGCTA TGTTCCCGGA GCAGGCGGGA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTGAGATT GTCGGGTGAG TTGAACGAAG ATTGGAAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAC GCCGCGAAG TCAAGCCCGA
2001 ACGCCTCGCC AAAAACACAG GCGCAGACCC GTACAACTTC AGCAATTTCA
2051 CACCCGTGCA CATATTCCGT TTCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGGCGG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TCGTCCGTT
2201 ACGAATTGGG CAAACACGCT AAATTGAGCC TCATCGGTAC GAACTTAAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAAACAA
2301 CTTCTATGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA

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This corresponds to the amino acid sequence <SEQ ID 2542; ORF 742.a>:

a742.pep

```

1  MVYGIAEADA GDSSVLTGG MYQKSREVPD FSGIILSCEN QKTAPFSSTP
51  ACNRPLQLPR NTYLGEDWSR LSADKYNLFS GFKHVFNDGW QLNAEVSYTK
101 NESDAKVGQF FLKNEHAAGL SDEDAVGFLT EKNEVIPFEP KDKALEKLKA
151 YRDETAKEYR ERKDDFVKNR FDNFAFEQYR SRRAAERKAG FDECM SAPFA
201 LDFICQGSWG DPGVDADKSE FVDKALAKEG IFNNAQRFP NSLYDSSFNR
251 KATANRRYSY MPLRHTKDDR QWGIKLDLTG TYGLFGREHD FVGYAYGDE
301 KIRSEYLEIY ERRHRVRPNT GATHGVYAGS CQGE PDGDL S PLVRGHKEP
351 DWQAYDEKGN RTVYAEECRN AKKIKTEPKL DAEGKQVYYY DEYSGSRTPV
401 YVDVYELDEK GNKIQETNPD GTPAFTGFSG TVPVWKT VKV ADDHVPALYN
451 YAKYLNTNKT HSLTAGTREN VTGRLHLLGG LHYTRYETSQ TKDMPVRYGQ
501 PASDFQTASS IKADQDHYTA KMQGHKLTPY AGITYDLTPQ QSIYGSYTKI
551 FKQQDNVDVS AKTVLPPLVG TNYEVGWKGA FLQGRNLNASF ALFYLEQKNR
601 TVVDFGYVPG AGGKQGSFQT VAKPIGKVS RGAEFELSGE LNEWDKVFAG
651 YTYNKSRYKN AAEVNAERLA KNTGADPYNF SNF TPVHIFR FGTSFHIPNT
701 GLTVGGGVSA QSGTSSLYNI RQGGYGLIDG FVRYELGKHA KLSLIGTNLN
751 GRTYFENNYN RTRGANNFYG EPRTVSMKLD WQF*

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a742/m742 98.5% identity in 783 aa overlap

	10	20	30	40	50	60
a742.pep	MVYGIAEADAGDSSVLTGGMYQKSREVPDFSGIILSCENQKTAPFSSTPACNRPLQLPR					
m742	MVYGIAEADAGDSSVLTGGMYQKSREVPDFSGIILPCENQKTAPFSSTPACNRPLQLPR					
	10	20	30	40	50	60
a742.pep	NTYLGEDWSRLSADKYNLFSGFKHVFNDGWQLNAEVSYTKNESDAKVGQFFLKNEHAAGL					
m742	NTYLGEDWSRLSADKYNLFSGFKHVFNDGWQLNAEVSYTKNESDAKVGQFFLKNEYAAGL					
	70	80	90	100	110	120
a742.pep	SDEDAVGFLTEKNEVIPFEPKDKALEKLKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR					
m742	SGEDAVGFLTEKNEVIPFEPKDKALEKLKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR					
	130	140	150	160	170	180
a742.pep	SRRAAERKAGFDECM SAPFALDFICQGSWGDPGVDADKSEFVDKALAKEGIFNNAQRFP					
m742	SRRAAERKAGFDECM SAPFALDFICQGSWGDPGVDADKSEFVDKALAKEGIFNNAQRFP					
	190	200	210	220	230	240
a742.pep	SRRAAERKAGFDECM SAPFALDFICQGSWGDPGVDADKSEFVDKALAKEGIFNNAQRFP					
m742	SRRAAERKAGFDECM SAPFALDFICQGSWGDPGVDADKSEFVDKALAKEGIFNNAQRFP					

1210

m742
SRRAAEKAGFDKCMSDPFALDFICQGSWGDGVDACKAEFVDKALAKEGIFNNAQRFP
190 200 210 220 230 240

a742.pep NSLYDSSFNRKATANRRYSYMLRHTKDDROWGIKLDLTGTYGLEFGREHDFVGYAYGDE

m742 NSLYDSSFNRKATANRRYSYMP^{LR}HTKDD^{RQ}WGIKLDLTGT^YGLFGR^{EH}DFVGYAYGDE
250 260 270 280 290 300

a742.pep · KIRSEYLEIYERRHRVRPNTGATHGVYAGSCOGEPDGDLSPLVRGHKEPDWOAYDEKGN

m742 KIRSEYLEIYERRYVRNPNTGATHGVYAGSCQEEDGDLSSPLVRGHKEPDWQAYDEKGN
310 320 330 340 350 360

370 380 390 400 410 420
a742.pep RTVYAEECRNAAKKIKTEPKLDAEGKOVYYYDEYSGSRTPVYVDVYELDEKGNKIOETNPD

m742 RTVYAECECRNAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQETNPD

430 440 450 460 470 480
a742.pep GTPAFTGFSGTVPVVKTKVKVADHDHVPALYNYAKYLN~~TK~~THSLTAGTRENVTGRHLHGG

m742 GTPAFTGPGSGTVPVVKTVKVVADHDVPAALYNKYALNTNKTHTSLTASTRENVVTGRLLHLLGG

 430 440 450 460 470 480

490 500 510 520 530 540
a742.pep LHYTRYETSQTKDMPVRYGCPASDFOTASSIKADODHYTAKMOGHKLTPYAGITYDLTPQ

m742 LHYTRYETSQTKDMPVRYGCPASDFQTASSIRADQDHYAKMQGHKLTPTYAGITYDLTPQ
 490 500 510 520 530 540

550 560 570 580 590 600
a742.pep OSIYGSYTKIFKQDNDVDVSAKTVLPPLVGTNYEVGWKGAFLOGRLNASFALFYLEOKNR

m742 QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAFLOGRLNASFALFYLEQKNR
 550 560 570 580 590 600

TVVDFGYVPGAGGKQGSFOTVAKPIGVVSRGAEEFELSGELNEDWKVFAGYTYNKSRYKN

m742 TVVDFGYYPGAGGKQGSFOTVAKPIGKVVSRGAEFELSGELNEDWKVVFAGYTYNKSRYKN
610 620 630 640 650 660

670 680 690 700 710 720
a742.pep. AAEEVNAERLAKNTGAOPYNESNETPVHIERFGTSEHIPNTGLTVGGGVSAQSGTSSLYNI

m742 AAEVNAERLAKNSSADPYNFSNFTPVHIFRFGTSEHIPNTGLTVGGGVSAQSGTSSLYNI
 670 680 690 700 710 720

730 740 750 760 770 780
a742.pep ROGGYGLIDGFEVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNEYGEPRVTYSMKLD

m742 RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRRTRGANNFYGEPRTVSMKLD

a742.pep WQFX

1111

m742 WQFX

a742/ p25184

sp|P25184|PUPA PSEPU

FERRIC-PSEUDOBACTIN

358

RECEPTOR

PRECURSOR

>q i | 94923 | p i r | | S 15169

1211

ferric-pseudobactin receptor precursor - *Pseudomonas putida* >gi145723 (X56605)
 pseudobactin uptake protein [*Pseudomonas putida*] Length = 819
 Score = 152 bits (381), Expect = 6e-36
 Identities = 110/356 (30%), Positives = 170/356 (46%), Gaps = 55/356 (15%)

Query: 436 KTVKVADDDHV-PALYNYAKYLNTNKTSLTAGTRFNVNTERLHLLGGLHYTRYETSQTKDM 494
 +T K DD + P + +Y +N+ +RFN+T LHL+ G + Y
 Sbjct: 511 QTPKPGDDEIIPGI-----QYNISNRQSGYFVASRFNLTDLHLILGARASNYRFDYAL-- 564

Query: 495 PVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTPYAGITYDLTPQQSIYGSYTKIFKQQ 554
 R G + ++ ++ +TPYAGI YDLT +QS+Y SYT IFK Q
 Sbjct: 565 -WRIGNEPAPYKM-----VERGVVTPYAGIVYDLTNEQSVYASYTDIFKPQ 609

Query: 555 DNVDVSAKTVPPLVGTNYEVGWKGAFLOGRNLNASFALFYLEQKNRTVVDFGYVPGAGGK 614
 +NVD++ K L P VG NYE+GWKG FL+GRLNA+ AL+ +++ N VP +GG
 Sbjct: 610 NNVDTGKP-LDPEVGKNYELGWKGEFLEGRNLNANIALYMKRDNLAESTNEVVPDSSGGL 668

Query: 615 QGSFQTVAKPIGKVVSARGAEFELSGELNEDWKVFAGYTYNKSRYKNAEVAERLAKNTG 674
 S + + ++G + ELSGE+ W VF GY++ ++
 Sbjct: 669 IAS-----RAVDGAETKGVDELSEVLPGWNVFTGYSHTRTE-----D 707

Query: 675 ADPYNFSNFTPVHIFRFTSFHIPN--TGLTVGGGVSAQSGTS---SLYN--IRQGGYGL 727
 AD + P+ FRF ++ +P LT+GGGV+ S ++ + YN + Q Y +
 Sbjct: 708 ADGKRLTPQLPMDTFRFWNTYRLPGEWEKLTGGGVNWNNSKSTLNFARYNSHVTQDDYFV 767

Query: 728 IDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLDWQF 783
 RY + + +L N+ + Y Y G+ YG PR ++ L + F
 Sbjct: 768 TSLMARYRINESLAATLNVNNIFDKKY----YAGMAGSYGHYGAPRNATVTLRYDF 819

g743.seq not found yet

g743.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2543>:

m743.seq
 1 ATGAATCAAA ATCATTTTTC ACTTAAATTT CTGACCGTTA TGCTGTTATC
 51 GGCTTACGGT GGTTCCTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
 101 ATACCGTCAG TCTGGATACG GTCAATGTAC GCGGCTCTCA TGCTTGTGTTG
 151 GGCAAGACCG AAAAGACCCG TTCTTATACG ATAGATCGGA TGTCACCCGC
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAC
 351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
 401 TGACCGTCAA TGTTGCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
 451 TCTCCGAGTA CCGATTGGC GGTATTGAC CATATTGAAG TTGTACGGGG
 501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGAGGA ACCGTCAATT
 551 TGATCCGTAA GTGA

This corresponds to the amino acid sequence <SEQ ID 2544; ORF 743>:

m743.pep
 1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALL
 51 GKTEKTRSYT IDRMSTATGM RIAGKDTPQS VSVITRSLD DKAVHTLEEA
 101 MKNVTTGVNVV RDSGLQTRFL SRGEYIDQIG EDGMTVNVAG RSGYTAKIDV
 151 SPSTDLAVYD HIEVVRGATG LTQSNSEPGG TVNLIRK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2545>:

a743.seq
 1 ATGAATCAAA ATCATTTTTC ACTTAAATTT CTGACCGTTA TGCTGTTATC
 51 GGCTTACGGT GGTTCCTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
 101 ATACCGTCAG TTTGGATACG GTCAATGTAC GCGGCTCTCA TGCTCTGTGCG
 151 GGCAAGACCG AGAAGACCCG TTCTTATACG ATAGATCGGA TGTCACCCGC
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAC

1212

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351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
401 TTACCGTCAA TGTTGCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
451 TCTCCGAGTA CCGATTGGC GGTATATGAC CATATTGAAG TTGTACGGGG
501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGTGGA ACCGTCAATT
551 TGATCCGTAA GCGA

```

This corresponds to the amino acid sequence <SEQ ID 2546; ORF 743.a>:

a743.pep

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1  MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALS
51  GKTEKTRSYT IDRSTATGM RIAGKDTPOS VSVITRSLD DKAVHTLEEA
101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGITVNVAG RSGYTAKIDV
151 SPSTD LAVYD HIEVVRGATG LTQSNSEPGG TVNLIRKR

```

a743/m743 98.9% identity in 187 aa overlap

	10	20	30	40	50	60
a743.pep	MNQNHFSLKI	LTVMLLSAYG	GSFADGVVPV	SDGNTVSLDT	VNVRGSHALS	SGKTEKTRSYT
m743	MNQNHFSLKI	LTVMLLSAYG	GSFADGVVPV	SDGNTVSLDT	VNVRGSHALS	LGKTEKTRSYT
	10	20	30	40	50	60
	70	80	90	100	110	120
a743.pep	IDRSTATGM	RIAGKDTPOS	VSVITRSLD	DKAVHTLEEA	MKNNTGVNVV	RDSGLQTRFL
m743	IDRSTATGM	RIAGKDTPOS	VSVITRSLD	DKAVHTLEEA	MKNNTGVNVV	RDSGLQTRFL
	70	80	90	100	110	120
	130	140	150	160	170	180
a743.pep	SRGFYIDQIG	EDGITVNVAG	RSGYTAKIDV	SPSTD LAVYD	HIEVVRGATG	LTQSNSEPGG
m743	SRGFYIDQIG	EDGMTVNVAG	RSGYTAKIDV	SPSTD LAVYD	HIEVVRGATG	LTQSNSEPGG
	130	140	150	160	170	180
a743.pep	TVNLIRKR					
m743	TVNLIRKX					

g744.seq not found yet

g744.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2547>:

m744.seq

```

1  ATGAAACCGT TAAAAACATT AGAATTTGGA TTTGTGGATG CTGCAAACTA
51  CAGAAGAAGA GAAAATAAAG ATTTATTTAA CCGAATATTT GTAAAAGGAG
101 AATATTTGGA TGAATTATGT GAACCAAATA TTTCTTTTTT AATCGGAGAA
151 AAGGGAACAG GAAAGACAGC ATATGCTGTT TATTTAACTA ATAACTTCTA
201 TAAAAACATA CATGCCACCTA CTAAGTTTGT TCGTGAAACC GATTATTCAA
251 AATTTATTCA GCTAAAGAAA GCAAGACACT TAACTGTTTC AGATTTTACA
301 AGTATTTGGA AAGTCATTTT ATATCTCTTG ATATCAAATC AAATCAAATG
351 TAAAGAAAAC GGAATATTAT CTTCATATAT TAATAAATTT AAAGCCTTAG
401 ATGAGGCTAT AAATGAATAT TATTATGGCG CTTTGATCCG GAAATTGTA
451 CAAGCAATAA CTTTAATAGA AAATCAAAA GAAGCTGCGG AAATGATTTT
501 TGGAAAATTT GTTAAACTAG GTGAAGAGGA ATCCCAACAA ATAACTTTTA
551 CAGAAAGTAA ATCCAAGCA AATTTAGGTT TTATTGAAAG AAAATTTAAA
601 AGCTTCCTTA CTCAGTTAAA GCTAAAAGAT AATCATATTT TGTTTATTGA
651 TGGGATAGAT ATTAGACCAT CACAGATTCC ATTTGATGAA TATCATGAGT
701 GTGTAAAAGG TCTTGCTAAC GCCATATGGA TGTAAATAA TGATATCTTC
751 CCTTCCTTAA AAGATAGTAA GGGAAAGGATG AGAGTGTGTG TATTGATTAG
801 ACCTGATATC TTTGATTCAT TAGGTTTACA AAATCAAAAT ACCAACTTC
851 AAGATAATTC AGTATTTTAA GACTGGAGGA CGGATTATAA ATCTTATAGA
901 AGTTCAAAGA TTTTGGCGT TTTTGATCAT CTTTGAGAA CCCAGCAAGA
951 AAAACAAGAT AGTTTAGAAA AAGGCAATC ATGGGATTAT TATTTCCAT
1001 GGAATGCTCC TAATTTACAT GATGAGTATA AAAATTTAAC TTCATTTATT
1051 AGCTTCCTTA GAAAATCGTA TTATCGACCT CGCGATATTC TTCAGATGCT
1101 TACTTTGCTA CAAAAAATA AGAAAAGTAA GGAAGATTAT GTCGTAGCAG
1151 AAGATTTTGA TAATACTTCT TTTCAAAGAG AATACTCGAT ATATTACTT
1201 GGTGAAATCA AAGATCATCT TTTGTTTTAT TATAGTCAAA GTGATTATCA
1251 AAATTTCTCG AAATTTTTTG AATTTTAAA CGGAAAGAT AGATTTAAAT

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1213

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1301 ATAGTGATTT TTTAAAAGCA TTTGAACGTT TGAAAAAGCA CTTACAAACA
1351 ACATCAGTGG AAATACCTAA ATTTATGAGT ACTGCTAATG AGTTTTTGCA
1401 ATTTTTATTT GACTTGAATG TTATTGCTTA TTTAGATAAC CCAGAAGATG
1451 AAACGAAACC ATATATCCAT TGGTGCTTA AAGATAGAAA TTATGCAAAAT
1501 ATTTCTCCTA AAATAAAAAC TGAAGCTGAA TATTTAATAT TTTCAGGATT
1551 ATCAAAAGCC CTTGATGTTG GTACTCCATT TAAGAACAAA CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2548; ORF 744>:

m744.pep

```

1 MKPLKTLFEG FVDAANYRRR ENKDLFNRIF VKGEYLDLCL EPNISFLIGE
51 KGTGKTAYAV YLTNNFYKNI HATTKFVRET DYSKFIQLKK ARHLTVSDFT
101 SIWKVILYLL ISNQIKCKEN GILSSIENKF KALDEAINEY YYGAFDPEIV
151 QAITLIENSK EAAEMIFGKF VKLGEZESQQ ITFTESKFQA NLGFIERKFK
201 DALSQLKLKD NHILFIDGID IRPSQIPFDE YHECVKGLAN AIWMLNNDIF
251 PSIKDSKGRM RVLLIRPDI FDSLGLQONQ TKLQDNSVFL DWRTDYKSYR
301 SSKIFGVFDH LLRTQEQKD SLEKGNWDY YFPWNAPNLH DEYKNLTSFI
351 SFLRKSYYRP RDILQMLTLL QKNKSKEDY VVAEDFDNTS FQREYSIYLL
401 GEIKDHLLEY YSQSDYQNFL KFFEFLNGKD RFKYSDELKA FERLKKHLQT
451 TSVEIPKFMS TANEFLQFLF DLNVIAYLDN PEDETKPYIH WCFKDRNYAN
501 ISPKIKTETE YLIFSGLSKA LDVGTPEFKNK Q*

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g745.seq not found yet

g745.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2549>:

m745.seq

```

1 ATGTTTGGC AACTGACCGT TGTTTCAGTA ACCGCCGTCA TTGCACTGGG
51 GACAATATTC ATCAATAAGA AAACCTCAAA GCAAAAGGCG ACATTAGATG
101 TTATTTGAA TGATTACCAA GATGCACAAT TTGTAGAAGC CGACAATCAT
151 ATTTGCGCTT ATATTCGCGG CACGGCAGTT GACGACAACA ACGCGCGGAT
201 CGACCTGTAT GAAATTTATC AAAATAAGGG CGGACAATGG GAAAAAGAGA
251 GAGGGCATT ACTTACCGTA ATCAATCGGC ACGAGTTTGA TGCGTGCGCA
301 ATCAACTCGG GAGTATTGGA TGAGGATTGG TTTAAACGGC TGCATTGCAC
351 CAACCTCATA AAATTGTGGA ATGCAGTTTC GCCTCTTGT ATGAAAATAC
401 GCGAAGAAGA ACGCAAAGAC ACAATATTTA GAGAGTTGGA AATTTTGTT
451 GCATTATGGA AAGCAAACCC CCTAAAGGCA TCTGATTTGT GA

```

This corresponds to the amino acid sequence <SEQ ID 2550; ORF 745>:

m745.pep

```

1 MFWQLTVVSV TAVIALGTIF INKKTSKOKA TLDVILNDYQ DAQFVEADNH
51 ISPYIRGTAV DDNNARIDLY EIYQNKGGQW EKERGHLLTV INRHEFYACA
101 INSGVLDEDL FKRLHCTNFI KLWNAVSPV MKIREEERKD TIFRELEILV
151 ALWKANPLKA SDL*

```

a745.seq not found yet

a745.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2551>:

g746.seq

```

1 ATGTCCGAAA ACAAAACAAA CGAAGTCCTG ACCGGTTACG AACAGCTGAA
51 ACGGCGCAAC CGCCGCCGCC TCGTAACGGC AAGCTCCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCACTCAGTT CCGATCCTGC CGACAGCAAT
151 CCGCACCCG AGGCCGCGCA AACCAGCGCA ACGGAAAGCC AAACGGCAAA
201 CACGGCACAA ACCCCTGCCT TGAATCCGC CGCCGAAAC GGGGAAACCG
251 CGGCCGACAA ACCGCAAGGAC TTGGCAGGCG AAGACAAGCC TTCTGCCGCC
301 GACAGCGAAA TCAGCGAGCC TGAACCGTA GCGCGCCGC TGGTGCTGAT
351 TAACGACCGG CTCGAAGACA GCAACATCAA AGGTTTGAA GAATCCGAGA
401 AACTGCAACA GGCAGAAACC GCCAAACCG AACCGAAGCA GGCAAAACAA
451 CGCCTGCCG AAAAAGTGC GGCACATGCC GACAGTACGG ATACGGTAGC
501 GGTGAAAAA CCGAAACGCA CTGCCGAACC CAAACCGCAA AAAGCGGAAC
551 GCACTGCCGA AGCCAAGCCC AAAGCCAAAG AAACCAAAAC CGCCGAAAAA
601 GTTGCCGACA AACCGAAAC TGCTGCCGAA AAACCAAAAC CGGATACGGC
651 AAGATCCGAC AGCGCGGTAA AAGAAGCGAA AAAGCCGAC AAGGCTGAAG
701 GCAAAAAGAC AGCCGAAAAA GACCGTTCGG ACGGCAAAAA ACACGAAACG

```

g746.pap

1	MSENKQNEVL	TGYEQLKRRN	RRRLVTASSL	VAASCILLAA	ALSSDPADSN
51	PAPQAGETGA	TESQTANTAQ	TPALKSNAEN	GETAADKPOD	LAGEDKPSAA
101	DEISEPENG	GAPLVLINDR	LEDSSIAKLE	ESEKLOQAE	AKTEPKQAKQ
151	RAAEKVSATA	DS ² PTVAVEK	PKRTAEPKPQ	KAERTAAEAR	KAKETKTEAK
201	VADKPKTAAE	KTKEPTAKSD	SAVKEAKKD	KAEGKKTAEK	DRSDGKKHET
251	AQKTOKADKT	KTAEKEKSGK	GAKKAAIQAG	YAEKERALS	QRKMKAAAGID
301	STITEITMDN	GKYYRVKSSN	YKNARDAERD	LNLRLVHGIA	GOV ² NE*

m746.seq

1	ATGTCGGA	ACAAACAAA	CGAAGTCTG	AGCGGTACG	AACAACCTCA
51	ACGGCGCAAC	CGCGCGCGCC	TCGTAAACGGC	AAGTTGCCTG	GTTCGCCCT
101	CTTCGATCCT	GCTGGCAGC	CCCTTCAGTT	CCGGCCCTGC	CGAACAGACT
151	CGCGCGGAAA	CGACGGCGGT	AGAAAACA	CGCGCAGTG	CGGCAACAAC
201	CCCTGCCTTG	AAATCGCCG	CCGACAACAC	GCAGCACTTG	GCAGGCGAAG
251	ACAAGCCTTC	TGCCCGCCAG	AGCGAAATCA	CGAGACCTGA	AAACGTAGCG
301	CGCGCGCTGG	TGCTGATTAA	CGAGCGCCCTC	GAAGACAGCA	ACATCAAAAGG
351	TTTGGAGAGCA	TCCGAGACCT	TGCAACAGGC	AGAAACCGCC	AAAACCGCAC
401	CGAAGCAGGC	AGAAACAACG	CGTGCAGAA	AAGTGCCGGC	AACCTGCCAG
451	AGTAGCGATA	CGGTAGCGGT	TGAAAACAACG	AAACGCATCT	CCGAAACA
501	ACCGCAAAA	CGGGAACGCA	CTGCCAAAGC	CAAGCCCAAA	GCCAAAGAAA
551	CCAAACCCG	CGAAAAGATT	GCCGACAAAC	CGAAACCTGC	CGCCGAAAAA
601	ACCAACCCGG	ATACGCGAA	ATCCGACAGC	CGGTAAAGAG	AAGCGAAAAA
651	AGCCGACAAG	GCTGAAGCA	AAAAAACAGC	CGAAAAGAGC	CGTTTCGACG
701	GCAAAAACA	CGAAACGGCA	CAAAAACCG	ACAAAGCGGA	CAAGACCCAA
751	ACCGCGAGA	AGGAANAATC	CGGTAATAAA	CGCGCCATTC	AGGCAGGTTA
801	TGCCGAAAA	GAACCGCGCT	TAAGCTTCCA	GCCGCAAAATG	AAGCGCGCGG
851	GATATGATTC	GACCATCACC	GAATATTGCA	CCGACATCCG	CAAACTTTAC
901	CGCGTCAAT	CAAGCAACTA	TAAAAACGTA	AGGGATAGCG	ACAACGCTATT
951	GAACAATAATG	CGCGTACACG	GTATCGCCGG	TCAGGTAACG	AATGAATAG

m746.pap

1	1	MSENKQNEVL	SGYBQKLRNN	RRRLVTSACL	VAASCILLAA	ALSSGPAEQT
51	1	AGETSGVENK	AAGAAQOTPAL	KSAADVKPQDL	AGEDPKPSAD	SEISEPENVG
101	1	APLVLINERL	EAGNINKLEA	SEKLQQAETA	KATPQKQAR	AAEKVPATAD
151	1	STDTVAVEPK	KRTAEAKPK	AERTAKAKPK	AKETKKHTEV	ADPKPTAAEK
201	1	TKPTAKASD	AVKEAKRQK	AESKTKAEKD	RSDGKKHTEA	QKTDKADTKT
251	1	RAKEKKSCKK	AAIQAGYAEK	ERALSLOQKM	KAAGIDSTIT	EIMTNGNKNY
301	1	TVKSSNYKVA	RDAERDLNKL	RVHGIGAQVT	NE*	

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 746 shows 89.9% identity over a 346 aa overlap with a predicted ORF (ORF 746) from *N. gonorrhoeae*:

m746/g746 89.9% identity in 346 aa overlap

	10	20	30	40	50	
m746.pep	MSENKQNEVL	SGYEQLKRRNRRLVT	ASCLVAASCI	LAAALSSGPAEQ	T-----	AGETSG
g746	MSENKQNEVL	TGYEQLKRRNRRLVT	ASSLVAASCI	LAAALSSDPADSN	PAPOAGETGA	
	10	20	30	40	50	60
	60	70	80	90	100	109
m746.pep	VENKAAGAA	QTPALKSAA-----	DKPQDLAGEDKPSA	ADSEISEPENVGAP	LVLINER	
	: : : : : :	: : : :	: : : : : :	: : : : : :	: : : : : :	
g746	TESQTANTA	QTPALKSAAENGETA	ADKPQDLAGEDKPSA	ADSEISEPENVGAP	LVLINDR	
	70	80	90	100	110	120

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```

      110      120      130      140      150      160      169
m746.pep  LEDSNIKGLEASEKLQQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPQ
      |||  |||  |||  |||  |||  |||  |||
g746      LEDSNIKGLEASEKLQQAETAKTEPKQAKQRAAEKVSATADSTDTVAVEKPKRTAEPKPQ
      |||  |||  |||  |||  |||  |||  |||
      130      140      150      160      170      180

      170      180      190      200*      210      220      229
m746.pep  KAERTAKAKPKAKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEK
      |||  |||  |||  |||  |||  |||  |||
g746      KAERTAEAKPKAKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAEGKKTAEK
      |||  |||  |||  |||  |||  |||  |||
      190      200      210      220      230      240

      230      240      250      260      270      280
m746.pep  DRSDGKKKHETAQKTDKADKTKTAEKEKSGK---KAAIQAGYAEKERALSQRKMKAAAGID
      |||  |||  |||  |||  |||  |||
g746      DRSDGKKKHETAQKTDKADKTKTAEKEKSGKAGKAAIQAGYAEKERALSQRKMKAAAGID
      |||  |||  |||  |||  |||  |||
      250      260      270      280      290      300

      290      300      310      320      330
m746.pep  STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
      |||  |||  |||  |||  |||
g746      STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
      |||  |||  |||  |||  |||
      310      320      330      340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2555>:

```

a746.seq
1  ATGTCCGAAA ACAAAACAAA CGAAGTCCTG AGCGGTTACG AACAACTCAA
51  ACGGCGCAAC CGCCGCCGCC TCGTAACGGC AAGTTGCCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCCCTCAGTT CCGGCCCTGC CGAACAGACT
151 GCGGCGGAAA CAAGCGGCGT AGAAAACAAA GCGGCAGGTG CGGCACAAAC
201 CCCTGCCTTG AAATCCGCGG CCGACAAACC GCAGGACTTG GCAGGCGAAG
251 ACAAGCCTTC TGCCGCCGAC AGCGAAATCA GCGAGCCTGA AAACGTAGGC
301 GCGCCGCTGG TGCTGATTAA CGACCGCCTC GAAGACAGCA ACATCAAAGG
351 TTTGGAAGCA TCCGAGAAAC TGCAACAGGC AGAACCAGCC AAAACCGCAC
401 CGAAGCAGGC AAAACAACGC GCTGCCGAAA AAGTGCCGGC AACTGCCGAC
451 AGTACGGATA CGGTAGCGGT TGA AAAACCG AAACGCACTG CCGAAACAAA
501 ACCGCAAAAA GCGGAACGCA CTGCCAAAGC CAAGCCCAAA GCCAAAGAAA
551 CCAAAACCGC CGAAAAAGTT GCCGACAAAC CGAAAACTGC CGCCGAAAAA
601 ACCAAACCGG ATACGGCAAA ATCCGACAGC GCGGTAAAAG AAGCGAAAAA
651 AGCCGACAAG GCTGAAAGCA AAAA PACAGC CGAAAAAGAC CGTTCGGACG
701 GCAAAAAACA CGAAACGGCA CAAAAACCG ACAAGCGGA CAAGACCAAA
751 ACCGCGGAGA AGGAAAAATC CGGTAAAAA GCCGCCATTC AGGCAGGTTA
801 TGCCGAAAAA GAACGCGCCT TAAGCCTCCA GCGCAAAATG AAGCGGCGG
851 GTATCGATTG GACCATCACC GAAATTATGA CCGACAACGG CAAAGTTTAC
901 CGCGTCAAT CAAGCAACTA TAAAPACGCA AGGGATGCCG AACGCGATTT
951 GAACAAATTG CGCGTACACG GTATCGCCGG TCAGGTAACG AATGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2556; ORF 746.a>:

```

a746.pep
1  MSENKQNEVL SGYEQLKRRN RRRLVTASCL VAASCILLAA ALSSGPAEQT
51  AGETSGVENK AAGAAQTPAL KSAADKPQDL AGEDKPSAAD SEISEPENVG
101 APLVLINDRL EDSNIKGLEA SEKLQQAETA KTAPEKQAKR AAEKVPTAD
151 STDTVAVEKP KRTAETKPQK AERTAKAKPK AKETKTAEKV ADKPKTAAEK
201 TRPDTAKSDS AVKEAKKADK AESKRTAEKD RSDGKKHETA QKTDKADKTK
251 TAEKEKSGKK AAIQAGYAEK ERALSQRKM KAAGIDSTIT EIMTDNGKVV
301 RVKSSNYKNA RDAERDLNKL RVHGIAGQVT NE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 746 shows 99.7% identity over a 332 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a746/m746; 99.7% identity in 332 aa overlap

```

      10      20      30      40      50      60
a746.pep  MSENKQNEVLSGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
      |||  |||  |||  |||  |||  |||
m746      MSENKQNEVLSGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
      |||  |||  |||  |||  |||  |||
      10      20      30      40      50      60

```


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	70	80	90	100	110	120
a746.pep	AAGAAQTALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDRLEDSNIKGLEA					
m746	AAGAAQTALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINERLEDSNIKGLEA					
	70	80	90	100	110	120
	130	140	150	160	170	180
a746.pep	SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDVAVEKPKRTAETKPKQAERTAKAKPK					
m746	SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDVAVEKPKRTAETKPKQAERTAKAKPK					
	130	140	150	160	170	180
	190	200	210	220	230	240
a746.pep	AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA					
m746	AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA					
	190	200	210	220	230	240
	250	260	270	280	290	300
a746.pep	QKTDKADKTKTAEKEKSGKKAIIQAGYAEKERALSQRKMKAAAGIDSTITEIMTDNGKVY					
m746	QKTDKADKTKTAEKEKSGKKAIIQAGYAEKERALSQRKMKAAAGIDSTITEIMTDNGKVY					
	250	260	270	280	290	300
	310	320	330			
a746.pep	RVKSSNYKNARDAERDLNKLVRVHGIAGQVTNEX					
m746	RVKSSNYKNARDAERDLNKLVRVHGIAGQVTNEX					
	310	320	330			

g747.seq not found yet

g747.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2557>:

m747.seq

```

1   CTGACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGGGTG CTCCCGCGA TGTACGAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTACAAACC
201 CCGTGAGATT GTCTTGGACG GTGACAAAAC CAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAGCCGCAA CGTTCTATAG TCAATTAAAA
301 TCAAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2558; ORF 747>:

m747.pep

```

1   LTPWADAYAD LRGKTKVMTT QMGASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPIYR HKTIIKPREI VLDGDKTKMG RSKSNEYGFR VAATFYSQLK
101 SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2559>:

a747.seq

```

1   CTAACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGTGTG CTCCCGCGA TGTACGAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTGCAAACC
201 CCGTGAGATT GTTTTGGACG GCGACAAAAC CAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAACCGCAA CGTTCTATAG TCAATTAAAA
301 TCAAAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2560; ORF 747.a>:

a747.pep

```

1   LTPWADAYAD LRGKTKVMTT QMCASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPIYR HKTICKPREI VLDGDKTKMG RSKSNEYGFR VTATFYSQLK
101 SK*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N. meningitidis*

ORF 747 shows 97.1% identity over a 102 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a747/m747 97.1% identity in 102 aa overlap

```

a747.pep      10      20      30      40      50      60
               LTPWADAYADLRGKTKVMTTQMCASRDVSKSAGWSVGIGLNVGKQLTDSVGLFDPYYR
               |||||
m747          10      20      30      40      50      60
               LTPWADAYADLRGKTKVMTTQMGASRDVSKSAGWSVGIGLNVGKQLTDSVGLFDPYYR
               |||||

a747.pep      70      80      90     100
               HKTICKPREIVLDGDKTKMGRSKSNEYGFRVTATFYSQLKSKX
               |||||
m747          70      80      90     100
               HKTIYKPREIVLDGDKTKMGRSKSNEYGFRVAATFYSQLKSKX
               |||||

```

a747/m80195

gi|150271 (M80195) outer membrane protein [*Neisseria meningitidis*] Length = 272

Score = 59.3 bits (141), Expect = 6e-09

Identities = 29/99 (29%), Positives = 51/99 (51%), Gaps = 4/99 (4%)

Query: 1 LTPWADAYADLRGKTKVMTTQMCASRDVSKSAGWSVGIGLNVGKQLTDSVGLFDPYYR 60
 + PW++ DL + K+ T +D+++ GW G+G N+GK+L +S +E P+Y+
 Sbjct: 174 INPWSEVKFDLNSRYKLNTGVNLKKDINQKTNGWGFGLGANIGKKLGESASIEAGPFYK 233

Query: 61 HKTICKPREIVL---DGD-KTKMGRSKSNEYGFRVTATF 95
 +T + E + GD + ++ EYG RV F
 Sbjct: 234 QRTYKESGEFSVTTKSGDVSLTIPKTSIREYGLRVGIKF 272

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2561>:

```

g748.seq
1 ATGAGTCAAA ACCAACC CGC ACRACCGACC AAACGCAATC TGTTCAAAAC
51 CGCCCTTGCC GTCGCGCAA TCGGCGCAAT CGGAGGTAT TTGCGCGCCA
101 AAAAACAGGG CGAAACCGCC GAACGCACCG CGGAAAGCCA AACTCGCCC
151 CAAGCCTATC CCTGCTACGG CGAACATCAG GCAGGTATCG TTACGCGCGC
201 GCAGCGCGTT TCCATTATGT GCGCCTTGA CTAACCGCG CAAAGTGCCA
251 AGCAGCTGGA AAACCTGTTC CGCACACTGA CGGCCGCGAT CGAGTTTCTC
301 ACCCAAGCGG GAGAATACCA AGACGGCGAC GACAAACTCC CGTCAGCCGG
351 CAGCGGCATT TTGGGTAAG CCTTCAACC CGACGGATTG ACCGTTACCG
401 TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGACT CAAAGACAAA
451 AAAACGGTTC ATTTGCAGGA AATGCGCGAC TTCCCAACG ATAAGCTGCA
501 AAAAAGCTGG TCGGACGGCG ATTTGAGCCT GCAAACTGCG GCCTTCACCC
551 CCGAAACCTG CCAAACCGCC CTGCGCGACA TCATCAAACA CACCGCCCAA
601 ACCGCCGTCA TCCGCTGGAG TATCGACGGG TGGCAGCTA AATCCGAACC
651 CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTCCGAGAC GGCACGGGCA
701 ACCCAAGGT TCCGATCCC AAAACCGCG ACGAGGTTT ATGACGGGG
751 GTGGCCGCCA ACAGCCTCGA CGAACCGGAG TGGCGGAAA ACGGCAGCTA
801 TCAGGCAGTC CGCCTTATCC GCCGCTTGT CGAGTTTGG GACAGGACGC
851 CGCTTCAAGA GCAAACCGAC ATTTTCGGG GCGGAAAATA CAGCGGGGCG
901 CCGATGGACG GCAAAAAGA AGCCGACCAA CCGATTTCG CCAAAGACCC
951 CGAGGGTGAT ATCAGCCCA AAGACAGCCA TATGCGCCTG CGGAATCCGC
1001 GCGATCCCGA ATTCCTCAA AAACACTGCC TCTTCGCGC CGCCTACAGC
1051 TATTCTCGCG GACCGCCTC AAGCGGACAG CTTGATGTC GGCTGGTGTT
1101 CGTCTGTAT CAGGCAATC TTGCCGACG TTTATCTTC GTGCAAAACC
1151 TCCTCAACGG CGAACCGCTG GAAGAATACA TCAGCCCTT CGGCGGCGGC
1201 TATTCTTTCG TCTTGCCCG CGTGGGAAA GCGGATTCT TGGACAAGG
1251 GCTGCCGGGC GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2562; ORF 748.ng>:

```

g748.pep
1 MSQNQPAQPT KRNLFKTALA VGAIGAIGGY FGGKKQGETA ERTAESQHSF
51 QAYPCYGEHQ AGIVTPRQAF SIMCAFDVTA QSAKQLENLF RLTARIEFL
101 TQGEYQDGD DKLPSAGSGI LGKAFNPDGL TVTVGVGSSL FDRGFLKDK
151 KTVHLQEMRD FPNDKLQKSW CDGDLSLQIC AFTPETCQTA LRDIKHTAQ
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLWIG
251 VAANSLDEPE WAKNGSYQAV RLIRRFVEFW DRTPLOEQTD IFGRRYKSSA
301 PMSKKKEADQ PDFAKDPEGD ITPKDSHMRL ANPRDPEFLK KHCLFRAYS
351 YSRGPASSGQ LDVGLVFVCY QANLADGFIF VQNLNGEPL EYISPFGGG

```

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401 YFFVLPGVGK GGFLGQGLPG V*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2563>:

```
m748.seq
1  ATGAGCAAAA AACACCCGC ACAACCGACC AGGCGCACTC TTTTAAAC
51  CGCGATCGCA GCCGGAGCAG TCGGCGCAAT CGGAGGTTAT CTCGGCGGCA
101 AAAAAACAGGG CGAAACCGCC GAACGCACCG CGGAAAGCCA AACTCGCCC
151 CAAGCCTATC CCTGCTACGG CGAACATCAG GCAGGCATCG TTACGCCGCA
201 GCAGGCGTTT TCGATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
251 AGCAGCTGGA AAACCTGTTC CGCACGCTGA CGGCCCGCAT CGAGTTCTC
301 ACCCAAGCGG GCGAATACCA AGACGGCGAC GACAAACTTC CGCCAGCCGG
351 CAGCGGCATT TTGGGCAAAG CCTTCAACCC CGACGGGTG ACCGTTACCG
401 TGGGGTGGG CAGCAGCCTG TTGACGGCC GGTTCGGACT CAAAGACAAA
451 AAACCGATTC ATTTGAGGA AATGCGCGAC TTCTCCAACG ATAAGCTGCA
501 AAAAAAGCTG TCGGACGGCG ATTTGAGCCT GCAAATCTGT GCCTTACCC
551 CCGAAACCTG CCAAGCCGCC CTGCGCGACA TCATCAAACA CACCGTCCAA
601 ACCGCCGTTA TCCGTGGAG TATCGACGGG TGGCAGCCA AATCGGAACC
651 CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTACGGGAC GGCACGGGCA
701 ACCCCAAAGT TTCCGATCCC AAAACTGCCG ACGAGGTTT GTGGACGGG
751 TGGGCGCCA ACAGCCTCGA CGAACCGGAG TGGGCGAAAA ACGGCAGCTA
801 CAGGCGAGTC GGCCTTATCC GCCACTTTGT CGAGTTTGG GACAGGACGC
851 CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GCGCGAAATA CAGCGGTGCG
901 CGGATGGAGC GCAAAAAAGA AGCCGACCAA CCGGATTTTG CCAAAGACCC
951 CGAGGTGAT ATCAGGCCCA AAGACAGCCA TATACGCCTG GCGAATCCGC
1001 GCGATCCCGA ATTCTCTAAA AAACACCGCC TCTTCCGCGC CGCCTACAGC
1051 TATTCGCGCG GACTCGCCTC AAGCGGACAG CTTGATGTCG GGCTGGTGT
1101 CGTCTGCTAT CAGGCAAACC TTCCGACGG ATTCACTTC GTGCAAAACC
1151 TCCTCAACGG CGAACCCTG GAAGAATACA TCAGCCCTT CGGCGGCGGC
1201 TATTTCTTGG TCTTGCCCG CGTGAAAAA GCGGCTTTT TGGGCAAGG
1251 GCTGCTGGGC GTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2564; ORF 748>:

```
m748.pep
1  MSKKQPAQPT RRTLFKTAIA AGAVGAIGGY LGGKKQGETA ERTAESQHSP
51  QAYPCYGEHQ AGIVTPQQAQ SIMCAFDVTA QSAKQLENLF RLTARIEFL
101 TQGGEYQDGD DKLPPAGSGI LGKAFNPDGL TTVGVGSSL FDGRFGLRDK
151 KPIHLQEMRD FSNDKLQKSW CDGDLSQLIC AFTPETCQAA LRDIKHTVQ
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLTWG
251 VAANSLDEPE WAKNGSYQAV RLIRHFVEFW DRTPLOEQTD IFGRRKYSGA
301 PMDGKKEADQ PDFAKDPEGD ITPKDSHRL ANPRDPEFLK KHRLFRRAYS
351 YSRGLASSGQ LDVGLVFVCY QANLADGFIF VQNLNGEPL EEYISPFGGG
401 YFFVLPGVEK GGFLGQGLLG V*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 748 shows 95.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. gonorrhoeae*

```
m748/g748 95.0% identity in 421 aa overlap

m748.pep      10      20      30      40      50      60
MSKKQPAQPTRRTLFKTAIAAGAVGAIGGYLGGKKQGETAERTAESQHSPOAYPCYGEHQ
g748          10      20      30      40      50      60
MSQNQPAQPTKRNLFKTALAVGAIGAIGGYFGGKKQGETAERTAESQHSPOAYPCYGEHQ

m748.pep      70      80      90     100     110     120
AGIVTPQQAQSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGGEYQDGD DKLPPAGSGI
g748          70      80      90     100     110     120
AGIVTPRQAQSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGGEYQDGD DKLPSAGSGI

m748.pep     130     140     150     160     170     180
LGKAFNPDGLTVTVGVGSSLFDGRFGLKDKKPIHLQEMRDFSNKLOKSWCDGDLSQLIC
g748         130     140     150     160     170     180
LGKAFNPDGLTVTVGVGSSLFDGRFGLKDKKTVHLQEMRDFPNKLOKSWCDGDLSQLIC

m748.pep     190     200     210     220     230     240
AFTPETCQAALRDIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP
```

	190	200	210	220	230	240
g748	AFTPETCQTALRDIHKHTAQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					
m748.pep	250	260	270	280	290	300
g748	KTADAEVLWTGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLEQETDIFGRKRKYSGA					
	250	260	270	280	290	300
m748.pep	310	320	330	340	350	360
g748	PMDGKKKEADQPDFAKDPESGDITPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ					
	310	320	330	340	350	360
m748.pep	370	380	390	400	410	420
g748	LDVGLVFVFCYQANLADGFI FVQNLLNGEPL E EYISPFGGGYFFVLPGVKGGFLGQGLLG					
	370	380	390	400	410	420
m748.pep	VX					
g748	VX					

```

a748.seq
1      ATGAGCAAAA  ACCAACCCGC  ACAACCGACT  AGGCGCACTC  TTTTAAAAAC
51     CGCGATCGCA  GCTGGAGCAG  TCGGCGCAAT  CGGAGGCTTAT  CTCGGCGGCA
101    AAAAACGGGG  CGAARACGCC  GAACGCACCG  CCGAAAGCCA  ACACCTCGCC
151    CAAGCCTATC  CTGCTACGG  CGAACATCGA  CGAGCAGTCCG  TTACGCCGCA
201    GCAGGCGTAT  TCGATTATGT  GCGCCTTCGA  CGTAACCGCG  CAAAGTGCCA
251    AGCAGCTGGA  AAACCTGTTC  CGCACGCTGA  CCGCCCGCAT  CGAGTTTCTC
301    ACCCAAGCGC  GCGCAATACA  AGACGGCGAC  GACAACATTC  CGCCAGCCGG
351    CAGCGGCAT  TTGGGCAAG  CCTTCAACCC  CGACGGGTTG  ACCGTTACCG
401    TGGGGGTGGG  CAGCAGCCTG  TTTGACGGCC  GGTTCGGACT  CAAAGACAAA
451    AAACCGATT  ATTTGCAGAA  AATTGCGGAC  TTCTCCAACG  ATAAGCTGCA
501    AAAAACGCTG  TCGCAGCGGC  ATTTGAGCCT  GCAAACTCTG  GCCTTACCC
551    CCGAAACCTG  CCAAGCCGCG  CTGGCGGACA  TCATCAAACA  CACCGTCCAA
601    ACCCGCGTTA  TCGCGTGGAG  TATCGACGGG  TGGCAGCCTA  AATCCGACAA
651    CGGCGCGAT  CGGCGCGCA  ACCTGTGTGG  CTTCGCCGCA  GGCACGGGCA
701    ACCCCAAGT  TTCCGACCCC  AAAACTGCCG  ACGAGGTTTT  GTGGACGGGG
751    GTGGCGGCCA  ACAGCCTCGA  CGAACCCGAG  TGGGCGAAAA  ACGGCAGCTA
801    TCAGGCAGTC  CGCCTATCT  GCGCACTTGT  TGAGTTTGG  GACAGGACGC
851    CGCTTCAAGA  GCAAAACGAC  ATTTTCGGGC  GGCCAAATA  CAGCGGCGCG
901    CCGATGGACG  GCAAAAAGA  AGCGGACCA  CCGGATTTTG  CCAAGAGCCC
951    CGAGGGGAAT  ACCACGCCCA  AAGCAGCCA  TATACGCTCA  GCGAATCCGC
1001   GCGATCCCGA  GTTCCTTAA  AAACACCGCC  TCTTCGCGCG  CGCCTACAGC
1051   TATTTCGCGC  GACTCGCCT  AAGCGGACAG  CTTGATGTCG  GGCTGTCTGT
1101   CGCTCTGCTA  CAGGCAAAAC  TTGCGCAGCG  ATTCACTTCC  GTGCAAAACT
1151   TCCTCAACGC  CGAAGCCCTG  GAAGAATACA  TCAGCCCCCT  CGGCGGCGGC
1201   TATTTTCTCG  TCTTGCCTCG  CGTGGA AAAA  GGC GGCTTTT  TGGGGCAAGG
1251   GCTGCTCGCC  GTATAA

```

```
a748..pep
1  MSKNQPAQPT  RRTLFKTAIA  AGAVGAIGGY  LGGKKRGETA  ERTAESQHP
51  QAYPCYGEHQ  AGIVTPQAAF  SIMCAFDVTA  QSAQLENLF  RLTARIEFL
101  TQGGEYQDGD  DKLPPAGSGI  LGKAFNDPGL  TVTVGVGSSL  FDGFRGLDK
151  KPIHLQEMRD  FSNDKLQKSW  CDGDLSLQIC  AFTPETCQAA  LRDIHKHTV
201  TAVIRWSIDG  WQKPSSEGM  AARNLSLQFD  DTGNPKVSD  KTADEVLTG
251  VAANSIDEPE  WAKNGSYQAV  RLRIHFVEFW  DRTPLEQETD  IFGRRKYSGA
301  PMDGKKEADQ  PDFAKDPEGN  TTPKDSHIRL  ANPRDPEFLK  KHRLFRFRAYS
351  YSRGLASSGQ  LDVGLVFVCY  QANLADGFIF  VQNLNLGEPL  EEYISPFGGG
401  YFFVLPGVEK  GGFLGGGLLG  V*
```

Computer analysis of this amino acid sequence gave the following results:

1220

Homology with a predicted ORF from *N. meningitidis*

ORF 748 shows 99.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. meningitidis*:

a748/m748 99.0% identity in 421 aa overlap

	10	20	30	40	50	60
a748.pep	MSKNQPAQPTRRTLFKTAIAAGAVGAIGGYLGGKKRGETAERTAESQHSPPQAYPCYGEHQ					
m748	MSKKQPAQPTRRTLFKTAIAAGAVGAIGGYLGGKKQGETAERTAESQHSPPQAYPCYGEHQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
a748.pep	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGGGEYQDGGDKLPPAGSGI					
m748	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGGGEYQDGGDKLPPAGSGI					
	70	80	90	100	110	120
	130	140	150	160	170	180
a748.pep	LGKAFNPDGLTVTVGVGSSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLQLQIC					
m748	LGKAFNPDGLTVTVGVGSSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLQLQIC					
	130	140	150	160	170	180
	190	200	210	220	230	240
a748.pep	AFTPETCQAALRDI IKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					
m748	AFTPETCQAALRDI IKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					
	190	200	210	220	230	240
	250	260	270	280	290	300
a748.pep	KTADEVLTWVGVAANSLDEPEWAKNGSYQAVRLIRHVEFWDRTPLEQETDIFGRRKYSGA					
m748	KTADEVLTWVGVAANSLDEPEWAKNGSYQAVRLIRHVEFWDRTPLEQETDIFGRRKYSGA					
	250	260	270	280	290	300
	310	320	330	340	350	360
a748.pep	PMDGKKEADQPDFAKDPEGNTTPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ					
m748	PMDGKKEADQPDFAKDPEGNTTPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ					
	310	320	330	340	350	360
	370	380	390	400	410	420
a748.pep	LDVGLVFVCYQANLADGFI FVQNLLNGEPL E EYISPFGGGYFFVLP GVEKGGFLGQGLLG					
m748	LDVGLVFVCYQANLADGFI FVQNLLNGEPL E EYISPFGGGYFFVLP GVEKGGFLGQGLLG					
	370	380	390	400	410	420
a748.pep	VX					
m748	VX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2567>:

g749.seq

```

1  ATGAGAAAT  TCAATTGAC  CGCATTGTC  GTGATGCTG  CCTTGGGTTT
51  GACCGCGTGC  CAGCCGCCGG  AGCGGAGAA  AGCCGCGCCG  GCCGCGTCCG
101  GTGAGACCCA  ATCCGCCAAC  GAAGGCGGTT  CGGTCCGTAT  CGCCGTCAAC
151  GACAATGCCT  GCGAACCGAT  GAATCTGACC  GTGCCGAGCG  GACAGGTGTG
201  GTTCAATATT  AAAAACRAACA  GCGGCCGCAA  GCTCGAATGG  GAAATCCTGA
251  AGGGCGTGAT  GGTGGTGGAC  GAACGCGAAA  ATATCGCCCC  GGGGCTTTTC
301  GACAAAATGA  CCGTAAacct  GCTGCCGGGC  GAATACGAAA  TGACCTGCGG
351  CCTTTTGACC  AATCCGCGCG  GCAAGCTGGT  GGTAGCCGAC  AGCGGCTTTA
401  AAGACACCGC  CAACGAAGCG  GATTTGGAAA  AACTGCCCCA  ACCGCTCGCC
451  GACTATAAAG  CCTACCTTCA  AGCGGAGGTT  AAAGAGCTGG  CGGCGAAAAC
501  CAAAACCTTT  ACCGAAGCCG  TCAAAGCAGG  CGACATTGAA  AAGGCGAAT
551  CCCTGTTTGC  CGCCACCCGC  GTCCATTACG  AACGCATCGA  ACCGATTGCC
601  GAGCTTTTCA  GCGAACTCGA  CCCCCTCATC  GATGCGTGTG  AAGACGACTT
651  CAAAGACGGT  GCGAAAGATG  CCGGGTTTAC  CGGCTTCCAC  CGTATCGAAC
701  ACGCCCTTGT  GGTGGAAAAA  GACGTATCCG  GCGTGAAGGA  AACC GCGGCC
751  AAAC TGATGA  CCGATGTCGA  AGCCCTGCAA  AAAGAAATCG  ACGCATTGGC

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1221

```

801 GttccctCCG GGCAAAGTGG TCGCGGCGCG GTCCGAAGT ATTGAAGAAG
851 CGCGGGGCGAG TAAATCAGC GCGGAAGAAG ACCgttaCAG CCACACCGAT
901 TTGAGCGACT TCCAAGCTAA TCGGACGGA TCTAAAAAA TCCTCGATT
951 GTTCCGTCCG TTGATTGAGG CAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATC TGGCGAAATA CCGCACCAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGAGC GAAGCCGACC GCAAAGCATT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2568; ORF 749.ng>:

```

g749.pep
1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIQAVN
51 DNACEPMNLT VPSGQVVFNI KNNSGRKLEW EILKGVVVVD ERENIAPLS
101 DKMTVTLPLG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLPQPLA
151 DYKAYVQGEV KELAAKTKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
201 ELFSELDPMV DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEAAGSKIS GEEDRYSHTD
301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRILGLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2569>:

```

m749.seq
1 ATGAGAAAT TCAATTGAC CGCATTGTC GTGATGCTT CTTAGETTT
51 GACCGCGTGC CAGCCGCCG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCACTAT CGCCGTCAAC
151 GACAAATGCTT GCGAACCGAT GGAATGACC GTGCCGAGCG GACAGGTGT
201 GTTCAATATT AAAACAACA GCGCCGCGAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGTAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCCT GTGCCGCGG GAATACGAAA TGAATGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAAACGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTTGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTACGTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAC
501 CAAAACCTTT ACCGAAGCGG TCAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTTCAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAAGTATGTA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAACGT ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GCGGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAA TCCTCGATT
951 GTTCCGTCCG CTGATCGAGG CAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2570; ORF 749>:

```

m749.pep
1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIQAVN
51 DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGVVVVD ERENIAPLS
101 DKMTVTLPLG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPMV DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRILGLK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 749 shows 96.1% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. gonorrhoeae*

m749/g749 96.1% identity in 388 aa overlap

```

          10      20      30      40      50      60
m749.pep MRKFNLALSVMALGLTACQPPEAEKAAPASGEAQTANEGGSVSIQAVNDNACEPMELT
          |||
g749      MRKFNLALSVMALGLTACQPPEAEKAAPASGETQSANEGGSVGIQAVNDNACEPMNLT
          10      20      30      40      50      60

```

1222

	70	80	90	100	110	120
m749.pep	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYENTCGLLT					
g749	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYENTCGLLT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m749.pep	NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
g749	NPRGKLVVADSGFKDTANEADLEKLQPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m749.pep	KAKSLFADTRVHYERIEPIAELEFSELDPVIDAREDDFKDGAAGTGFHRIEYALWVEK					
g749	KAKSLFAATRIVHYERIEPIAELEFSELDPVIDACEDDFKDGAAGTGFHRIEHALWVEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
g749	DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEAAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
	310	320	330	340	350	360
m749.pep	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG					
g749	LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTDNFKOVNEILAKYRTKDGFTYDKLS					
	310	320	330	340	350	360
	370	380	389			
m749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
g749	EADRKALQAPINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2571>:

a749.seq

```

1  ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51  GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCAGTAT CGCCGTCAAC
151 GACAATGCCT CGCAACCGAT SGAAGTACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA SCGCCGCCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
351 TCTTTTGACC AATCCGCGCG CAAAGCTGGT GGTAAACGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTATGTTC AAGCGAAGTC AAAGAGCTGG TGGCGAAAC
501 CAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC GCACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTCCAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAAGTATGTA CCGATGTGTA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCCTCCG GCGAAGGTGG TCGGCGGGCG GTCCGAAGTG ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GCGGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCGAAAAAAA TCGTCGATTT
951 GTTCCGTCGG TTGATCGAGA CCAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTGT AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2572; ORF 749.a>:

a749.pep

```

1  MRKENLTALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIQVN
51  DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGMVVVD ERENIAPLGS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEAD LEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGAASEL IEEVAGSKIS GEEDRYSHTD

```

1223

301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYOKLG EADRKALQAS INALAEDLAQ LRGILGLK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 749 shows 99.7% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. meningitidis*:

a749/m749 99.7% identity in 388 aa overlap

a749.pep	10	20	30	40	50	60
	MRKFNLTALSVM	LALGLTACQP	PEAEKAAPAS	GGEAQTANEG	GSVSI	AVNDNACEPMELT
m749	MRKFNLTALSVM	LALGLTACQP	PEAEKAAPAS	GGEAQTANEG	GSVSI	AVNDNACEPMELT
a749.pep	70	80	90	100	110	120
	VPSGQVFN	IKNNSGRKLE	WEILKGMV	VDERENIAP	GLSDKMTVT	ILLPGEYEMTCGLLT
m749	VPSGQVFN	IKNNSGRKLE	WEILKGMV	VDERENIAP	GLSDKMTVT	ILLPGEYEMTCGLLT
a749.pep	130	140	150	160	170	180
	NPRGKLVV	TDGSGFKDT	ANEADLEKLS	QPLADYKAY	VQGEVKEL	VAKTKTFTEAVKAGDIE
m749	NPRGKLVV	TDGSGFKDT	ANEADLEKLS	QPLADYKAY	VQGEVKEL	VAKTKTFTEAVKAGDIE
a749.pep	190	200	210	220	230	240
	KAKSLFAD	TRVHYERIE	PIAELFSE	LDPVIDARE	DDFKDGAK	DAGFTGFHRIEYALWVEK
m749	KAKSLFAD	TRVHYERIE	PIAELFSE	LDPVIDARE	DDFKDGAK	DAGFTGFHRIEYALWVEK
a749.pep	250	260	270	280	290	300
	DVSGVKEI	AAKLMTD	VEALQKEI	DALAFPPG	KVVGASEL	IEEVAGSKISGEEDRYSHTD
m749	DVSGVKEI	AAKLMTD	VEALQKEI	DALAFPPG	KVVGASEL	IEEVAGSKISGEEDRYSHTD
a749.pep	310	320	330	340	350	360
	LSDFQANVDG	SKKIVDLFR	PLIETKNK	ALLEKTD	TNFKQVNEI	LAKYRTKDG
m749	LSDFQANVDG	SKKIVDLFR	PLIETKNK	ALLEKTD	TNFKQVNEI	LAKYRTKDG
a749.pep	370	380	389			
	EADRKALQAS	INALAEDLA	QLRGILGLKX			
m749	EADRKALQAS	INALAEDLA	QLRGILGLKX			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2573>:

g750.seq

```

1  GTGAAACCGC GTTTTATTG GGCAGcctGC GCCGTCTGC CGGCCGCCCTG
51  TTCGCCCGAA CCTGCCCGCG AAAAACTGT ATcgcCCGCA TCCCAAGCCG
101 CATCCACACC TGTCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC
151 GTTGTGCCGA AGAATCCCGA ACgcgtcgcc gtgtAcgaCt ggGCCGCCGTt
201 ggaTACGCTG ACCGAGCCGG GCGTGAATGT GGGCGCAACC ACCGCGCCGG
251 TGCGCGTGGA CTATTGCGAG CCTGCATTG ACAAGCGCGC AACGGTGGGG
301 ACGCTGTTTG AGCCCGATTG CGAATCCCTG CACCGCCACA ATCCGCAGTT
351 TGTCATTACC GCGCGGCCCG GTGCGGAAGC GTATGAACAG TTGGCGAAAA
401 ACGCGACCAC CATAGATTG ACGGTGGACA ACGGCAATAT CCGCACCAGC
451 GGCGAGAAGC AGATGGAGAC CCTGTCGCGG ATTTTCGGTA AGGAAGCGCG
501 CGTGGCGGAA TTGAATGCGC AGATTGACGC GCTGTTCCGC CAAAAGCGCG
551 AAGCCGCCAA AGGCAAAGGA CGCGGCTGG TGCTGTCGGT TACAGGCAAC
601 AAGGTGTCCG CCTTCGGCAC GCAATCGCGG TTGGCAAGTT GGATACACGG
651 CGACATCGGC CTGCCGCCCG TGGACGAATC TTACGCAAC GAAGGGCACG
701 GGCAGCCCGT TTCCTTCGAA TACATCAAAG AGAAAAACCC CGGCTGGATT
751 TTCATCATCG ACCGCACCGC CGCCATCGGG CAGGAAGGGC CGGCTGCCCT
```


g750.pap

1	VKPRFVYWAA	AVLPAACSP	PAEKTVTSAA	SQAASATPVAT	LVPTARGDA
51	VPKNPEPRAV	YVDWAAIDL	TAPKCVNGAT	TAPVRVDYLQ	LTADKAATVS
101	TEFQPDCESL	HRHNPFQVIT	GGPGAEEYEQ	LAKNATTIDL	TVDNGNIKTS
151	GKQAMETLSR	IFSGKEARVA	LNAQIDALFA	KGRKAAAGRG	RGLVLSVTNG
201	KVSAMFTQSR	LASWINGDIG	LPNVDSELSR	EGHPQPSYFE	YIEKKNPGWI
251	FIIDRTAAIG	QEGPAAEVL	DNALVCGTNA	WKRKQIIVMP	AAIYIVAGGA
301	RQILQAEEQL	KAFAEKAEPV	AAQ*		

m750.seq

1	GTGAAACCGC	GTTTTATTATG	GGCAGCCTGC	GCCGTCTCTGC	TGACCGCCTG
51	TTFCGCCCGAA	CCTGCCGCCCG	AAAAAAGCTGT	ATCCGCGCGCA	TCCGCATCTG
101	CGCCGACGCT	ACCGCTGCCG	ACCGCGCGGG	CGCATGCCGT	TGTGCGGAAG
151	AATCCCGAAC	GCCTGCGCGT	GTACAGACTGG	CGCGCGTGG	ATACGCTGAC
201	CGAATTGGGC	GTGAATTGTGG	CGCGCAACCGC	CGCGCCGGTG	CGCGTGGATT
251	ATTTGACAGC	TGCATTGTGAC	AAGGCGCCAA	CCGTGGGGGAC	GCTGTTCCGAG
301	CCCGATTACG	AAGCCCTGCA	CCGCTACAAT	CTCTAGCTTG	TCAATTACCGG
351	CGGGCGGGG	CGGGAAGCTAT	ATGAACAGTT	AGCGAAAAAC	CGGACCACCA
401	TAGATCTGAC	TGTGGACAAC	GGCAATAATC	GCACCGCGCG	CGAAAAGCAG
451	ATGGAGACCT	GGTGGCGGAT	TTTCGCGAAG	GAAGCGCGGG	CGCGCGAATT
501	GAAAGCGCAG	ATTGACGCGC	TGTTCCGCCA	AACGCGCGAA	CGCGCCAAAG
551	GCAAAAGGAG	CGGGCTGGT	CTGTCGGTGA	CGGGCAACAA	GGTGTCCGCC
601	TTCGGACCGC	AGTCGCGGTT	CGCAAGTTTG	ATACACGGCG	ACATCGGCCCT
651	ACCGCCTGTA	GACGAATCTT	TACGCAACGA	GGGGCAGCGG	CAGCCTGTTT
701	CCTTCCGAATA	CATCAAAAGG	AAAAAGCCCG	ATTGGAATTT	CATCATCGAC
751	CGTACCGCGC	CCATCGGGCA	GGAAGGGCCG	CGGGCTGTCT	AAGATTATGGA
801	TAAACGCCGTG	GTACGCGCCA	CGAACGCTTG	GACGCGCAAG	CAATCATCTG
851	TCATGCTCGC	CGGGAAGCTAC	ATTGTCCCGG	CGCGCGCGCG	GCAGTTGATT
901	CAGCGCGGCG	AGCAGTTGAA	GGCGGCGCTT	AAAAAGGCAG	AACCCGTTGC
951	GGCGGGGAAA	AAGTAG			

m750.psp

1	VKPRFYWAAC	AVLLTACSPV	PAAEKTVSAA	SASAATLTVP	TARGDAVVPK
51	NPERVAHYCW	AALDTLTTEL	VNVGATTAPV	RDVYLQPAFV	KAATVTGTFQ
101	PDYEAALHYN	PQLVITGGPV	AEAYEQLAQN	ATTIDLTVDN	GNIRTSGEKE
151	METLARIFPK	EARAAELKAK	IDALFAQTRF	AAKKGKGRVL	LSVTNGKGLV
201	FTQZSRLASL	IHGDIPLPPV	DESLRNEHGK	QPVSFYFKEI	KNPWFIFIID
251	RTAATGQGGP	AAVEVLNDAL	VRGTNWKRRK	KIIVMPAANY	IVAGGAQLII
301	QAAGQLKAAK	KKAEFVAAGK	K*		

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 750 shows 93.8% identity over a 322 aa overlap with a predicted ORF (ORF 750) from *N. gonorrhoeae*

m750/g750 93.8% identity in 322 aa overlap

	10	20	30	40	50
m750.pep	VKPRFYWAACAVLLTACSP	EPAAEKTVSAASASA----	ATLTVPTARGDAVVPKN	PERVA	
		:			
g750	VKPRFYWAACAVLPAACS	EPAAEKTVSAASQAASTP	VATLTVPTARGDAVVPKN	PERVA	
		:			
	10	20	30	40	50
	60	70	80	90	100
m750.pep	VYDWAALDTLTELGVNG	ATTAPVRVDYLQPAFDK	AATVGLTFEPDYEA	LHRYNPQLVIT	
g750	VYDWAALDTLTEPGVNG	ATTAPVRVDYLQPAFDK	AATVGLTFEPDCES	LHRYNPQFVIT	
	70	80	90	100	110
	120	130	140	150	160
m750.pep	GGPGAERYEQLAKNATT	IDLTVDNGNIRTSGE	KMETLARIFGKEARA	AEKAQIDALFA	

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g750      GGPGEAEYEQIAKNATTIDLTVDNGNIRTSGEKOMETLSRIFGKEARVAELNAQIDALFA
          130      140      150      160      170      180

          180      190      200      210      220      230
m750.pep  QTREAAKKGKGRGLVLSVTGNKVSFQTSRLASWIHGDIGLPPVDESIRNEGHGQPVSF
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g750      QKREAAKKGKGRGLVLSVTGNKVSFQTSRLASWIHGDIGLPPVDESIRNEGHGQPVSF
          190      200      210      220      230      240

          240      250      260      270      280      290
m750.pep  YIKEKNPDWIFIIDRTAAIGQEGPAAVEVLNVLVRCGTNNAWKRRKQIIVMPAANYIVAGGA
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g750      YIKEKNPDWIFIIDRTAAIGQEGPAAVEVLNVLVRCGTNNAWKRRKQIIVMPAANYIVAGGA
          250      260      270      280      290      300

          300      310      320
m750.pep  RQLIQAAEQKAAFKKAEFVAAGKX
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g750      RQLIQAAEQKAAFEKAEFVAQX
          310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2577>:

```

a750.seq
1  GTGAAACCGC  GTTTTATTG  GGCAGCCTGC  GCCGTCCTGC  TGACCGCCTG
51  TTCGCCCGAA  CCGTCCGCGG  AAAAACTGT  ATCCGCGCGA  TCCGCATCTG
101 CCGCCACACT  GACCGTGCCG  ACCGCGCGG  GCGATGCCGT  TGTGCCGAAG
151 AATCCCGAAC  GCGTCGCCGT  GTACGACTGG  GCGGCGTTGG  ATACGCTGAC
201 CGAATTGGGT  GTGAATGTGG  GCGCAACCAC  CGCGCCGGTG  CGCGTGGATT
251 ATTTGCAGCC  TGCATTGAC  AAGCGCGCAA  CGGTGGGGAC  GCTGTTCCGG
301 CCCGATTACG  AAGCCCTGCA  CCGCTACAAT  CCTCAGCTTG  TCATTACCGG
351 CGGSCCGGGC  GCGGAAGCGT  ATGAACAGTT  GCGGAAAAAC  GCGACCACCA
401 TAGATCTGAC  GGTGGACAAC  GGCAATATCC  GCACCAGCGG  CGAAAAGCAG
451 ATGSAGACCT  TGGCGCGGAT  TTTCGGCAAG  GAAGCGCGCG  CGGCGGAATT
501 GAAGGCGCAG  ATTGACGCGC  TGTTCGCCCA  AACGCGCGAA  CGCGCCAAAG
551 GCAAAGGACG  CGGGCTGGTG  CTGTCGGTTA  CGGGCAACAA  GGTGTCCGCC
601 TTCGGCACGC  AGTCGCGGTT  GGCAAGTTGG  ATACACGGCG  ACATCGGCTT
651 ACCGCTGTGA  GACGAATCTT  TACGCAACGA  GGGGCACGGG  CAGCCTGTTT
701 CCTTCGAATA  CATCAAAGAG  AAAAAACCCG  ATTGGATTTT  CATCATCGAC
751 CTATCCGCGC  CCATCGGGCA  GGAAGGGCCG  GCGGCTGTCG  AAGTATTGGA
801 TAACGCGCTG  GTACGCGGCA  CGAACGCTTG  GAAGCGCAAG  CAAATCATCG
851 TCATGCTGTC  CGCGAAGTAC  ATTGTCGCGG  GCGGCTCGCG  GCAGTTGATT
901 CAGGCGGCGG  AGCAGTTGAA  GGAGGCGTTT  GAAAAGGCAG  AACCCTGTCG
951 GCGGGGAAA  GAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2578; ORF 750.a>:

```

a750.pep
1  VKPRFYWAAC  AVLLTACSPE  PAAEKTVSAA  SASAATLTVP  TARGDAVVPK
51  NPERVAVYDW  AALDTLTELG  VNVGATTAPV  RVDYLQPAFD  KAATVGTLEF
101 PDYEALHRYN  PQLVITGGPG  AEAYEQLAKN  ATTIDLTVDN  GNIRTSGEKQ
151 METLARIFGK  EARAELKAQ  IDALFAQTRE  AAKGKGRGLV  LSVTGNKVSF
201 FGTQSRLASW  IHGDIGLPPV  DESLRNEGHG  QPVSFYEIKE  KNPDWIFIID
251 RTAAIGQEGP  AAVEVLNVL  VRGTNAWKRR  QIIVMPAANY  IVAGGSRLI
301 QAAEQLEKAF  EKAEPVAAGK  E*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 750 shows 98.8% identity over a 321 aa overlap with a predicted ORF (ORF 750) from *N. meningitidis*:

```

a750/m750  98.8% identity in 321 aa overlap

          10      20      30      40      50      60
a750.pep  VKPRFYWAACAVLLTACSPEPAAEKTVSAAASAATLTVPARGDAVVPKNPERVAVYDW
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m750      VKPRFYWAACAVLLTACSPEPAAEKTVSAAASAATLTVPARGDAVVPKNPERVAVYDW
          10      20      30      40      50      60

          70      80      90      100     110     120
a750.pep  AALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLEFDPYEALHRYNPQLVITGGPG
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m750      AALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLEFDPYEALHRYNPQLVITGGPG

```

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	70	80	90	100	110	120
	130	140	150	160	170	180
a750.pep	AEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARIFGKEARAAELKAQIDALFAQTRE					
m750	AEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARIFGKEARAAELKAQIDALFAQTRE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a750.pep	AAKGKGRGLVLSVTGNKVSFAFGTOSRLASWIHGDIGLPPVDESLRNEGHGQPVSFYEYIKE					
m750	AAKGKGRGLVLSVTGNKVSFAFGTOSRLASWIHGDIGLPPVDESLRNEGHGQPVSFYEYIKE					
	190	200	210	220	230	240
	250	260	270	280	290	300
a750.pep	KNPDWIFIIDRTAAIGQEGPAAVEVDNALVRGTNAWKRKQIIVMPAANYIVAGGSRQLI					
m750	KNPDWIFIIDRTAAIGQEGPAAVEVDNALVRGTNAWKRKQIIVMPAANYIVAGGARQLI					
	250	260	270	280	290	300
	310	320				
a750.pep	QAAEQLKEAFEKAEPVAAGKEX					
m750	QAAEQLKAFFKAEPVAAGKKX					
	310	320				

g751.seq not found yet

g751.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2579>:

m751.seq..

```

1  ATGGGCTTGGG  GTATGTTTGC  CACAACCCAA  GCCGATAGAG  CGGTAAGGTC
51  TGCAACTGCA  CCTAAAGAAA  TGTGGTTCCA  TAAGAAGATA  ATAGATGAAA
101 AAACAGGTAA  AGTATCCTTT  GATACCAGAC  AAATTGAGTC  ATTGAATGAT
151 TTAAGCAAGG  AAGAACTGGC  AAGCATTCAA  GACACAAATG  GCAAAGTTAT
201 TACTGTGTCT  AATCCTGGTA  TTTTCAATAA  TCGAGAAGAT  TCATTAAGCA
251 ACGCAGCAAA  ACAAATCGT  AATAGTACAA  ACGGTAGTGG  TGTATTGCA
301 GTCATGAATC  CTCCAACAGG  GAAATATAAA  TCTGATTCTA  ATAACAAAAT
351 AAAAGATTTT  TTATGGCTCG  GTTCAAGTCT  TGTCTCTGAA  CTGATGTATG
401 TCGGTTACGA  CCAATTAAAT  AATAAAGTGT  TCCAAGGCTA  TTTACCCAAA
451 ACCAATTCAG  AAAAAGTCAA  TCAAGATATT  TATCGAGAGG  TTCAAAAAAT
501 GGGTAACGGC  TGGTCGGTTG  ATACCAAGTA  TCACAGTCGT  GGGGGAATTA
551 CAGCAAGCGT  TTCCTTAAAA  GATTGGGTAA  ACAATCAAAA  ACAAATGGC
601 ATTGCCCCAA  TCAGAAAAGC  ACGTTTCTAT  GGTACAGCCA  CAAATGTGCA
651 GAATGATTAC  GCCGATGTTT  TACAGAAAAA  CGGCTATACC  TATACGGGTG
701 CAGACGGCAA  AACTTATAAC  AGCGGATCCT  ACTCAATCGT  GCATGATAAA
751 GATTTTGTGG  GGAACAAATG  GATACCTTTC  TTGCTAGGAA  CCAATGACAC
801 CACACAAGGT  ACATGTAAGG  GGTGTGCTGA  TTCGCATAGC  AGTTATTTTG
851 CGGAGGTGCC  AAAAGCAGGT  ACAAAGAAT  TTGATGACTA  TGTAATAATA
901 TGGGGTGAAG  TTGAATATGA  CGCTCAAGGT  AAGCCAATTA  ACAAATCTAA
951 ACCCATACTG  GTAGAACCAG  ACAAACAA  AGATAATGAA  AAATATGAAA
1001 AAGAAGCTTT  CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2580; ORF 751>:

m751.pep..

```

1  MAWSMFATTQ  ADRAVRSATA  PKEMNFHKKI  IDEKTGKVSF  DTRQIWSLND
51  LSKEBLASIQ  DTNGKVITVS  NPGIFNNRED  SLSNAAKQNR  NSTNGSGVIA
101 VMNPPTGKYK  SDSNNKIKDF  LWLGSSLVSE  LMYVGVDQLN  NKVPQGYLPK
151 TNSEKLNQDI  YREVQKMGNG  WSVDTSNHSR  GGITASVSLK  DWVNNQKQNG
201 IAPIRKARFY  GTATNVQNDY  ADVLQKNGYT  YTGADGKTYN  SGSYSIVHDK
251 DFGVGNKIWF  LLGTNDTTQG  TCKGLCYSHS  SYFAEVPKAG  TKEFDDYVKI
301 WGEVEYDAQG  KPINKSKPIL  VEPNKTNDNE  KYEKEAP*

```

a751.seq not found yet

a751.pep not found yet

g752.seq not found yet

g752.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2581>:

m752.seq..

```

1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAAT TGCCAAGCTG CTGAATTCTT
101 CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAAATCAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTCTG CATTCCCGAC TCTTTCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGA AAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTTGC ACCGCATTGC
651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTGCATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTT TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTGAAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCTGCCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTAAACCT ATTTATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTTG GAGCACTACA TTTCCGACAA ACAAAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATT TTAGTAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTAT TGGAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2582; ORF 752>:

m752.pep

```

1  MKISRPPEFT LLQOEYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51  DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQKPIDFPF
101 EHGFWFICPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRELLKSLIM
151 EEAITSAQLE GAATTRKQVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNPPLSVEMI LDHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFH PVVQAIILHF LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPQYAK SYLYAETDDL
351 DLTYFIYYQC DIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIETAQ EIANQYGISL NTARSDSLKL GEYRFLVPFK
451 SGNALAYVAP QDILLERLEKK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2583>:

m752-1.seq

```

1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAAT TGCCAAGCTG CTGAATTCTT
101 CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAAATCAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTCTG CATTCCCGAC TCTTTCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGA AAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTTGC ACCGCATTGC

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```

651 TACCACTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTGCATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTGTG ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTTATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTGG GAGCACTACA TTTCCGACAA ACAAAAACAC CAACAGGAAT
1151 TCAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAATTTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTACCGATTT GAGTAAACTC GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTAT TGGAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2584; ORF 752-1>:

m752-1.pep

```

1 MKISRPEFT LLQEYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51 DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAVKSRK KIQKPIDFPF
101 EHQFWFCIPD SLOARLHLID KSCGSSIGTS SLGGFGRSEQ NRELLKSLIM
151 EEAITSAQLE GAATTRKVK DMLKSORKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDLHRIATSN AIENKREPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFIH PVVQAILLHF LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
351 DLYFYIYYQC DIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIETAQ EIANQYGISL NTARSDLSKL GEYRFLVPPK
451 SGNALYVAP QDLLERLEKK

```

a752.seq not found yet

a752.pep not found yet

g753.seq not found yet

g753.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2585>:

m753.seq

```

1 ATGCCCATCA CTCCACCCTT AAACATCATC TCTCCTAAAC TCTACCCCAA
51 TGAACAATGG AACGAAAGCG AAGCACTCGG TGCCATCACT TGGCTATGGT
101 ATCAGTCGCC TACGCATCGC CAAGTACCTA TTGTGGAGAT GATGACGTAT
151 ATATTGCCCTG TGTAAAAAAA CGGGCAGTTC GCTTTGTTTT GCAAGGGTAC
201 CCAACCAATC GGTATATCT CATGGGCTTA TTTTGATGAA GTGGCGCAGG
251 CGCATTATTT AGAATCTGAC CGCCATTTGC GTGACAACAG CGATTGGAAC
301 TGTGGCGACA ATATTGGCT GATTCAATGG TTTGCGCCAT TGGGACACAG
351 TCATCAAATG CGCTCAGCTG TCGGCCAGTT ATTCCTAGT ACGACAGTAC
401 CGGCCTTGTA TCATAAAGGG AGCGATAAGG GTTTGAGAAT TTAACTTTT
451 AAAACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2586; ORF 753>:

m753.pep

```

1 MPITPPLNII SPKLYPNEQW NESEALGAI T WLWYQSPTHR QVPIVEMMTY
51 ILPVLKNGQF ALFCKGTQPI GYISWAYFDE VAQAHYLED RHLRDNSDWN
101 CGDNIWLIQW FAPLGHSHQM RSAVRQLFPS TTVRALYHKG SDKGLRILTF
151 KT*

```

a753.seq not found yet

a753.pep not found yet

g754.seq not found yet

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g754.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2587>:

```

m754.seq
1  ATGATGAAGT CTATCCTCAC CGTATCCGGA AATCGTATGC GTAAACCCAG
51  AATCACCTAT TTGGATGTTT GGGCAAACGA TGAAAGAATC GGTACTTTGG
101 AAAAGGGGGC CATGTATCGG TTCGCATACG ACAATCCCAA TTCTTCGTTG
151 CTGGGCGCTGC ATTATCAAGA CAGAAGCAAG GTATATATCA GCAACAATAT
201 GCCGCATATC TTTGCACAGT ATTTTCCGGA AGGCTTTTTC GATGCACACA
251 TCACAAGCAA ATATGCTTTT CATGATGCGC CTTTGAAGA CAATGAGATG
301 CTGCGCTTGG CAATTCTGTG CAGAGAGACT TTGGGTCGGA TACATGTGCG
351 CTGTAATGAC CCGCTTTTTA ATGAATGGAT TGACGGGTTG GAGATGAAAA
401 ATCCAAGAAT ATTGACTGAA CGGGATTTCG TGGGCATAAA TGCCCGACAG
451 GTTTTTTCAGC AATATATGCG AGAAATCTTC CATCAGCGCC GTTTCGTCAG
501 TGTATCCGGG ATACAGCAGA AGATGTCCTT AGATGCCATC CGCAGAAATA
551 CCAAGCAAAC TGCCTCATAT ATTGCCAAG GTTTTGATGC ATCCGAATAT
601 CCTTGCTTGG CTGCCAATGA ATTTTATATG ATGCAGACCA TCAACAAGC
651 CGGCATTGCC GTTGCACAGA CCAGCCTGTC GGAAGATTCA TCAGTCTTAT
701 TGGTACGTCG GTTTGATGTC AGTGAACAGG GTTATTTTTT AGGGATGGAA
751 GACTTTACCA GTCTGCGCCA GTATTCGGTA GAAGATAAAT ATAAAGGCAG
801 TTATGCGGCT ATGACACAGA TTATCCGACA GATATCCGGC AGACCAGATG
851 AAGATTAAAT CCATTCTTTT AATCAGCTTG CTGCCAGTTG CATATTGAAA
901 AACGGCGATG CACACCTCAA AAATTTTCA GTACTCTATC ATGACGAATA
951 CGATGTTCGT CTTGCACCTG TCTATGATGT ATTGGATACA TCAATATACA
1001 GGGTTGGAAC ACAAGGAATT TTTGATGCTT ATGACGATAC GCTGGCATTG
1051 AACCTGACTA ACCACGGTAA GAAACATAT CCTTCCAAGA ATACATTGTT
1101 GGATTTTGCT GAGAAATATT GCGATTGGG AAGAGAAGAT GCATCCTTTA
1151 TGATAGATAC AATCGTTCAA GCTAAAGAAC AGGTTCTTGT TAAATACTCG
1201 GATGTATTGC GTGAGAATGA ATGGTTGGCG CAGAAGTGGC ATTTTATCCC
1251 GGATGAAAAT GAAGAAGGTC TACCGTTTAC ATTCGGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2588; ORF 754>:

```

m754.pep
1  MMKSILTVSG NRMKRPRITY LDVWANDERI GTLEKGAMYR FAYDNPNSSL
51  LGLHYQDRSK VYISNNMPHI FAQYFPEGFL DAHITSKYAF HDAFPEDNEM
101 LRLAILCRET LGRIHVRCND PLFNEWIDGL EMKNPRILTE RDLLGINARQ
151 VFQQYMAEIF HHGRFVSVSG IQQKMSLDAL RRNTKQTASY IAKGFDASEY
201 PCLAANEFLC MQTIKQAGIA VAQTSLSSEDS SVLLVRRFDV SEQGYFLGME
251 DFTSLRQYSV EDKYKGSYAA IAQIIRQISG RPDEDLIHFF NQLAASCILK
301 NGDAHLKNFS VLYHDEYDVR LAPVYDVLDL SIYRVGTQGI FDAYDDTLAL
351 NLTNHGKTTY PSKNTLLDFA EKYCDLGRED ASFMIDTIVQ AKEQVLVKYS
401 DVLRENEWLA QKWHFIPDEN EEGLPFTFR*

```

a754.seq not found yet

a754.pep not found yet

g755.seq not found yet

g755.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2589>:

```

m755.seq..
1  ATGAGCCGTT ACCTGATTAC CTTTGATATG GATACCAACT GCCTGAAAGA
51  CAATTACCAC GGAAATAACT ATACCAATGC CTACTCCGAT ATTAACCAAC
101 TCTTGGCTAG ACATGGATTT GAGAACATTC AGGGCAGTGT TTATCTAGGC
151 CGTGAAGGCA TCAGTGAAGC ACACGGAACA ATAGCCATTC AGGAACTGAC
201 CGCTCGGTTT GATTGGTTTT ACTCCTGTAT TTCAAACATT AAGTTTTACC
251 GCCTTGAAAG TGATTGAAC GCACAATTTA TCGCTGATGG TGTGTATCAA
301 GCCAAACAGG CTTTCCTTCA ACGTGTTGAA CAACTTCGTA TATCCCTAAC
351 AGAAGCTGGA TTGTCTGATG AGCAAATCAA TCAGGTTCTG GAAAAACAGA
401 AATTTGAATT GGAAAGTCCT AACCTGAAAT TAAATTAA

```

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This corresponds to the amino acid sequence <SEQ ID 2590; ORF 755>:

```
m755.pep..
  1 MSRYLITFDM DTNCLKDNYH GNNYTNAYS D IKTILARHGF ENIQGSVYLG
 51 REGISEAHGT IAIQELTARE DWFYSCISNI KFYRLESDLN AQFIADGVYQ
101 AKQAFLLQ RVE QLRISLTEAG LSDEQINQVL EKQKFELESP NLKLN*
```

a755.seq not found yet

a755.pep not found yet

g756.seq not found yet

g756.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2591>:

```
m756.seq
  1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
 51 CAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTGGGAA
301 TACCTGAAGC AGGTTGCTTC GGAACGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTGCAG AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2592; ORF 756>:

```
m756.pep
  1 MTANFAQTLV EIQDSLRYRVV STVOYGDNDL KRLTADKRKQ YELNFKISEG
 51 STRVESDFKE TLVRFRDML ODMPPKIRSA TLVALTLLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DFVQIGRRSY
151 SREDISEANR RAERVYPYAE LVSDGNFTAV LSDIGD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2593>:

```
a756.seq
  1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
 51 NAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTGGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTGCAG AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2594; ORF 756.a>:

```
a756.pep
  1 MTANFAQTLV EIQDSLXRVV STVOYGDNDL KRLTADKRKQ YELNFKISEG
 51 STRVESDFKE TLVRFRDML QDMPPKIRSA TLVALTLLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DFVQIGRRSY
151 SREDISEANR RAERVYPYAE LVSDGNFTAV LSDIGD*
```

m756 / a756 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
m756.pep	MTANFAQTLVEIQDSLRYRVVSTVOYGDNDLKRLTADKRKQYELNFKISEGSTRVESDFKE					
a756	MTANFAQTLVEIQDSLXRVVSTVOYGDNDLKRLTADKRKQYELNFKISEGSTRVESDFKE					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m756.pep	TLVRFGRDMLQDMPPKIRSATLVALTTLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
a756	TLVRFGRDMLQDMPPKIRSATLVALTTLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m756.pep	RLAESQERITSAILKGARGADFVQIGRRSYSREDISEANRRAERVYPYGAELVSDGNFTAV					
a756	RLAESQERITSAILKGARGADFVQIGRRSYSREDISEANRRAERVYPYGAELVSDGNFTAV					
	130	140	150	160	170	180
m756.pep	LSDIGDX					
a756	LSDIGDX					

g757.seq not found yet

g757.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2595>:

```

m757.seq
1  ATGAAAATAC TCGCTTTATT AATTGCCGCT ACCTGTGCTT TATCTGCGTG
51  TGGCAGCCAA TCTGAAGAAC AACCGGCATC TGCACAACCC CAAGAGCAGG
101 CACAATCCGA ATTA AAAACC ATGCCGGTAA GCTATACCGA CTATCAATCA
151 GCAGCCCAATA AAGGGCTGAA TGACCAAAAA ACCGGTCTGA CCCTTCCTGA
201 ACATGTTGTC CCTATCGACA ATGCCGGAAG AAAGAATCTG CTGCATGACT
251 TTTCAGACGG CCTCACAAATC TTAACCGTTG ATACCGATAA AGCCGACAAA
301 ATTACTGCTG TCCGAGTAGT CTGGAATACA GATGCAATGC CTCAAAAAGC
351 GGAAAAACTG TCCAAAGCTG CCGCAGCCTT GATTGCGGCA ACCGCTCCGG
401 AAGACCGCAC AATGCTGCGT GATACGGCGC ACCAAATCGA AATGGCGATT
451 GACAGCCATA ATGCGCAAAA AGAGCCAACC CGAGAATGGG CGCGTGGTGG
501 GATTGCTTAT AAAGTCACTG TTACCAATTT ACCGAGCGTG GTTTTGACGG
551 CAAAAGCTGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2596; ORF 757>:

```

m757.pep (lipoprotein)
1  MKILALLIAA TCALSACGSQ SEEQPASAQP QEQAQSELKT MPVSYTDYQS
51  AANKGLNDQK TGLTLPEHVV PIDNAEGKNL LHDFSDGLTI LTVDTDKADK
101 ITAVRVVWNT DAMPQKAEL SKAAPALIAA TAPEDRTMLR DTGDQIEMAI
151 DS:NAOKEPT REWARGGIAY KVTVTNLPVS VLTAKAE*

```

a757.seq not found yet

a757.pep not found yet

g758.seq not found yet

g758.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2597>:

```

m758.seq
1  ATGAACAATC TGACCGTGTT TACCCGTTTC GATACCGATT TGGCGACGCT
51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCGGTT ACAGACCATC
101 AGGGCAAACCT GGTGGAAATT CCCGTCTGCT ACGGCGGCGA ATACGGCCCG
151 GATTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCGGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251 CCGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCGGC
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCCGTCG GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
451 CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGACAGAA GGATTGAGCC
501 ATGA

```


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This corresponds to the amino acid sequence <SEQ ID 2598; ORF 758>:

```
m758.pep
  1  MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGGEYGP
 51  DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101  RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPT
151  LLAAGDQVRF VAERIEP*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2599>:

```
a758.seq
  1  ATGAACAATC TGACCGTGTT CACCCGTTTC GATACCGATT TGGCGACGCT
 51  TGCCGATGAA TTGCAAIATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101  AGGGCAAACCT GGTGAAATTT CCCGTCTGCT ACGGCGGCGA ATACGGCCCG
151  GATTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201  CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251  CTGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301  CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTCGCTCG GTATCGGCGG
351  CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401  TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
451  CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGCAGAAA GGATTGAGCC
501  ATGA
```

This corresponds to the amino acid sequence <SEQ ID 2600; ORF 758.a>:

```
a758.pep..
  1  MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGGEYGP
 51  DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101  RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPT
151  LLAAGDQVRF VAERIEP*
```

m758 / a758 100.0% identity in 167 aa overlap

	10	20	30	40	50	60
m758.pep	MNNLTVFTRFDTDLATLADE LQYVWEHTAVTDHQGKLVEIPVCYGGGEYGPDLAEVAAFHQ					
a758	MNNLTVFTRFDTDLATLADE LQYVWEHTAVTDHQGKLVEIPVCYGGGEYGPDLAEVAAFHQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m758.pep	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPA GSVGIGGSQT					
a758	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPA GSVGIGGSQT					
	70	80	90	100	110	120
	130	140	150	160		
m758.pep	GVYPFASPGGWQIIGRTELP LFRADLNPPTLLAAGDQVRFVAERIEPX					
a758	GVYPFASPGGWQIIGRTELP LFRADLNPPTLLAAGDQVRFVAERIEPX					
	130	140	150	160		

g759.seq not found yet

g759.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2601>:

```
m759.seq
  1  ATGCGCTTCA CACACACCAC CCCATTTTGT TCCGTATTGT CCACCCTCGG
 51  TCTTTTGGCC GTTTCCTCTG CTTACTCATC CATTGTCCGC AACGATGTCTG
101  ATTACCAATA TTTTCGCGAC TTTGCCGAAA ATAAAGGCGC GTTCACCGTA
151  GGTGCAAGCA ATATTTCCAT CCAAGACAAG CAAGGCAAAA TATTAGGCAG
201  GGTTCTCAAC GGCATCCCCA TGCCCCGACTT CCGCGTCAGC AACCGCCAAA
251  CCGCCATCGC CACCCTGGTT CACCCCAAT ACGTCAACAG TGTCAAACAC
301  AACGTCGGCT ACGGTTCCAT ACAATTCGGC AACGACACCC AAAATCCAGA
351  AGAACAAAGC TATACCTACC GCCTCGTATC ACGCAACCCG CACCCGACT
401  ACGACTACCA CCTTCCCCGC CTCAACAAAC TGTTACCGA AATCTCACCT
```

451 ACCGCACTCA GCAGCGTACC CTTGCTTGGA AACGGCCAGC CAAAGGCCAA
 501 TGCCTACCTC GATACCGACC GCTTCCCCTA CTTTCTACGA CTCGGCTCAG
 551 GCACGCAACA AGTCCGCAAA GCAGACGGCA CGCGTACAG AACCGCCCCG
 601 GCATACCAAT ACCTGACCGG CGGCACGGCG CTGAAAGTAT TGGGGTTCCA
 651 AAACCCAGGC TTA CTGCTCG GCGGCAGCCT GACCGACCAA CCCCTTAACA
 701 CCTACGCAAT CGCCGGAGAC AGCGGTTCCT CCCTGTTTGC CTTGACAAAG
 751 CATGAAAACC GCTGGGTGCT TGCGGGCGTA CTCAGCACCT ACGCCGGCTT
 801 CGATAATTTT TTCAACAAAT ACATCGTCAC GCAACCCGAA TTCATCCGTT
 851 CCACCATCCG CCAATACGAA ACCCGGCTGG ATGTCGGGCT GACCACCAAC
 901 GAACTCATAT GGCGGACAA CGGTAATGGC AACAGCACCC TGAAGGGCT
 951 CAACGAACGC ATCACCTGCT CCATTGCAAA CCCTTCGCTT GCCCCACAAA
 1001 ACGACAGCAG GCACATGCCG TCTGAAGATG CCGGCAAAAC GCTCATCCTA
 1051 TCCAGCAGGT TCGACAACAA AACACTGATG CTGGCAGACA ATATCAACCA
 1101 AGGCGCAGGC GCATTGCTAGT TCGACAGCAA CTTACCCGTC GTCCGTAATA
 1151 ACCACACATG GCAAGGTGCA GCGCTTATCG TAGCCGACGG CAAACGCGTC
 1201 TTCTGGCAAG TCAGCAACCC CAAAGGCGAC CGGCTCTCCA AACTGGGCGC
 1251 AGGCACGCTT ATCGCCAACG GACAAGGCAT CAACCGGGC GACATCAGCA
 1301 TCGGGGAAGG CACTGTCGTA CTCGCCCAA AAGCTGCTTC AGACGGCAGC
 1351 AAACAAGCAT TCAACCAAGT CCGCATCACC AGCGGCAGGG GCACGGCCGT
 1401 CCTCGCCGAC AGCCAGCAAA TCAAACCCGA AAACCTCTAT TTCGGCTTCA
 1451 GGGCGGACG GCTCGACCTC AACGGCAACA ACCTTGCTT TACCCATATC
 1501 CGCCATGCGG ACGGCGGCGC GCAAATCGTC AATCACAAAC CTGACCAAGC
 1551 CGCGACACTG ACGCTGACCG GCAACCCCGT CCTCAGTCCC GAGCATGTGG
 1601 AGTGGGTGCA ATGGGGCAAC CGTCCGCAAG GCAACGCGGC GGTTCACGAA
 1651 TACATCAACC CGCACCGCAA CCGTCGGACC GACTACTTCA TACTCAAACC
 1701 CGGCGGCAAC CCGCGCGAAT TTTTCCCGTT AAATATGAAA AACTCAACAA
 1751 GCTGGCAATT TATCGGCAAC AACAGGCAAC AGGCCGCCGA ACAAGTCGCC
 1801 CAAGCCGAAA ATGCCCGCCC CGACCTGATT ACCTTCGGCG GATACTTGGG
 1851 TGAAAACGCG CAAACGGGCA AAGCCGCGCC GAGTTACAGC AAAACCAATG
 1901 AAGCAGCCAT AGAAAAAACC CGCCATATCG CAAATGCCGC CGTATACGGC
 1951 CGGCCCGAAT ACCGTTACAA CGGCGCACTC AACCTGCACT ATCGTCCCAA
 2001 ACGCACCGAC AGCAGCTGTG TGCTCAACGG CCGCATGAAC CTTAACGGGG
 2051 AAGTCTTGAT TGAGGGCGGC AATATGATTG TGTCAGGCAG GCCCGTACCC
 2101 GATGCTTACG ACCACCAGGC CAAACGCGAA CCCGTTCTTG AAAACGAATG
 2151 GACCGCAGGC AGCTTCAAGG CTGCACGGTT CACCGTCGCA AACCATGCCC
 2201 GACTGACGGC AGGCGGCAAT ACCGCGCATC TGGACGGCGA CATAACCGCA
 2251 TACGATCTGT CCGGCATCGA CCTCGGCTTT ACCCAAGGCA AAACACCGGA
 2301 ATGCTACCGC TCCTACCATG GCGGCAGCAC CCACTGCACA CCCAACGGCG
 2351 TTTTAAAAGC GAAAACTAT CTGCACTAC CTGCAACGCA AGTACGCGGC
 2401 GACATTACCC TTAACGACCG TTCAGAGCTC CGCCTGGGCA AAGCACACCT
 2451 GTAGGCGAGC ATCCGTGCCG GCAAAGACAC CGCAGTCCGC ATGGAAGCAG
 2501 ACAGCAACTG GACACTTTCC CAGTCCAGCC ACACCGGCGC ACTGACGCTT
 2551 GACCGCGCAC AAATTACCCT GAACCCGAT TCGGCCAATA ATACACACAA
 2601 CAACCGCTTC AACACACTGA CCGTCAACGG CACACTTGAC GGGTTCGGCA
 2651 CATTCGATT CTTGACCGGC ATCGTCCGAA AACAAAATGC CCCCCCCTC
 2701 AAACCTGGAAG GGGACAGCGG CGGCGCATTC CAAATCCACG TCAAAAACAC
 2751 CGGACAAGAA CCTCAAAACA CCGAATCGCT TGCCTTGTG AGCCTCAATC
 2801 CGAAACACAG CCACCAAGCC CGATTACCCC TCCAAAACGG CTATGCCGAT
 2851 TTGGGTGCCCT ACCGCTACAT CCTCCGCAAA AACAAACAG GATACAGCCT
 2901 GTACAACCCG CTCAAAGAGG CCGAATTTCA AATTGAAGCC ACGCGTGCGG
 2951 AACATGAGCG CAACCAACAG GCATACAACC AATTACAGGC AACCGACATC
 3001 AGCAGACAGG TTCAACATGA CTCTGACGCG ACCAGGACAG CACTACAGGC
 3051 CTGGCAGAAC AGTCAAACCG AACTTGCCCG CATCGACAGC CAAGTCCAAT
 3101 ATCTGTCCGC CCAATTGAAA CAGACAGACC CGCTGACCGG CATTCTGACG
 3151 CGTGCCCAA ACCTGTGTG CGCACAGGA TACAGTGGC ATATCTGCCG
 3201 TCAGGTTGCC AAAGCCGCGG ACACGAACGA CCGTCACTC TTCGAAACCG
 3251 AACTGGATAC GTATATAGAA CGGTGAGAAA TGGCCGAACT CGAACTTGAC
 3301 AAAGCACGGC AAGGCGGCGA TGCGCAAGCC GTCGAAACAG CCCGGCACGC
 3351 CTACCTGAAC GCACTCAACC GTCTGTCCCG ACAAATCCAC AGTTTGAAAA
 3401 CCGCGCTTGC CGGCATCCGT ATGCCGAACC TGGCCGAAC TATCAGCCGG
 3451 TCGGCCAACA CCGCCGTTTC CGAACAGGCC GCCTACAATA CCGGCCGGCA
 3501 ACAGGCGGGA CGCCGCATCG ACCGCCACCT TACCGATCCG CAGCAGCAAA
 3551 ACATCTGGCT GGAACCCGGT ACGCAACAAA CCGACTACCA TAGCGGCACA
 3601 CACCGTCCCT ACCAACAAAC TACCAACTAT GCACATATCG GCATCCAAC
 3651 CGGCATCACC GACCGTCTCA GTGTGCGTAC GATTTTAACC GATGAGCGCA
 3701 CAAACAACCG TTTTGATGAA GCGGTATCCG CCCGAAACCG CAGCAACGGC

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3751 GCACATCTGT TCGTCAAAGG GGAACACGGC GCACTCTTTG CCGCGGCAGA
3801 TTTAGGCTAC AGCAACAGCC GTACCCGATT TACCGATTAT GACGGGGCTG
3851 CCGTCCGCGG CCACGCATGG GATGACAGCA TCAACACCGG CATCAAAATC
3901 GATACCGGCA TCAACCTCAG ACCCTATGCC GGCATCCGTA TAAACCGCAG
3951 CAACGGCAAC CCGTACGTAC TCGACGGCGC AGAGATAAAC AGCCCGGCGC
4001 AAATCCAAAC CACATGGCAT GCCGGCATCC GTCTCGATAA AACCCTCGAA
4051 CTGGGTCAAG CCAAGCTGAC CCCCGCCTTC AGCAGCGATT ACTACCATAC
4101 CCGCCAAAAC AGCGGTTCCT CCCTCAGCGT CAACGACCGT ACCTTACTGC
4151 AGCAAGCCCG CCACGGCACA CTGCATACCC TGCAAAATCGA CGCCGGATAC
4201 AAAGGCTGGA ACGCCAAACT TCATGCCGCT TACGGCAAAG ACAGCAACAC
4251 CGCCGCCAC AAACAGGCAG GAATCAAAAT AGGCTACAAC TGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2602; ORF 759>:

```

m759.pep
1  MRFTHTTTPFC SVLSTLGLFA VSPAYSSIVR NDVDYQYFRD FAENKGAFTV
51  GASNISIQDK QGKILGRVLN GIPMPDFRVS NRQTAIATLV HPQYVNSVKH
101 NVGYGSIQFG NDTQNPEEQA YTYRLVSRNP HEDYDYHLPR LNKLVTEISP
151 TALSSVPLLG NGQPKANAYL DTDREFPYFVR LGSQTQVVRK ADGTRTRTAP
201 AYQYLTGGTP LKVLGFQNHG LLVGGSLTDQ PLNTYAIAGD SGSPLFAFDK
251 HENRWVLAGV LSTYAGFDNF FNKYIVTQPE FIRSTIRQYE TRLDVGLTTN
301 ELIWRDNGNG NSTLQGLNER ITLPIANPSL APQNDSRHMP SEDAGKTLIL
351 SSRFDNKTLM LADNINQAG ALQFDSNFTV VGKNHTWQGA GVIVADGKRV
401 FQVQSNPKGD RLSKLGAGTL IANGQGINQG DISIGEGTVV LAQKAASDGS
451 KQAFNQVGIT SGRGTAVLAD SQQIKPENLY FGFRGGRDL NGNNLAFTHI
501 RHADGGAQIV NHNPDQAATL TLTGNPVLSP EHVEWVQWGN RPQGNAAVYE
551 YINPHNRNRT DYFILKPGGN PREFFPLNMK NSTSWQFIGN NRQQAEEQVA
601 QAENARPLI TFGGYLGENA QTGKAAPSYS KTNEAAIEKT RHIANAAVYG
651 RPEYRYNGAL NLHYRPKRTD STLLLNGGMN LNCEVLIEGG NMIVSGRPVP
701 HAYDHOAKRE PVLENEWTDG SFKAARFTLR NHARLTAGRN TAHLDGDITA
751 YDLSGIDLGF TQKKTPECYR SYHSGSTHCT PNAVLKAENY RALPATQVRG
801 DITLNDREL RLKKAHLYGS IRAGKDTAVR MEADSNWTL SSSHTGALT
851 DGAQITLNPD FANNTNHRF NTLTVNGTLD GFGTFRELTG IVRKQNPPL
901 KLEGDSTRGAF QIHVKNTGQE PQTTESLALV SLNPKHSHQA RETLQNGYAD
951 LGAYRYILRK NNGGYSLYNP LKEAELQIEA TRAEHERNQQ AYNQLQATDI
1001 SRQVQHSDA TRQALQAWQN SQTELARIDS QVQYLSAQLK QTDPLTGILT
1051 RAQNLCAAQG YSADICRQVA KAADTNDLTL FETELDTYIE RVEMAESELD
1101 KARQGGDAQA VETARHAYLN ALNRLSRQIH SLKTGVAGIR MPNLAEELIS
1151 SANTAVSEQA AYNTGRQAG RRIDRHLDTP QQONIWLETG TQQTQDYHSGT
1201 HRPYQTTNY AHIGIQTGIT DRLSVGTILT DERTNNRFE GVSARNRSNG
1251 AHLFVKGENG ALFAAADLGY SNSRTRETDY DGAAVRRHAW DAGINTGIKI
1301 DTGINLRPYA GIRINRSNGN RYVLDGAEIN SPAQIQTTWH AGIRLDKTVE
1351 LGQAKLTPAF SSDYYHTRQN SGSALSVNDR TLLQQAAGHT LHTLQIDAGY
1401 KGWNAKLHAA YGKDSNTARH KQAGIKIGYN W*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2603>:

```

g760.seq (partial)
1  AACCAACGCA ACACCCGTTA CGCCGCATTG GGCAAACGCG TGATGGAAGG
51  CGTTGAGACC GAAATCAGCG GTGCGATTAC ACCGAAATGG CAAATCCATG
101 CAGGTTACAG CTATCTGCAC AGCCAAATCA AAACCGCCGC CAATCCACGC
151 GACGACGGCA TCTTCTGCT GGTGCCCAAA CACAGCGCAA ACCTGTGGAC
201 GACTTACCAA GTTACGCCCG GGCTGACCGT CGGCGCGCGC GTGAACGCGA
251 TGAGCGGCAT TACTTCATCT CCAGGGATGC ATGACGGCGG TTATGCCACG
301 TTCGATGCGA TGGCGGCATA CCGCTTCACG CCCAAGCTGA AGCTGCAAAT
351 CAATGCCGAC AACATCTTCA ACCGCCATTA CTACGCCCGC GTCGGCGGCA
401 CGAACACCTT TAACATTCCC GGTTCGGAGC GCAGCCTGAC GGCAAACCTG
451 CGTTACAGTT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2604; ORF 760.ng>:

```

g760.pep (partial)
1  NNRNTRYAAL GKRVMGCVET EISGAITPKW QIHAGYSYLH SQIKTAANPR
51  DDGIFLLVPK HSANLWTTYQ VTPGLTVGGG VNAMSGITSS AGMHAGGYAT
101 FDAMAAYRFT PKLKLQINAD NIFNRHYAR VGGTNTFNIP GSERSLTANL
151 RYSF*

```

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2605>:

```
m760.seq
1  ATGGGACAGT TTATGTCAGT TTTCCGCATC AATATGACCG CCGCCACGGT
51  TTTGGCAGCA CTCTCGTCTT CGGTTTTTGC CGCACAAACG GAAGGTTTGG
101 AAACCGTCCA TATTAAGGGT CAGCGTTCTT ACAACGCGAT TGCCACCGAG
151 AAAAAACGGC ATTACAGCTC GTTTGCCGCC ACCGTCGGTA CAAAAATCCC
201 CGCTTCTTTG CGCGAAATTC CGCAATCCGT CAGCATCATT ACCAACCAGC
251 AGGTCAAAGA CCGCAATGTT GATACGTTTG ACCAGTTGGC ACGCAAAACG
301 CCCGGCCTGC GCGTGTGAG CAACGACGAC GGACGCTCTT CGGTTTACGC
351 GCGCGGTTAC GAATACAGCG AATACAACAT CGACGGCCTG CCCGCGCAGA
401 TGCAGAGTAT CAACGGCAGC CTGCCCCAACC TGTTCGCCTT CGACCGCGTG
451 GAAGTGATGC GCGGGCCGAG CGGACTGTTC GACAGCAGCG GCGAGATGGG
501 CGGCATCGTG AATCTGGTGC GCAAACGCCC GACCAAAGCG TTCCAAGGTC
551 ATGCGGCGGC AGGTTTCGGT ACGCACAAC AATATAAGC CGAGGCGGAC
601 GTATCGGGCA GCCTCAATTC AGACGGCAGC GTGCGCGGCC GCGTGATGGC
651 GCAGACCGTC GCGCGCTCTC CGCGTCCCGC CGAGAAAAAC AACC GGCGCG
701 AAACCTTCTA CGCGCGCGCG GATTGGGACA TCAACCCCGA TACGGTTTTG
751 GCGCGGGGCT ATCTTTACCA GCAACGCGCG CTCGCGCGCT ACAACGGCCT
801 GCCTGCCGAT GCCAATAACA AATTACCGTC CCTGCCGCAA CACGTATTTG
851 TCGCGCGCGA TTGGAACAAA TTAAAAATGC ACAGCCACGA CGTGTTCGCC
901 GATTTGAAAC ATTACTTCGG CAACGGCGGC TACGGCAAAG TCGGTATGCG
951 CTATTCGGAT CGGAAAGCCG ATTCCAATTA TACGTTTTCG GCGAGCAAAC
1001 TCAACAATAC CGGACAAGCC GACGTAGCGG GTTTGGGTAC GGACATTAAA
1051 CAAAAAGCCT TTGCGGTTGA CGCAAGTTAC AGCCGTCCGT TTGCCTTGGG
1101 CAACACCGCC AACGAATTTG TGATTGGTGC AGACTACAAC CGCTTGCGCA
1151 GTACTAATGA ACAAGGGCGT TCGACTTTGT CAAAAAGCGT CGCTTTAGAT
1201 GGTTTCCGCG CTTTGCCTTA TAACGGCATA CTTCAGAACG CCCGCGCGCG
1251 AAACAAAGGT TTCAATCACT CCGTTACCGA AGAAAACCTC GACGAAACCG
1301 GTTTGTATGC CAAGACGGTG TTCCGTCCTC TGGAAAGGTT GTCGTTGATT
1351 GCAGGCGGAC GTGTAGGACA TCACAAAATC GAGTCGGGCG ACGGCAAAAC
1401 CCTGCATAAA GCTTCGAAAA CCAAATTTAC AAGCTACGCC GGCGCGGTTT
1451 ACGATATAGA CGGCAGCAAC AGCCTGTACG CTTCCGCCTC CCAACTCTAC
1501 ACACCGCAAA CCAGCATCGG CACCGACGGC AAGCTGCTCA AACC GGCGCA
1551 AGGCAACCAG TTTGAAATCG GCTACAAAGG CAGCTACATG GACGACCGCC
1601 TCAATACCCG GGTTCGTTTC TACCGCATGA AGGATAAAAA CGCGCGCGCA
1651 CCGCTGGACT CAAACAACAA AAAAACCCTG TACGCCGCAT TGGGCAAAAC
1701 CGTGATGGAA GGTGTTGAGA CCGAAATCAG CGGCGCGATG ACACCGAAAT
1751 GGCAAATCCA TGCAGGTTAC AGCTACCTGC ACAGCCAAAT CAAAACCGCC
1801 TCCAATTCGC GCGACGAAGG CATCTTCTTG CTGATGCCCA AACACAGCGC
1851 AAACCTGTGG ACGACTTACC AAGTTACGTC CGGGCTGACC ATCGGCGGCG
1901 GCGTGAACGC GATGAGCGGC ATTACTTCAT CTGCAGGGAT ACATGCAGGC
1951 GGTTATGCCA CGTTCGATGC GATGGCGGCA TACCGCTTCA CGCCCAAAC
2001 GAAGCTGCAA ATCAACGCCG ACAACATCTT CAACCGCAT TACTACGCC
2051 GCGTCGGCAG CGAGAGCACC TTAAACATTC CCGGTTCCGA GCGCAGCCTG
2101 ACGGCAAACC TCGGTTACAG TTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2606; ORF 760>:

```
m760.pep
1  MQQFMSVFRI NMTAATVLAA LSSSVFAAQT EGLETVHIKQ QRSYNAIATE
51  KNGDYSSFAA TVGTKIPASL REIPQSVSII TNQQVKERNV DTFDQLARKT
101 PGLRVLNSDD GRSSVYARGY EYSEYNIDGL PAQMOSINGT LPNLFAPDRV
151 EVMRGP SGLF DSSGEMGGIV NLVRKRPTKA FQGHAAAGFG THKQYKAED
201 VSGSLNSDGS VRGRVMAQTV GASPRPAEKN NRRETFYAAA DWDINEDTVL
251 GAGYLYQQR LAPIYNGLPAD ANNKLP SLPQ HVFVGADWNK FKMHS HDVFA
301 DLKHYFGNGG YGKVMRYSD RKADSNYTFA GSKLNNTGQA DVAGLGTDIK
351 QKFAFVDASY SRPFALGNTA NEFVIGADYN RLRSTNEQGR STLKSV ALD
401 GFALPYNGI LQNRAGNKG FNHSVTEENL DETGLYAKTV FRPLEGLSLI
451 AGGRVGH HKI ESGDGKTLHK ASKTRKTSYA GAVYDIDGSN SLYASASQLY
501 TPQTSIGTDG KLLKPREGNQ FEIGYKGSYM DDRLNTRVSF YRMKDKNAAA
551 PLDSNNK KTR YAALGKRVME GVETEISGAM TPKWQIHAGY SYLHSQIKTA
601 SNRDEGI FL LMPKHSANLW TTYQVTSGLT IGGGVNAMSG ITSSAGIHAG
651 GYATFDAMAA YRFTPKLKLQ INADNIFNRH YYARVGSEST FNIPGSERSL
701 TANLRYSF*
```

1236

m760 / g760 91.6% identity in 154 aa overlap

	530	540	550	560	570	580
m760.pep	YKGSYMDRLNTRVSYRMRKDKNAAPLDSNNKKTRYAALGKRVMEGVETEISGAMTPKW					
				:		
g760			NNRNRTRYAALGKRVMEGVETEISCAITPKW			
			10	20	30	

	590	600	610	620	630	640
m760.pep	QIHAGYSYLHSQIKTASNSRDEGIFLLMPKHSANLWTTYQVTSGLTIGGGVNAMSGITSS					
g760	QIHAGYSYLHSQIKTAAANPRDDGIFLLVPKHSANLWTTYQVTPGLTVGGGVNAMSGITSS					
	40	50	60	70	80	90

	650	660	670	680	690	700
m760.pep	AGIHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYARVGSESTENIPGSESLTANL					
g760	AGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYARVGSTNTENIPGSESLTANL					
	100	110	120	130	140	150

	709
m760.pep	RYSFX
g760	RYSFX

g761.seq not found yet

g761.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2607>:

m761.seq

1	ATGAAATAT	CATTTCATTT	AGCTTTATTA	CCCACGCTGA	TTATTGCTTC
51	CTTCCCTGTT	GCTGCCGCCG	ATACGCAGGA	CAATGGTGAA	CATTACACCG
101	CCACTCTGCC	CACCGTTTCC	GTGGTCGGAC	AGTCCGACAC	CAGCGTACTC
151	AAAGGCTACA	TCAACTACGA	CGAAGCCGCC	GTTACCCGCA	ACGGACAGCT
201	CATCAAAGAA	ACGCCGCAAA	CCATCGATAC	GCTCAATATC	CAGAAAAACA
251	AAAATTACGG	TACGAACGAT	TTGAGTTCCA	TCCTCGAAGG	CAATGCCGGC
301	ATCGACGCTG	CCTACGATAT	GCGCGGTGAA	AGCATTTTCC	TGCGCGGTTT
351	TCAAGCCGAC	GCATCCGATA	TTTACCGCGA	CGGCGTGCGC	GAAAGCGGAC
401	AAGTGCGCCG	CAGTACTGCC	AACATCGAGC	GCGTGGAAT	CCTGAAAGGC
451	CCGTCTTCCG	TGCTTTACGG	CCGCACCAAC	GGCGGCGGCG	TCATCAACAT
501	GGTCAGCAAA	TACGCCAACT	TCAAACAAAG	CCGCAACATC	GGAGCGGTTT
551	ACGGCTCATG	GGCAAACCGC	AGCCTGAATA	TGGACATTAA	CGAAGTGCTG
601	AACAAAACG	TCGCCATCCG	TCTCACCGGC	GAAGTCGGGC	GCGCCAATTC
651	GTTCCGCAGC	GGCATAGACA	GCAAAAATGT	CATGGTTTCG	CCCAGCATTA
701	CCGTCAAAC	CGACAACGGC	TTGAAGTGGA	CGGGGCAATA	CACCTACGAC
751	AATGTGGAGC	GCACGCCCGA	CCGCAGTCCG	ACCAAGTCCG	TGTACGACCG
801	CTTCGGACTG	CCTTACC CGA	TGGGGTTCGC	CCACCGGAAC	GATTTTGTC
851	AAGACAAGCT	GCAAGTTTGG	CGTTCCGACC	TTGAATACGC	CTTCAACGAC
901	AAATGGCGTG	CCCAATGGCA	GCTCGCCAC	CGCACGGCGG	CGCAGGATTT
951	TGATCATTTC	TATGCAGGCA	GCGAAAATGG	CAACTTAATC	AAACGTAAC
1001	ACGCCTGGCA	GCAGACCGAC	AACAAAACCC	TGTCGTCCAA	CTTAACGCTC
1051	AACGGCGACT	ACACCATCGG	CCGTTTGA	AACCACCTGA	CCGTAGGCAT
1101	GGATTACAGC	CGCGAACACC	GCAACCCGAC	ATTGGGTTTC	AGCAGCGCCT
1151	TTTCCGCCTC	CATCAACCCC	TACGACCGCG	CAAGCTGGCC	GGCTTCGGGC
1201	AGATTGCAGC	CTATTCTGAC	CCAAAACCGC	CACAAAGCCG	ACTCTACGG
1251	CATCTTTGTG	CAAAACATCT	TCTCCGCCAC	GCCCGATTG	AAATTCGTCC
1301	TCGGCGGCGG	TTACGACAAA	TACACCTTTA	ATTCCGAAAA	CAAACTCACC
1351	GGCAGCAGCC	GCCAATACAG	CGGACACTCG	TTCAGCCCCA	ACATCGGCGC
1401	AGTGTGGAAC	ATCAATCCCG	TCCACACACT	TTACGCCTCG	TATAACAAAG
1451	GCTTCGGCGC	TTATGGCGGA	CGCGGCGGCT	ATTTGAGCAT	CGATACGTTG
1501	TCTTCCGCGC	TGTTCAACGC	CGACCCGAG	TACACCCGCC	AATACGAAAC
1551	CGGCGTGAAA	AGCAGTIGGC	TGGACGACCG	CCTCAGCACT	ACGTTGTCTG
1601	CCTACCAAAT	CGAACGCTTC	AATATCCGCT	ACCGCCCCGA	TCCAAAAAAC
1651	AACCCTTATA	TTTATGCGGT	TAGCGGCAAA	CACCGTTCGC	GCGGCGTGGA

1237

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1701 ATTTGTCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT
1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTGAA TAATACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCGGACCG AAAACCTCTA CGGCGAAATC GGCCTAACCG
1901 GTACAGGCAA ACGCTACGGT TACAACCTAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2608; ORF 761>:

m761.pep

```

1 MKISFHLALL PTLIIASFPV AAADTDQNGE HYTATLPTVS VVGQSDTSVL
51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSX YANFKQSRNI GAVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNMVVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDREGL PYRMGFAHRN DFKVDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQT D NKTLSNLTL
351 NGDYITIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFLVGGRYDK YTFENSENKL
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTL
501 SSAVENADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRDPKPN
551 NPYIYAVSGK HRSRGVLSA IGQIIPKKLY LRGS LGVMQA KVVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT
651 LPGAARVDAM LGWNHKNVNV TFAANLLNQ KYWRSDSMPG NPGYTARVN
701 YRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2609>:

a761.seq

```

1 ATGAAATAT CATTTCATT AGCTTTATTA CCCACGCTGA TTATTGCTTC
51 CTTCCTGTT GTCGCCGCG ATACGCAGGA CAATGGTGAA CATTACACCG
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC
301 ATCGACGCGC CCTACGATAT GCGCGGCGAA AGCATTTTCC TCGCGCGCTT
351 TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACGC AAAAGCGGGC
401 AGGTGCGCGC TAGCACCGCC AACATCGAGC GCGTGAAAT CCTGAAAGGT
451 CCGTCTCCG TGCTTTATGG GCGTACCAAC GCGGCGGGTG TCATCAACAT
501 CGTCAGCAAA TAGCCCAACT TCAACAAGAG CCGTAATATC GGTACGGTTT
551 ATGGTTCGTG GGCAAACCGC AGCCTGAATA TGGACATCAA CGAAGTGCTG
601 AAAAAAAGC TCGCCATCCG TCTCACCAGC GAAAGTCGGC GCGCCAATTC
651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATT
701 CCGTCAAACT CGACAACGGC TTGAAGTGGA CCGGGCAATA CACCTACGAC
751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG
801 CTTCGGACTG CCTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTC
851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCACGAC
901 AAATGGCGTG CCCAATGGCA GCTCGCCAC CGCACGGCGC GCGAGGATT
951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAAT
1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC
1051 AACGGCGACT ACACCATCGG CCGTTTGTAA AACCACCTGA CCGTAGGCAT
1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT
1151 TTTCCGCTC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC
1201 AGATTGCAGC CTATTCTGAC CCAAAACCGC CACAAAGCCG ACTCCTACGG
1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCGATTTCG AAATTCGTCC
1301 TCGGCGGCGG TTACGACAAA TACACCTTTA ATTCGAAAA CAACTCACC
1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC
1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCTCG TATAACAAAG
1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CGATACGTTG
1501 TCTTCGCGCG TGTTCACGCG CGACCCGAG TACACCCGCC AATACGAAAC
1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACCTGTCTG
1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCCGA TCCAAAAAAC
1651 AACCCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCGC GCGGCGTGGA
1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

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1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTTGAA TAACACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGCCTAACCG
1901 GTACAGGCAA ACGCTACGGT TACGACTCAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GTTCAATCAA AAATATTGGC
2051 GTTCGACTC TATGCCGGT AATCCGCGC GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2610; ORF 761.a>:

```

a761.pep
1  MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
51  KGYINYDEAA VTRNGQLIKE TPQTIOTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSX YANFKQSRNI GTVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYDFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAQQTQ DNKTLSSNLT
351 NGDYTIGREE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFLVGGRYDK YTFENSENKL
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFAFYGG RGGYLSIDTL
501 SSAVENADPE YTRQYETGVK SSWLDDRLLT TLSAYQIERF NIRYRPPDPK
551 NPYYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGSIGVMOA KVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YDSRNKEVTT
651 LPGAARVDAM LGWNHKNVNV TFAANLFNQ KYWRSDSMPG NPRGYTARVN
701 YRF*

```

m761 / a761 99.6% identity in 703 aa overlap

	10	20	30	40	50	60
m761.pep	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYINYDEAA					
a761	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYINYDEAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m761.pep	VTRNGQLIKETPQTIOTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
a761	VTRNGQLIKETPQTIOTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m761.pep	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRTNGGGVINMVSXYANFKQSRNI					
a761	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRTNGGGVINMVSXYANFKQSRNI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m761.pep	GAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPSITVKLDNG					
a761	GTVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPSITVKLDNG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m761.pep	LKWTGQYTYDNVERTPDRSPKSVYDFGLPYRMGFAHRNDFVKDKLQVWRSLEYAFND					
a761	LKWTGQYTYDNVERTPDRSPKSVYDFGLPYRMGFAHRNDFVKDKLQVWRSLEYAFND					
	250	260	270	280	290	300
	310	320	330	340	350	360
m761.pep	KWRAQWQLAHRRTAAQDFDHFYAGSENGNLIKRNIAWQQTDNKTLSSNLTNGDYTIGREE					
a761	KWRAQWQLAHRRTAAQDFDHFYAGSENGNLIKRNIAWQQTDNKTLSSNLTNGDYTIGREE					
	310	320	330	340	350	360
	370	380	390	400	410	420

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```

m761.pep      NHLTVGMDYSREHRNPTLGFSASFASINPYDRASWPASGRQLPILTQNRHKADSYGIFV
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a761          NHLTVGMDYSREHRNPTLGFSASFASINPYDRASWPASGRQLPILTQNRHKADSYGIFV
               370      380      390      400      410      420

               430      440      450      460      470      480
m761.pep      QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a761          QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
               430      440      450      460      470      480

               490      500      510      520      530      540
m761.pep      YNKGFPYGGGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDRLSTTLLSAYQIERF
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a761          YNKGFPYGGGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDRLSTTLLSAYQIERF
               490      500      510      520      530      540

               550      560      570      580      590      600
m761.pep      NIRYRPDPKNNPYIYAVSGKHSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a761          NIRYRPDPKNNPYIYAVSGKHSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
               550      560      570      580      590      600

               610      620      630      640      650      660
m761.pep      RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYSRNKEVTTLPGFARVDAM
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a761          RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYDSRNKEVTTLPGFARVDAM
               610      620      630      640      650      660

               670      680      690      700
m761.pep      LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNERGYTARVNYRFX
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a761          LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNERGYTARVNYRFX
               670      680      690      700

g762.seq Not yet found
g762.pep Not yet found

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2611>:

```

m762.seq
1  ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTTTTAC GATAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT
301 AGTTTTATGG ACTTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTCTT
401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2612; ORF 762>:

```

m762.pep
1  MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT
51  LLLFIENFV TKSIYMAIIY PILYFTTIKK YYPYSRKVII LLSLALSIYF
101 SEMDFYFFSI YSDNLSYETE PLHLIPIII NFFSLLVSNF ILSFINK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2613>:

```

a762.seq
1  ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTTTTAC GATAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT

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1240

301 AGTTTATGG ACTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
 351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTTTCT
 401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

This corresponds to the amino acid sequence <SEQ ID 2614; ORF 762.a>:

a762.pep
 1 MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT
 51 LFLLFIFNFV TKSIYMAIIY PLYFFTIKK YYPYSRKVII LLSLALSIYF
 101 SFMDYFFFSI YSDNLSYETE PLHLYIPIII NFFSLLVSNF ILSFINK*

m762 / a762 100.0% identity in 147 aa overlap

	10	20	30	40	50	60
m762.pep	MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
a762	MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m762.pep	TKSIYMAIIYPILYFFTIKKYYPYSRKVIIILLSLALSIYFSFMDYFFFSIYSDNLSYETE					
a762	TKSIYMAIIYPILYFFTIKKYYPYSRKVIIILLSLALSIYFSFMDYFFFSIYSDNLSYETE					
	70	80	90	100	110	120
	130	140				
m762.pep	PLHLYIPIIIINFFSLLVSNFILSFINKX					
a762	PLHLYIPIIIINFFSLLVSNFILSFINKX					
	130	140				

g763.seq not yet found

g763.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2615>:

m763.seq
 1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTCCCGTTTG
 51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
 101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTGCCACTA
 151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGC
 201 GCGCGAGCAA CATTGCGCTG ATTTTCAAGC GTCCCATAC CAGCGTGATG
 251 CAGTGCAGCG ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCCATGTA
 301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATT CTCCACCCG
 351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
 401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
 451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
 501 TTATTTCAAC GTTTTACTCA GCGAGACAC CGTTGCCGCC CATGCGGCGG
 551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
 601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA
 651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
 701 AAAACCAAGT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC
 751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA
 801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
 851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
 901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
 951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAG
 1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTTATC CGGCGGAGAA
 1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC
 1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
 1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT
 1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
 1251 CGGCATCCGC AACCAGGCTG AAGTAATACG GGCGCGCGAG GAAGTCGCCC
 1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
 1351 TTGCGCTTGG TGAAAGAGAG CGGTTAGGG TTGGAACCG TATTTCGCGA
 1401 ATAA

1241

This corresponds to the amino acid sequence <SEQ ID 2616; ORF 763>:

```
m763.pep
1  MTLNLNLMIMO DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQO HSADFQASHY QRDVAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMOQLAL OSSGOALRAA
301 QNSRYPTVSA HVGYNQNNLYT SSAQNNDYHY RGKGMVGVQ LNLPLYTGGE
351 LSGKIHEAEA QYGAAEAQLT ATERHIKLA V RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2617>:

```
a763.seq
1  ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
51  CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTTCAC CTTGCCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GGCGCAGCAA CATTCGGCTG ATTTTCAAGC GTCCCATTA CAGCGTGATG
251 CAGTGCAGCG ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATT TTTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGCGCG
551 AAAAAGAGGC TTATGCCCGC CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA
651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
701 AAAACCAAGT GAACGACTAC ACCGGCCTGG ACAGCAAACA AATCGAGGCC
751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCAAGC TGGAACGTTA
801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGCGAGCA
901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC
1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
1151 ATACCGAAAC CGGTCCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT
1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GGCGCGGCG AGAGTCGCCC
1301 AAGCAGAAAC GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
1351 TTGCGCTTGG TGAAAGAGAG CGGTTAGGG TTGGAAACGG TATTTGCGGA
1401 ATAA
```

This corresponds to the amino acid sequence <SEQ ID 2618; ORF 763.a>:

```
a763.pep
1  MTLNLNLMIMO DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQO HSADFQASHY QRDVAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TGLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMOQLAL OSSGOALRAA
301 QNSRYPTVSA HVGYNQNNLYT SSAQNNDYHY RGKGMVGVQ LNLPLYTGGE
351 LSGKIHEAEA QYGAAEAQLT ATERHIKLA V RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*
```

m763 / a763 99.8% identity in 467 aa overlap

```

          10      20      30      40      50      60
m763.pep  MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
          |||||
a763      MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
          10      20      30      40      50      60
```

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m763.pep	70	80	90	100	110	120
	LPEAWRAAQHSADFQASHYQRDAVRARQQQAKAFLPHVSANASYQRQP	PSISSTRETQ				
a763	LPEAWRAAQHSADFQASHYQRDAVRARQQQAKAFLPHVSANASYQRQP	PSISSTRETQ				
m763.pep	130	140	150	160	170	180
	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLKVAESYFNVLLSRD	TVAA				
a763	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLKVAESYFNVLLSRD	TVAA				
m763.pep	190	200	210	220	230	240
	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAQEI	IAVLAEKQTYENQLNDY				
a763	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAQEI	IAVLAEKQTYENQLNDY				
m763.pep	250	260	270	280	290	300
	TGLDSKQIEAIDTANLLARYLPKLERYSLDEWQRIALSNNHEYRMQQLALQSSGQALRAA					
a763	TGLDSKQIEAIDTANLLARYLPKLERYSLDEWQRIALSNNHEYRMQQLALQSSGQALRAA					
m763.pep	310	320	330	340	350	360
	QNSRYPTVSAHVGYNQNLTYSSAQNNDYHYRGKGM	SVGVQLNPL	PLYTG	GELSGKIHEAEA		
a763	QNSRYPTVSAHVGYNQNLTYSSAQNNDYHYRGKGM	SVGVQLNPL	PLYTG	GELSGKIHEAEA		
m763.pep	370	380	390	400	410	420
	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAQERVLE	SSRLK	LKSTETG	QQYGIR		
a763	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAQERVLE	SSRLK	LKSTETG	QQYGIR		
m763.pep	430	440	450	460		
	NRLEVIRARCEVAQAEQKLAQARYKFMLAYLRLVKESGLG	LET	VFAEX			
a763	NRLEVIRARCEVAQAEQKLAQARYKFMLAYLRLVKESGLG	LET	VFAEX			

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g764.seq not found yet

g764.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2619>:

m764.seq

```

1   ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCTCGATACA TTACTGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAATT GAAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGCTTTTGT CCCGCGCATT TGGAACCTGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCCTT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCGGGCAA AACGGTGTCT GCGGGGCGCA GCAAAACCAT CCAGCCGCTG
301 GAAACGGCGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CGGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GCGCGAGGAG CAGAAGCTGG TTTGCGTGGG GCGGATCGAG CAGCAGAAAA
701 CAGCAGACTA CCGCCGTTTG CGGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAG
801 TACGCGCGGT CAGATGAGGC AGATTCAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGCT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CCGCAGCAGC TGATGACAAT ACAGTCGCTT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCTACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGATTGC GCCCGATGAC GACAAAATGG ACGTGGAAAT
1101 TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGCTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAAGCAGT GAATCTGACG GCGGGCATGA ATGTCACGGC GGAGATTAAA
1351 ACGGGTAAAC GCGGGTGCT GATTATCTG TTAAGCCCGC TGCAAAACCA
1401 ATTGGACGAA AGCTTTAGGG AGCGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2620; ORF 764>:

m764.pep

```

1   MFFSALKSFL SRYITVWRNV WAVRDQLKPP KRTAEQAFI PAHLELTDTF
51  VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPI
101 ETAVVKAVHV RDGOHVKQGE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSALRGHQ AELQSAKAQE QKLVSVAIE QKKTADYRRL RADNFISEHA
251 FLEQSKSVS NWNLESTRG QMRQIAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVIAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVSHDAV SHEQLGLVYT AVVSLDKHTL NIDGKAVNLT AGMNVTAIEIK
451 TGKRRVLDYL LSPLQTKLDE SFRER*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2621>:

a764.seq (partial)

```

1   ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCCCCTGACA TTACCGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAATT GGAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGCTTTTGT CCCGCGCATT TGGAACCTGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCCTT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCGGGCAA AACGGTGTCT GCGGGGCGCA GCAAAACCAT CCAGCCGCTG
301 GAAACGGTGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGC3GC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CGGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GCGCGAGGAG CAGAAGCTGG TTTGCGTGGG GCGGATCGAG CAGCAGAAAA

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```

701 CAGCAGACTA CCGCCGTTTG CGGGCCGACA ATTTTATTTC GGAACATGCG
751 TTTTGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAG
801 TACGCGCGGT CAGATGAGGC AGATTGAGC GGCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACGCGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGCCACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGGTTGC GCCCGATGAC GACAAAATGG ACGTGGAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAA

```

This corresponds to the amino acid sequence <SEQ ID 2622; ORF 764.a>:

```

a764.pep (partial)
1 MFFSALKSFL SRYITVWRNV WAVRDQLEPP KRTAEEOAFL PAHLELTDTP
51 VSAAPKWAAR FIMAFALLAL LSWFSGKIDI VAAASGKTVS GGRSKTIQPL
101 ETVVVKAVHV RDGQHVKGGE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSALRGHQ AELQSAKAE QKLVSVAIE QOKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVVAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVSHDAV SHEQLGLVYT AVVSLDKHTL NIDGK

```

m764 / a764 99.3% identity in 435 aa overlap

m764.pep	10	20	30	40	50	60
	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEEOAFLPAHLELTDTPVSAAPKWAAR					
a764	10	20	30	40	50	60
	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEEOAFLPAHLELTDTPVSAAPKWAAR					
m764.pep	70	80	90	100	110	120
	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVVKAVHVRDQHVKGGE					
a764	70	80	90	100	110	120
	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETVVVKAVHVRDQHVKGGE					
m764.pep	130	140	150	160	170	180
	TLAELEAVGTSDSDVVQSEQAALQAAQLSKLRYEAVLAALESRTVPHIDMAQARSLGLSDAD					
a764	130	140	150	160	170	180
	TLAELEAVGTSDSDVVQSEQAALQAAQLSKLRYEAVLAALESRTVPHIDMAQARSLGLSDAD					
m764.pep	190	200	210	220	230	240
	VQSAQVLAQHQQYQAWAAQDAQLQSALRGHQAEQKLVSVAIEQQOKTADYRRL					
a764	190	200	210	220	230	240
	VQSAQVLAQHQQYQAWAAQDAQLQSALRGHQAEQKLVSVAIEQQOKTADYRRL					
m764.pep	250	260	270	280	290	300
	RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIAAIAQAEQNRVLNTQNLKRDTLDA					
a764	250	260	270	280	290	300
	RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIAAIAQAEQNRVLNTQNLKRDTLDA					
m764.pep	310	320	330	340	350	360
	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVIAPDD					
a764	310	320	330	340	350	360
	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVVAPDD					
m764.pep	370	380	390	400	410	420
	DKMDVEVLVLNKDIGFVEQGQDAVVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT					

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|||||
a764      DKMDVEVLVLNKGDIGVEQGDVAVVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT
              370      380      390      400      410      420

              430      440      450      460      470
m764.pep  AVVSLDKHTLNIDGKAVNLTAGMNVTAIEIKTGKRRVLDYLLSPLQTKLDESFRERX
|||||
a764      AVVSLDKHTLNIDGK
              430

```

g765.seq not yet found

g765.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2623>:

```

m765.seq
1  ATGTTAAGAT GCCGTCCGAA ATCCGTTTIG GATTGAGACG GCATTTTTTT
51 GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCTTTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGTGCGG TCGTTGCTGA TGTTACGGT CATGATTCCG CCACAATGAA
201 CGCTGCGGCT GCCAAAGATT ATATGAAAC GGTGAGTTA AACAACTCTG
251 CCGGCAATGT CGATAACCACA TCCAGAACAG CCCGCAGGGT GCAGGCAGTA
301 TTTCGACGTA TGCTGCCTTA TGCCGATGCG GCAAATAATA CCAGCCATAA
351 GTTGTACTGG AAAATGACGG TTTTCAAAAA CGATGAGCTG AACCGGTGGG
401 CAATGCCCGG TGGAAAAATG GCGTTTTATA CGGGGATAGT CGACAACTC
451 AAGCTGACCG ATGACGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 CGCCTGCGAT GAACACGGTA AAAATAAGGT CGGGCAGCAA ATCTTGACCA
551 ATACGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAT
601 ACTAATCCGG AATTGGTCGG ATTGGGTATG GATATTTTGG GGACGTACGG
651 TCTTACCTTG CCTTATAGCC GCAGCTTGGA AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCGGC CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAACACGAC CAAACCGGCT TTATTTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTGTTGCC GACCGTTATG CCGGTTTATG AGCAAAGTGT CAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2624; ORF 765>:

```

m765.pep
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKYEI SFLPSFKRIL CLSAVISVLG
51 ACAVVADVYG HDSATMNAAA AKDYMKTVEL NKSAGNVDTT SRTARRVQAV
101 FRRMLPYADA ANNTSHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTDEIAAI MGHEMTHALH EHGKNKVQQ ILNTAAQIG TQIILDKPD
201 TNPELVGLGM DILGTYGLTL PYSRSLEEEA DEGGMLMAQ AGYHPAAVR
251 VWEKMNQEND QNGFIYAITS THPTNNARIE NLKRLLTVM PVYEQSVRNK
301 GRVNRKRRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2625>:

```

a765.seq
1  ATGTTAAGAT GCCGTCCGAA ATCCGTTTIG GATTGAGACG GCATTTTTTT
51 GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCTTTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGTACGG TCGTTGCTGA TGTTACGGT CAGGATTCCG CCACAATGAA
201 TGCTGCGGCT GCCGAAGATT ATATGAAAC GGTGAGTTG AACAACTCTG
251 CCGGCAATGT CGATACTACA TCCAAAACAG CCCGTAGGGT GCAGGCAGTA
301 TTTCGACGTA TGTTGCCTTA TGCCGATGCG GCAAATAATA CCGGCCATAA
351 GTTGTACTGG AAAATGACGG TTTTCAAAAA CGATGAGCTG AACCGGTGGG
401 CAATGCCCGG CGGAAAAATG GCGTTTTATA CGGGGATAGT CGATAAACTT
451 AAGCTGACCG ATGGCGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 TGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGAAA ATCTTGACTA
551 ATATGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAC
601 ACTAATCCGG AATTGGTCGG ATTGGGTATG GATATTTTGG GGATGTACGG
651 CATTACCTTG CCTTATAGCC GCAGCTTGGA AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCAGC CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAACACGAC CAAACCGGCT TTATTTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTGTTGCC GACCGTTATG CCGGTTTATG AGCACAGTGT TAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2626; ORF 765.a>:

```

a765.pep
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKYEI SFLPSFKRIL CLSAVISVLG

```

1246

```

51  ACTVVADVYG QDSATMNAAA AEDYMKTVEL NKSAGNVDTT SKTARRVQAV
101 FRRMLPYADA ANNTGCHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTGGEIAAI MGHETHALH EHGKKNVQK ILTNMAAQIG TQIILDKKPD
201 TNPELVGLGM DILGMYGITL PYSRSL EEEA DEGGMMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAIT THPTNNARIE NLKRLLPVMPVYEHVSRNK
301 GRVKNKRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 765 shows 96.18% identity over a 309 aa overlap with a predicted ORF (ORF 765) from *N. meningitidis*:

m765 / a765 96.1% identity in 309 aa overlap

```

              10      20      30      40      50      60
m765.pep    MLRCRPKSVLSDSGIFLKFNLRSKPKYEISFLPSFKRILCLSAVISVLGACAVVADVYG
              |||
a765         MLRCRPKSVLSDSGIFLKFNLRSKPKYEISFLPSFKRILCLSAVISVLGACTVVADVYG
              10      20      30      40      50      60

              70      80      90      100     110     120
m765.pep    HDSATMNAAAADYMKTVELNKSAGNVDTTSTARRVQAVFRRMLPYADAANNTSHKFDW
              |||
a765         QDSATMNAAAADYMKTVELNKSAGNVDTTSTARRVQAVFRRMLPYADAANNTGHKFDW
              70      80      90      100     110     120

              130     140     150     160     170     180
m765.pep    KMTVFKNDELNAWAMPGGKMAFYTGIVDKLKLTDDEIAAIMGHEMTHALHEHGKKNVQK
              |||
a765         KMTVFKNDELNAWAMPGGKMAFYTGIVDKLKLTDGEIAAIMGHEMTHALHEHGKKNVQK
              130     140     150     160     170     180

              190     200     210     220     230     240
m765.pep    ILTNAAQIGTQIILDKKPDNPELVGLGMDILGTYGLTPYSRSL EEEA DEGGMMLMAQ
              |||
a765         ILTNMAAQIGTQIILDKKPDNPELVGLGMDILGMYGITLPYSRSL EEEA DEGGMMLMAQ
              190     200     210     220     230     240

              250     260     270     280     290     300
m765.pep    AGYHPAAAVRVWEKMNQENDQNGFIYAITSTHPTNNARIENLKRLLPVMPVYEQSVRNK
              |||
a765         AGYHPAAAVRVWEKMNQENDQNGFIYAITSTHPTNNARIENLKRLLPVMPVYEHVSRNK
              250     260     270     280     290     300

              310
m765.pep    GRVKNKRRRX
              |||
a765         GRVKNKRRRX
              310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2627>:

```

g767.seq
1  ATSAAGTTTA AACATCTGTI GCCGCTGCTG CTGTCGGCAG TGTGTGCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCTCTCA AGAACAGCCG GGAAAAATTG AGGTTTGGGA ATTTTTCGGC
151 TATTTTTCGCG TACATTGCCA TCATTTCGAT CCTTTGTAT TGAAGCTGGG
201 CAAGGCATTG CCGTCTGATA CTTATCTGCG GACGGAGCAC GTGGTCTGGC
251 GGCTTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCGGT CAAGCTGTGCG
301 GGTTTGAAAT ATCAGGCAAA CTCTGCTGTG TTTAAAGCAG TTTACGAACA
351 AAAAAATCCGT TTGGAAAAACA GGGCTGTTGC CGGGAATGG GCTTTATCTC
401 AAAAAAGGTTT TGACGGCAAA AAAGTATGAT GCGCTATGA TCCCCCGGAA
451 GCTGCGCGCCG TCGCATTAAT AATGCAGAAA CTGACGGAAC AATACGGTAT
501 TGACAGCAGC CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGATGGCGGC GTTCTACGA TTAAGAATT GGTGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGCCCTCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2628; ORF 767.ng>:

```

g767.pep
1  MKFKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQP GKIEVLEFFG
51  YFCVHCHHFD PLLLLKGLAL PSDTYLRTEH VVWRPEMLGL ARMAAAVKLS

```

m767.seq

1	ATGAAGCTCA	AACATCTGTT	GCCGCTGCTG	CTGTCGGCAG	TGTTGTCCGC
51	GCAGGCATAT	GCCCTGACGG	AAGGGGAAGA	CTATCTTTGTG	TTGGAATAAC
101	CCATTCTCTCA	AGAACAGTCG	GCATAAAATTG	AGGTTTGTGA	ATTTTTCGGC
151	TATTTCTGCG	TAGACTTGCCA	TGATTTGCAT	CGTTTGTATT	TGAAACTGGG
201	CAAGGCATTG	CCGTCTGATG	CCTATTTGAG	CGAGGAGCAG	GTGGTCTGGC
251	AGCCTGAAAT	GTCGGGTTTG	CGTAGGATAG	GCGCTGCCCT	CAATTTGTGCG
301	GGTTTGAAT	ATCAGGCAAA	CCCTGCTGTG	TTTAAAGCAG	TTTACGAACA
351	AAAAATCCGT	TTGAAAAACA	GGTCGGTTGC	CGGAAATATG	GCTTTGTCTC
401	AAAAAGCCCT	TGACGGCAAA	AAACTGATGC	GCGCTATATG	TTCGCCCGAA
451	GCTGCCGCGC	CCGCATTAAA	AATCGACAAA	CTGACGGAA	AATACCGCAT
501	CGACAGCAGC	CCGACCGTTA	TTGTCGGCGG	AAAATACCGC	GTTATCTTCA
551	ATAACGGCTT	TGACGGCGCG	GTTCAATACGA	TTAAAGATAT	GGTGTGCCAAA
601	GTCAAGGAAG	ATGCAAGGCG	TCAGACCCCT	GCTGTACAGA	AATAG

m767.pwp

1	MKLKHLPL	LSAIVLSAQAY	ALTEGEDYLV	LDKPIPEQES	GKIEVLEFFG
51	YFCVCHHFD	PLLLKLKGAL	PSDAYLRTEH	VVNOPEMLGL	ARMAAAVNLS
101	GLKYQANPAV	FKAVYEQKIR	LENRSVAGKV	ALSQKGFDBG	KLMRAYDSPE
151	AAAAALKMQK	LTVQYRIDST	PTVIVGGKYE	VIFNNGFDGG	VHTIKELVAK
201	VREERKROTP	AEQK*			

Homology with a predicted ORF from *N. gonorrhoeae*

m767/g767 95.8% identity in 214 aa overlap

	10	20	30	40	50	60
g767.pep	MKFKHLLPLLLSAVLSAQAYALTEGEDYLVLDKPIPQEQPGKIEVLEFFGYFCVHCHHFD					
m767	MLKLHLLPLLLSAVLSAQAYALTEGEDYLVLDKPIPQEQSGKIEVLEFFGYFCVHCHHFD					
	10	20	30	40	50	60
g767.pep	PLLLKLGKALPSDTYLRTEHVVRPEMLGLARMAAAVKLSGLKYQANSVAFKAVYEQKIR					
m767	PLLLKLGKALPSDAYLRTEHVVRQPEMLGLARMAAAVNLKGLKYQANPAVFKAVYEQKIR					
	70	80	90	100	110	120
g767.pep	LENRAVAGKQWALSQKGFQGGKLMRAYDSPEAAAAVKMQKLTEQYRIDSTPTVIVGGKYR					
m767	LENRSVAGKQWALSQKGFQGGKLMPAYDSPEAAAAVKMQKLTEQYRIDSTPTVIVGGKYR					
	130	140	150	160	170	180
g767.pep	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKXX					
m767	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKXX					
	190	200	210			

a767.seq

1	ATGAAGCTCA	AACATCTGTT	GCCGCTGCTG	CTGTGCGCAG	TGTTGTCCGC
51	CGAGGCATAT	GCCTCTACGG	AAGGGAAGA	CTATCTTGTG	TATGATAAAC
101	CCATTCTCTA	AAACAGCTGC	GGCAAAAATT	AGGTTTGGTA	TTTTTCCGCG
151	TATTTCGCG	TACATTGCCA	TCATTTCTGAT	CCTTTGTTAT	TGAAATTGGG
201	CAAGGCATTC	CGCTCTGATG	CCATTTTAAAG	GACGCGACAC	TGGTCTCGGC
251	AGCCTTGAAT	CGCTGGCTTG	CGAAGAAATG	CTGCTCCGCT	CAAGCTGTCA
301	GCTTTGAAT	ATCAGGCAAA	CCCTGCCGTG	TTTAAAGCAG	TTTACGAACA
351	AAAAATCCGT	TGGAAACAAA	GGTCGGTTGC	CGCAAAATAG	GCTTTGCTCT
401	AAAAATCGCT	TGACGGCAAA	AAACTGATTT	CGGCAATTCG	CTCTCCGCGC

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451 GCAGCGGCTG CTGCATCAA AATGCAGCAA TTGACGGAAC AGTACCGCAT
501 CGACAGTACG CCGACCGTTG TCGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGACGGCGGT GTTCATACGA TTAAGAATT GGTGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2632; ORF 767.a>:

```

a767.pep
  1 MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQKQS GKIEVLEFFG
  51 YFCVHCHHFD PLLLKLKAL PSDAYLRTEH VVWQPEMLGL ARMAAAVKLS
 101 GLKYQANPAV FKAVYEOKIR LENRVAEKW ALSQKGFQK KLMRAYDSPA
 151 AAAAASKMQQ LTEQYRIDST PTVVVGKYYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 767 shows 96.7% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. meningitidis*:

m767/a767 96.7% identity in 214 aa overlap

	10	20	30	40	50	60
a767.pep	MKLKHLLPLL	LSAVLSAQAY	ALTEGEDYLV	LDKPIPQKQS	GKIEVLEFFG	YFCVHCHHFD
m767	MKLKHLLPLL	LSAVLSAQAY	ALTEGEDYLV	LDKPIPQKQS	GKIEVLEFFG	YFCVHCHHFD
	70	80	90	100	110	120
a767.pep	PLLLKLKALP	SDAYLRTEH	VVWQPEMLGL	ARMAAAVKLS	GKLYQANPAV	FKAVYEOKIR
m767	PLLLKLKALP	SDAYLRTEH	VVWQPEMLGL	ARMAAAVKLS	GKLYQANPAV	FKAVYEOKIR
	130	140	150	160	170	180
a767.pep	LENRVAEKWALS	QKGFQKLMRAY	DSAAAAASKM	QOLTEQYRID	STPTVVVGK	YYR
m767	LENRVAEKWALS	QKGFQKLMRAY	DSAAAAASKM	QOLTEQYRID	STPTVVVGK	YYR
	190	200	210			
a767.pep	VIFNNGFDGGV	VHTIKELVAK	VREERKRQTP	AVQKX		
m767	VIFNNGFDGGV	VHTIKELVAK	VREERKRQTP	AVQKX		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2633>:

```

g768.seq
  1 ATGAATATCA AACAAATGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
  51 TGCCACGCAG GCAGCCCGCG AAAAACCCTG ATCCGCCGCC CAAACCGCGC
 101 AACATTCAGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
 151 GGTCAATTGC ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCCG
 201 CATATACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC
 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
 301 TATACAAATG TTGCCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAGG
 351 GATGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2634; ORF 768.ng>:

```

g768.pep
  1 MNIKQLITAA LIASAAFATQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE
  51 GHLHNAVNI PVDQIVRRIE AAPDKDTPVN LYCRSGRAE AALQELKKAG
 101 YTNVANHG GY EDLLKKGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2635>:

```

m768.seq
  1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
  51 TGCCACGCAG GCAGCCCGCG AAAAACCCTG ATCCGCCGCC CAAACCGCGC
 101 AACATCCGGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
 151 GGCATTTCG ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCCG
 201 CATACACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC

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251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
 301 TATACAAATC TTGCCAATCA CGCGCGTTAT GAAGACCTGC TCAAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2636; ORF 768>:

m768.pep

1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHPAVWI DVRSEQEFSE
 51 GHLHNAVNI PVDQIVRRIHE AAPDKDTPVN LYCRSGRRAE AALQELKEAG
 101 YTNVANHGGY EDLLKKG MK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 768 shows 96.6% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. gonorrhoeae*

m768/g768 96.6% identity in 119 aa overlap

	10	20	30	40	50	60
g768.pep	MNIKQLITAA	LIASAAFAAQ	AAPQKPVSA	QTAQHSVWID	DVRSEQEFSE	GHLHNAVNI P
m768	MNIKHLITAA	LIASAAFAAQ	AAPQKPVSA	QTAQHPAVWI	DVRSEQEFSE	GHLHNAVNI P
	10	20	30	40	50	60
	70	80	90	100	110	120
g768.pep	V	DQIVRRIE	EAAPDKDTP	VNLYCRSGRR	AEALQELK	KAGYTNVANHGGYEDLLKKG MKX
m768	V	DQIVRRIE	EAAPDKDTP	VNLYCRSGRR	AEALQELK	KAGYTNVANHGGYEDLLKKG MKX
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2637>:

a768.seq

1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
 51 TGCCGCGCAG GCAGCCCCGC AAAAACCCTG ATCCGCCGCC CAAACCCGCG
 101 AACATTCAGC CGTTTGGATC GATGTCCGCA GCGAACAGGA ATTTAGCGAA
 151 GGTCAATTGC ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCCG
 201 CATAACAGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC
 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAACTGAA AAAAGCAGGC
 301 TATACGAATG TTGCCAATCA CGCGCGTTAT GAAGACCTGC TCAAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2638; ORF 768.a>:

a768.pep

1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSVWIDVRSEQEFSE
 51 GHLHNAVNI PVDQIVRRIHE AAPDKDTPVN LYCRSGRRAE AALQELKKG
 101 YTNVANHGGY EDLLKKG MK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 768 shows 99.2% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. meningitidis*:

m768/a768 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
a768.pep	MNIKHLITAA	LIASAAFAAQ	AAPQKPVSA	QTAQHSVWID	DVRSEQEFSE	GHLHNAVNI P
m768	MNIKHLITAA	LIASAAFAAQ	AAPQKPVSA	QTAQHPAVWI	DVRSEQEFSE	GHLHNAVNI P
	10	20	30	40	50	60
	70	80	90	100	110	120
a768.pep	V	DQIVRRIE	EAAPDKDTP	VNLYCRSGRR	AEALQELK	KAGYTNVANHGGYEDLLKKG MKX
m768	V	DQIVRRIE	EAAPDKDTP	VNLYCRSGRR	AEALQELK	KAGYTNVANHGGYEDLLKKG MKX
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2639>:

g769.seq

```

1   TTGATAATGG TTATTTTSTA TTTTATTTT TGTGGGAAGA CATTTATGCC
51  TGCACGAAAC AGATGGATGC TGCTGCCTTT ATTGGCAAGC GCGGCATACG
101 CCGAAGaAAC ACCgtgCGAA CCGGATTGA GAAGCCGTCC CGAGTTCAGG
151 CTTCATGAAG CGGAGGTCAA ACCGATCGAC AGGAGAGAAG TACCGGGGCA
201 GGTGCGGGAA AAAGGAAAAG TTTTGCAGGT TGACGgcGAA ACCCTGCTGA
251 AAAATCCCGA ATTGTTGTCG CGTGCCATGT ATTCCGCAGT GGTCTCAAAC
301 AATATTGCCG GTATCCGCGT GATTTTGCCG ATTTACCTAC AACAGGCGCG
351 GCAGGATAAG ATGTTGGCAC TTTATGCACA AGGGATTTTG GCGCAGGCAG
401 AGGGCAGGGT GAAGGAGGCG GTTTCCTATT ACCGGGAATT GATTGCCGCC
451 CAACCCGACG CGCCCGCCGT CCGTATGCGT TTGGCGGCGG CATTTGTTGA
501 AGACAGGCAG AACGAGGCGG CGGCAGACCA GTTCGACCCG CTGAAACAG
551 AAGATCTGCC GCCGAGCTT ATGGAGCAGG TCGAGCTGTA CCGCAAGGCA
601 TTGCGCGAAC GCGATGCGTG GAAGSTAAAC GCGGGTTTCA GCGTTACCCG
651 CGAACACAAT ATCAACCAAG CCCCNAACA GCAGCAGTAC GGCAATTGGA
701 CTTTCCCGAA ACAGGTGGAC GGCAGGCAG TCAATTACCC GTTCGGCGCG
751 GTGAAATAAT GGTGCTGTA AAACGGCTGG TACACGACGG CGGGCGGCGA
801 CGTGTCGCGG AGGGTTTATC CGGGGAATAA GAAATCAAC GATATGACGG
851 CAGGTGTTTC CGGCGGCATC GGTTTTGCCG ACCGGCGTAA AGATGTCGGG
901 CTGGCAGTGT TCCACGAACG CCGCACCTAC GGCAACGACG CTTATTCTTA
951 CGCCAACGGC GCACGCCTTT ATTTCAACCG TTGGCAAAAC CCGAGATGGC
1001 AAACGCTGTC TTCGGCGGAG TGGGGGCGTT TGAAGAATAC GCGCCGGCGG
1051 CTTTCCGACA ATACCCATTT GCAAATTTCC AATTGCTGCG TGTTTTACCG
1101 GAATGCGCGC CAATATTGGA CGGGCGGTTT GGATTTTAC CCGCAGCGCA
1151 ACCCCGCCGA CCGTGGCGAC AATTTCAACC GTTACGGCCT GCGCTTTGCC
1201 TGGGGGCGAG AATGGGGCGG CAGCGGCGTG TCTTCGCTGT TCGGCTCGG
1251 CGTGGCGAAA CGGCATTATG AAAAACCCGG CTCTTCAGC AGTTTAAAG
1301 GGGAAAGGCG CAGGGATAAA GAATCGGACA CATCTTGAG CCTTTGGCAC
1351 CGGGCATTGC ATTTCAAAGG CATCACGCGC CGCCTGACGC TGTGCGACCG
1401 CGAAACGTGG AGCAACGATG TGTTAAACGA ATACGAGAAA AACAGGGCGT
1451 TTGTCGAGTT TAACAAACG TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2640; ORF 769.ng>:

g769.pep

```

1   LIMVIFYFYF CGRTFMPARN RMMLPLLAS AAYAEETPCE PDLRSRPEFR
51  LHEAEVKPID REKVPQVRE KGKVLQVDGE TLLKNPELLS RAMYSAVVSN
101 NIAGIRVILP IYLQARQDK MLALYAQGIL AQAEGRVKEA VSHYRELIAA
151 QPDAPAVRMR LAAALFEDRQ NEAAADQFDR LKTEDLPPQL MEQVELYRKA
201 LREERDAWKVN GGFSVTREHN INQAPKQQQY GNWTFPKQVD GTAVNYRFGA
251 EKKWSLKNWV YTTAGGDVSG RVYPGNKKFN DMTAGVSGGI GFADRRKDVG
301 LAVFHERRTY GNDAYSANG ARLYFNRWQT PRWQTLSSAE WGRLLKNTRRA
351 RSDNTHLQIS NSLVFYRNAR QYWTGGLDFY RERNPADRGD RERNRYGLRFA
401 WQGEWGGSLG SSLFRLGVAK RHYEKPFFFS SPKGERRRDK ESDTSLSLWH
451 RALHFKGITP RLTLSHRETW SNDVFNEYEK NRAFVEFNKT F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2641>:

m769.seq

```

1   TTGATAATGG TTATTTTSTA TTTTGTGGG AAGACATTTA TGCCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAARACACC GCGCGAACCG GATTTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC GATCGACAGG GAGAAGGTGC CGGGGCGAGT
201 GCGGGAAGAA GGAAGAGTTT TGCAGATTGA CGCGAAGACC CTGCTGAAAA
251 ATCCCGAATT GTTGTCCTCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCGGGTA TCCGCGTTAT TTGCGCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCATTACC GGAATTGAT TGCCGCCCAA
451 CCCGACGCGC CGGCGGTCG TATGCGTTTG CGGGCAGCAT TGTTTGAAAA
501 CASGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCCTG AAGGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTGC AGCTGTACCG CAAGGCATTG
601 CGCGAACGCG ATGCGTGGAA GGTAAATGCG GGCTTCACGC TCACCCGCGA
651 ACACAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAATGGT CGCTGAAAA CGGCTGGTAC ACGACGGCGG GCGGCGACGT
801 GTCCGGCAGG GTTTATCCGG GGAATAAGAA ATTTAACGAT ATGACGGCAG
851 CCGTTTCCGG CGGCATCGGT TTGCGCGACC GCGCAAGAGA TGCGGGCTG
901 GCAGTGTTCC ACGAACGCGC CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA CGCCTTTATT TCAACCGTGG GCAACCCCG AAATGGCAAA
1001 CCGTGTCTTC GCGGAGTGG GGGCGTTTGA AGAATACGCG CCGGGCGCGT
1051 TCCGACAATA CCCATTGCA AATTTCCAAT TCGCTGGTGT TTTACCGGAA
1101 TGCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACCGC GAGCGCAACC
1151 CGGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCTGCG CTTTGCCTGG
1201 GGGCAGGAAT GGGGCGGCG CCGCTGTCT TCGCTGTTC GCCTCGGCGC

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1251

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1251 GGCAGAACCG CATTATGAAA AACCCGGCTT TTTACGCGGT TTAAAGGGG
1301 AAAGCCCCAG CGATAAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCGG
1351 GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCGCGA
1401 AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGTTTG
1451 TCGAGTTTAA TAAACGTTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 2642; ORF 769>:

```

m769.pep
  1 LIMVIFYFCG KTFMPARNRW MLLLPILASA AYAETPREP DLRSRPEFRL
 51 HEAEVKPIDR EKVPQVREK GKVLIQDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIAAQ
151 PDAPAVRMRL AAALFENRQN EAAADQFDRL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTRHNI NQAPKRQYQ KWTFFKQVDG TAVNYRLGAE
251 KKWSLKNWY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRTYG NDAYSYTNGA RLYFNRWQTP KWQTLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRYGLRFAW
401 GQEWGSGSLG SLLRLGAAKR HYEKPGFFSG FKGERRRDKE LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDVFNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 769 shows 95.1% identity over a 492 aa overlap with a predicted ORF (ORF 769) from *N. gonorrhoeae*

```

m769/g769 95.1% identity in 492 aa overlap

      10      20      30      40      50      59
g769.pep LIMVIFYFYFCGKTFMPARNRWMLL-PLLASAAYAEETPCEPDLSRPEFRLHEAEVKPI
      |||||  |||||  |||||  |||||  |||||  |||||
m769     LIMVIFY--FCGKTFMPARNRWMLLLPLLASAAYAEETPREPDLSRPEFRLHEAEVKPI
      10      20      30      40      50

      60      70      80      90     100     110     119
g769.pep DREKVPQVREKKGKVLQVDGETLLKNPELLSRAMYSVVSNNIAGIRVILPIYLQQAQQD
      |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769     DREKVPQVREKKGKVLQIDGETLLKNPELLSRAMYSVVSNNIAGIRVILPIYLQQAQQD
      60      70      80      90     100     110

      120     130     140     150     160     170     179
g769.pep KMLALYAQGILAQAEGRVKEAVSHYRELIAAQPDAPAVRMRLAAALFEDRQNEAAADQFD
      |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769     KMLALYAQGILAQADGRVKEAISHYRELIAAQPDAPAVRMRLAAALFENRQNEAAADQFD
      120     130     140     150     160     170

      180     190     200     210     220     230     239
g769.pep RLKTEDLPQOLMEQVELYRKALRERDAWKVNGGFSVTRHNIHQAPKQOQYGNWTFPKQV
      |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769     RLKAENLPPOLMEQVELYRKALRERDAWKVNGGFSVTRHNIHQAPKQOQYGNWTFPKQV
      180     190     200     210     220     230

      240     250     260     270     280     290     299
g769.pep DGTAVNYRFGAEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDV
      |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769     DGTAVNYRLGAEEKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDA
      240     250     260     270     280     290

      300     310     320     330     340     350     359
g769.pep GLAVFHERRTYGNDAISYANGARLYFNRWQTPRWQTLSSAEWGRGLKNTRRARSNDNTHLQI
      |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769     GLAVFHERRTYGNDAISYANGARLYFNRWQTPRWQTLSSAEWGRGLKNTRRARSNDNTHLQI
      300     310     320     330     340     350

      360     370     380     390     400     410     419
g769.pep SNSLVFYRNARQYWTGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGLSLFLGVA
      |||||  |||||  |||||  |||||  |||||  |||||  |||||
m769     SNSLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGLSLFLRLGAA
      360     370     380     390     400     410

      420     430     440     450     460     470     479
g769.pep KRHYEKPFGFFSSFKGERRRDKESDTSLSLWHRALHFKGITPRLTSLSHRETSNDVFNEYE
      |||||  |||||  |||||  |||||  |||||  |||||  |||||

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m769      KRHYEKPGFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYE
          420      430      440      450      460      470

          480      490
g769.pep  KNRAFVEFNKTFX
          |||||
m769      KNRAFVEFNKTFX
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2643>:

```

a769.seq
1  TTGATAATGG TTATTTTITA TTTTGTGGG AAGACATTTA TGCCTGCCAG
51  AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACC GCGCGAACCG GATTTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC AATCGACAGG GAGAAGGTAC CGGGGCAGGT
201 CGGGGAAAAA GGAAAAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GCTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTACC GGAATTGAT TGTCGCCCAA
451 CCCGACGCGC CGCCGCTCCG TATGCGTTG GCGGCGGCAT TGTTTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCTG AAGGCGGAAA
551 ACCTGCCCGC GCAGCTGATG GAGCAGGTG AGCTGTACCG CAAGGCATTG
601 CGCGAACGCG ATGCGTGGAA GGTAAATGGC GGCTTCAGCG TTACCCGCGA
651 ACACAATATC AACCAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGGCGG GCGGCGACGT
801 GTCCGGCAGG GTTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 GCGTTTCCGG CGGCATCGGT TTTGCCGACC GGCCAAAGA TGCCGGGCTG
901 GCAGTGTTC ACGAACGCGC CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA GCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 CGTTGTCTTC GCGGAGTGG GGGCGTTGA AGAATACGCG CCGGCGCGGT
1051 TCCGACAATA CCCATTGCA AATTTCGAAT TCGCTGGTGT TTTACCGGAA
1101 TGCGGCGCAA TATTGGATGG GCGGTTTGA TTTTACCGC GAGCGCAACC
1151 CCGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCCTGCG CTTTGCCTGG
1201 GGGCAGGAAT GGGCGGCGAG CGGCCTGTCT TCGCTGTGTC GCCTCGGCGC
1251 GCGCAACCGG CATTATGAAA AACC CGGCTT TTTACGCGT TTTAAAGGGG
1301 AAAGGCGCAG GGATAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCGG
1351 GCATTGCATT TCAAGGCAT CACGCCGCGC CTGACGTGT CGCACCGCGA
1401 AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAT CGGCGCGTTG
1451 TCGAGTTTAA TAAAACGTTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 2644; ORF 769.a>:

```

a769.pep
1  LIMVIFYFCG KTFMPARNRW MLLPLLASA AYAETPREP DLSRPEFRL
51  HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQDDKM LALYAQGILA QADGRVKEAI SHYRELIVAQ
151 PDAPAVRMRL AAALFENRQN EAAADQFDRL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTREHNI NQAPKRQYQG KWTFFPKQVDG TAVNYRLGAE
251 KKWGLKNQWY TTAGDVSGR VYPGNKKEND MTAGVSGGIG FADRRKDAGL
301 AVFHERRYWG NDAYSYTNGA RLYFNWQTP KWOTLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRVGLRFAW
401 QQEWGGSGLS SLLRLGAAKR HYEKPGFFSG FKGERRRDKE LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDVFNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 769 shows 99.8% identity over a 490 aa overlap with a predicted ORF (ORF 769) from *N. meningitidis*:

```

m769/a769  99.8% identity in 490 aa overlap

          10      20      30      40      50      60
a769.pep  LIMVIFYFCGKTFMPARNRWMLLLPLLASAAYAETPREPDLSRPEFRLHEAEVKPIDR
          |||||
m769      LIMVIFYFCGKTFMPARNRWMLLLPLLASAAYAETPREPDLSRPEFRLHEAEVKPIDR
          10      20      30      40      50      60

          70      80      90      100     110     120
a769.pep  EKVPQVREK GKVLQIDGETLLKNPELLSFAMYSVVSNNIAGIRVILPIYLQQAQDDKM

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m769					
	EKVP	GGVREK	GKVLQID	GETLLKN	PELLSRAMYS
	70	80	90	100	110
	120				
a769.pep	130	140	150	160	170
	LALYA	OGILAQ	ADGRVKEA	ISHYRELI	VAQPDAPAV
m769	130	140	150	160	170
	LALYA	OGILAQ	ADGRVKEA	ISHYRELI	VAQPDAPAV
a769.pep	190	200	210	220	230
	KAENL	PPQLMEQ	VELYRKAL	RERCAWK	VNGGFSVT
m769	190	200	210	220	230
	KAENL	PPQLMEQ	VELYRKAL	RERDAWK	VNGGFSVT
a769.pep	250	260	270	280	290
	TAVNY	RLGAEKK	WSLKN	GWYTTAG	GDVSGRV
m769	250	260	270	280	290
	TAVNY	RLGAEKK	WSLKN	GWYTTAG	GDVSGRV
a769.pep	310	320	330	340	350
	AVFH	ERTYGN	DAYS	SYTNGAR	LYFNRWOT
m769	310	320	330	340	350
	AVFH	ERTYGN	DAYS	SYTNGAR	LYFNRWOT
a769.pep	370	380	390	400	410
	SLVF	YRNARQ	YWMGGL	DFYRERN	PADRGDN
m769	370	380	390	400	410
	SLVF	YRNARQ	YWMGGL	DFYRERN	PADRGDN
a769.pep	430	440	450	460	470
	HYEK	PGFFSG	FKGERR	RDKE	LNTSLSL
m769	430	440	450	460	470
	HYEK	PGFFSG	FKGERR	RDKE	LNTSLSL
a769.pep	490				
	RAFV	EFNKTF	X		
m769	490				
	RAFV	EFNKTF	X		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2645>:

g770.seq

1	ATGAACAGAC	TGCTACTGCT	STCTGCCGCC	GTCCTGCCGA	CTGCCTGCCG
51	CAGCGGGCAA	ACCGATAAAA	TCGGACGGGC	AAGTACCGTT	TTCAACATST
101	TGGGCAAAAA	CGACCGTATC	GAAGTGAAG	GATTCGACGA	TCCCGACGTT
151	CAAGGGGTTG	CCTGTTATAT	TTCTGATGCA	AAAAAAGGCG	GCTTGAAGSA
201	AATGGTCAAT	TTGGAAGAGG	ACCGGTCGCA	CGCATCGGTT	TCGTGCGTTC
251	AGACGGCATC	TTTGATTCTT	TTTGACGAAA	CCGCCGTGCG	CAAACCGAAA
301	GAAGTTTTC	AGCGCGGTAC	GGGCTTCGCG	TTCAAGAGCC	GGCAGATTGT
351	CCGTATTATC	GACCCCAAAC	GCAAGGCCTT	CGCCTATTTC	GTTTACAGCG
401	ATAAAATCGT	CCAAGGATCG	CCGAAAAATT	CCTTAAGCGC	GGTTTCCTGT
451	TTCCGCAGCG	GCATACCGCA	AACCGACGGG	GTGCAAGCCG	ATACTTCCGG
501	CAAACTGCTT	GCCGGCGCCT	GCATTATTTC	CAACCCGATA	AAAAATCCCG
551	ACAAACGCTG	A			

This corresponds to the amino acid sequence <SEQ ID 2646; ORF 770.ng>:

g770.pep

1	MNRLLLSAA	VLPTACSGSE	TDKIGRASTV	FNMLGKNDRI	EVEGFDDPJV
51	QGVACYISYA	KKGLKEMVN	LEEDASDASV	SCVQTASSIS	FDATAVRKPK
101	EVFKRGTGFA	FKSRQIVRY	DPKRAFAFYL	VYSDKIVQGS	PKNSLSAVSC
151	FGSGIPQTDG	VQADTSGKLL	AGACIIISNPI	KNPKDR	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2647>:

m770.seq

1	ATGAACAGAC	TGCTACTGCT	GTCTGCCGCC	GTCCTGCTGA	CTGCCTGCCG
51	CAGCGGGCAA	ACCGATAAAA	TCGGACGGGC	AAGTACCGTT	TTCAACATAC

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```

101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCCTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCGTGCG CAAACCGAAA
301 GAAGTTTCA AACACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAATCAT CCAAGGCTCG CCGAAAAAT CTTAAGCGC GGTTCCTGT
451 TTCGGCGCGC GCATACCGCA AACCAGTGGG GTGCAAGCCG ATACTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAATCICG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2648; ORF 770>:

```

m770.pep
1  MNRLLLLSAA VLLTACSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKHGASFA FKSRIQVRY DPKRRTFAYL VYSDKIIQGS PKNSLSAVSC
151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENLDRK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 770 shows 93.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. gonorrhoeae*

m770/g770 93.5% identity in 186 aa overlap

	10	20	30	40	50	60
g770.pep	MNRLLLLSAAV	LPTACSGE	TDKIGRASTV	FNILGKNDR I	EVEGFDDPDV	QGVACYISYA
m770	MNRLLLLSAAV	LPTACSGE	TDKIGRASTV	FNILGKNDR I	EVEGFDDPDV	QGVACYISYA
	10	20	30	40	50	60
g770.pep	KKGGLKEMVN	LEEDASDASV	SCVQTASSIS	FDETA VRKPK	EVFKHGASFA	FKSRIQVRY
m770	KKGGLKEMVN	LEEDASDASV	SCVQTASSIS	FDETA VRKPK	EVFKHGASFA	FKSRIQVRY
	70	80	90	100	110	120
g770.pep	DPKRRTFAYL	VYSDKIIQGS	PKNSLSAVSC	FGGGIPQTDG	VQADTSGNLL	AGACMISNPI
m770	DPKRRTFAYL	VYSDKIIQGS	PKNSLSAVSC	FGGGIPQTDG	VQADTSGNLL	AGACMISNPI
	130	140	150	160	170	180
g770.pep	KNPDKRX	:				
m770	ENLDRKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2649>:

```

a770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCGG
51  CAGCGCGCAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCACATAC
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCCTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCGTGCG CAAACCGAAA
301 GAAGTTTCA AACACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAATCAT CCAAGGCTCG CCGAAAAAT CTTAAGCGC GGTTCCTGT
451 TTCGGCGCGC GCATACCGCA AACCAGTGGG GTGCAAGCCG ATACTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAATCCCG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2650; ORF 770.a>:

```

a770.pep
1  MNRLLLLSAA VLLTACSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKHGASFA FKSRIQVRY DPKRRTFAYL VYSDKIIQGS PKNSLSAVSC

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151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENPDKR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 770 shows 99.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. meningitidis*:

m770/a770 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
a770.pep	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPFDVQGVACYISYA					
m770	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPFDVQGVACYISYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a770.pep	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKVEVFKHGASFAFKSRQIVRYY					
m770	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKVEVFKHGASFAFKSRQIVRYY					
	70	80	90	100	110	120
	130	140	150	160	170	180
a770.pep	DPKRRTFAYLVYSDKIIQGSPPKNSLSAVSCFSGGGIPQTDGVQADTSGNLLAGACMISNPI					
m770	DPKRRTFAYLVYSDKIIQGSPPKNSLSAVSCFSGGGIPQTDGVQADTSGNLLAGACMISNPI					
	130	140	150	160	170	180
a770.pep	ENPDKRX					
m770	ENLDRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2651>:

g771.seq

1	ATGGATTAT	TATCGGTTTT	CCACAAATAC	CGTCTGAAAT	ATGCGGTGGC
51	GGTGCTGACG	ATGCTGCTTT	TGGCGGCAGT	CGGGCTGCAC	GCTTCCGTAT
101	ATCGCACCTT	CACGCCCGAA	AACATCCGCA	GCCGCCTCCA	ACAAAGCATT
151	GCCCATACCC	ACCGGAAAAT	CTCGTTTGAT	GCGGATATAC	GGCGCAGGCT
201	TCTGCCCCGC	CCGACCGTCA	TCCTGAAAAA	CCTGACCATT	ACCGAACCCG
251	ACGGCGGCGG	GGTCGCCGTT	TCCGTCAAAG	AAACAAAAT	CGGATTGAGC
301	TGGAAAAACC	TGTGGTCGGA	TCGGATACAG	GTTGAAAAAT	GGGTGGTTTC
351	GGGTGCGGAT	CTTGCCCTGA	CGCGCGACAG	AAACGGCGCT	TGGAACATCC
401	AAGACCTGTT	CGACGGCGCG	AAACACTCCG	CCTCAGTCAA	CGGCATTATC
451	GTCGAAAACA	GCACCGTCCG	CCTCAATTTT	CTGCAGCAAC	AGCTTATCCT
501	GAAGGAAATC	AGCCTCAACC	TGCAATCCCC	CGATTCTGCG	GGGCAGCAGT
551	TTGAAAGTTC	GGGCATACTG	GTTTGAGAA	AGCTGTCCGT	CCCGTGAAAA
601	AGCAGGGGGC	TGTTCTTTC	AGACGGCATC	GGCAGCCTCG	AAATCTCACC
651	GTTCCATTTT	GAAGCTTCCA	CTTCGCTGGA	CGGACACGGC	ATCACCATT
701	CCACCACCGG	CAGCCCTTCT	GTCCGCTTCA	ACGCCGGCGG	AGCGGATGCC
751	GCCGGGCTCG	GCTTGCCTGC	AGACACTTCC	TTCCGCAACC	TCCACCTGAC
801	CGCGCAAATC	CCCGCACTGG	CACTCAAAAA	CAACAGCATC	AAAACCGGCA
851	CGGTCAACGG	CACGTTTACC	GCCGGCGGCG	AAATATGCCG	ATGGGACGGT
901	TCGTTCAAAC	TCGACAAAGC	CAACCTGCAC	TCCGGCATCG	CCAACATCGG
951	CAACGCCGAA	ATCTCCGGCA	GCTTCAAAC	ACCGCGCCTT	CAAACCAATT
1001	TCTCCCTCGG	CTCGCCGTTG	GTTTGGAGTC	GGGACAAACG	GCTGGACGCC
1051	CCCGCCCTGC	ACATATCGAC	CCTTCAGGAT	ACCGTCGACC	GCCTGCCGCA
1101	ACCCCGTTTC	ATCAGCCGGC	TCGACGGTTC	GCTGTCCATA	CCGAATCTGC
1151	AAATATTGAA	TGCCGAATTA	AACGGCACAT	TCGACCGCCA	ACCCGTTGCC
1201	GCAAAATTC	AATATACGCG	GGAAGGCGCA	CCGCACCTGG	AAGCCGCGCG
1251	CGCGCTGCAA	AAATTAAC	TCGCCCCCTA	TCTTGACGAA	TTCGGCAAC
1301	AAAACGGCAA	AATATTTCCC	GACATCTCG	GCAGGCTGTC	CGGCAACGTC
1351	GAGGCACACC	TCAAATCGG	CAGCATCCAA	CTCCCCGGCT	TGCAACTGGA
1401	CGATATGGAA	ACCTACCTCC	ACGCCGACAA	AGACCATATC	GCGCTCAGCC
1451	GTTTCAAGCT	AGGGCTTTAC	GGCGGCCATA	CCGAAGGCGG	CATCAGCATC
1501	GCCAACACCC	GTCCCGCCAC	TTACCGCTCG	CAACAGAATG	CAAGCAACAT
1551	CCAAATCCAA	CCGCTGCTGC	AAGACCTGTT	CGGCTTCCAC	AGCTTCAGCG
1601	GCAACGGCGA	TGCGGTGATC	GACCTGACCG	CAAGCGGCGA	AAACCGCAAA
1651	CAGCTTATCC	GCTCGTGCA	AGGCAGCCTG	TCGCTGAATA	TTTCCAACGG
1701	CECGTGGCAC	GGCATCGATA	TGGACAGCAT	TTTAAAAAAC	GGCCTTTCGG

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1751  GGAATACTC  GGGCAGCACA  CCCTTCTACC  GATTACGCT  CAACAGCGAA
1801  ATTTAGACG  GCATCAGCCG  CCACATCGAT  ACCGAAGTCT  TCTCCGACAG
1851  CCTCTATGTT  ACCAGCAACG  GCTATACCAA  TCTGGATACG  CAGGAATTGT
1901  CTGAAGATGT  CTTATCCGCG  AACGCCGTCC  ATCCGAAAAA  CAAACCGATT
1951  CCCCTGAAAA  TCACCGGTAC  GGTGGACAAG  CCGTCCATTA  CCGTCGATTA
2001  CGGCAGGCTG  ACCGGCGGCA  TCAATTCCGC  CAAAGAGAAA  CAGAAAATCC
2051  TCGAAGACAC  CCTGCTGGAA  CAATGGCAGT  GGCTCAAACC  TAAAGAACCG
3051  TAA

```

This corresponds to the amino acid sequence <SEQ ID 2652; ORF 771.ng>:

```

g771.pep
1  MDLLSVFHKY  RLKYAVAVLT  MLLLAAVGLH  ASVYRTFTPE  NIRSRLQQSI
51  AHTHRKISFD  ADIRRRLLPR  PTVILKNLTI  TEPDGGRVAV  SVKETKIGLS
101 WKNLWSDRIQ  VEKVVVSGAD  LALTFDRNGA  WNIQDLFDGA  KHSASVNRRI
151 VENSTVRLNF  LQQQLILKEI  SLNLQSPDSS  GQOFESSGIL  VWRKLSVPWK
201 SRGLFLSDGI  GTPEISPFHF  EASTELDGHG  ITISTGSPS  VRFNAGGADA
251 AGLGLRADTS  FRNLHLTAQI  PALALKNNIS  KGTGVNGTFT  AGGEYARWDG
301 SEKLDKANLH  SGIANIGNAE  ISGSFKTPRL  QTNFSLGSPL  VWSRDNLDA
351 PRLHISTLDQ  TVDRLPQPRF  ISRLDGSLSI  PNLQNWNAEL  NGTFDRQVPA
401 AKFKYTREGA  PHLEAAAAAQ  KLNLAPLYOE  FRQONGKIFP  DILGRLSGNV
451 EAHKIGISIQ  LPGLQLDDME  TYLHADKDHI  ALSRFKSGLY  GGHTEGGISI
501 ANTRPATYRL  QQNASNIQIQ  PLLQLFGFHF  SFSGNGDAVI  DLTASGENRK
551 QLIRSLQGS  SLNISNGAWH  GIDMESILKN  GLSGKISGST  PFYRFTLNSE
601 ISDGISRHID  TELFSDSLYV  TSNGYTNLDT  QELSEDVLIR  NAVHPKNKPI
651 PLKI*GTVDK  PSITVDYGR  TGGINSRKEK  QKILEDTLLE  QWQWLKPKPE
701 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2653>:

```

m771.seq
1  ATGGATTAT  TATCGGTTTT  CCACAAATAC  CGTCTGAAAT  ATGCGGTGGC
51  CGTGCTGACG  ATACTGCTTT  TGGCGGCAGT  CGGGCTGCAC  GCTTCCGTAT
101 ATCCGACCTT  CACGCCTGAA  AACATCCGCA  GCCGCCTACA  ACAAGCATT
151 GCACACACAC  ACCGAAAAAT  CTCGTTTGAT  GCGGACATTC  AGCGCAGGCT
201 CCTGCCCCGG  CCGACCGTCA  TCCTGAAAAA  CCTGACCATT  ACCGAACCCG
251 GCGCGGACCA  GACTGCCGTT  TCCGTCCAAG  AAACCAAAAT  CGGATTGAGC
301 TGGAAAAAAC  TGTGGTCGGA  TCAGATACAG  ATTGAAAAAT  GGGTGGTTTC
351 GAGTGGCGAA  CTTGCCCTGA  CGCGCGACGG  GAAAGGTGTT  TGGAACATCC
401 AAGACCTGAT  CGACAGCCAA  AAACGCCAAG  CCTCAGTCAA  CCGCATTATC
451 GTCGAAAAAC  GCACCGTCCG  CCTCAATTTC  CTCGAGGAAC  AGCTTATCTC
501 GAAGGAAATC  AACCTCAACC  TGCAATCCCC  CGATTCTGTC  GGGCAGCCGT
551 TTGAAAGTTC  GGGCATACTG  GTTTGGGGAA  AGCTGTCCGT  CCCGTGGAAA
601 AGCAGGGGGC  TGTTCCTTTC  AAACGGCATC  GGCCCGCCCG  AAATCTCACC
651 GTTCCATTTC  GAAGCTTCCA  CTTGCGTGGA  CGGACACGGC  ATTACCATTT
701 CCACCACCGG  CAGCCCTTCT  GTCCGCTTCA  ACGCCGCGCG  AGCGGATGCC
751 GCCGGCCTCG  GCCTGCGTGC  AGACACTTCC  TTCCGCAACC  TCCACCTGAC
801 CGCCCAAAAT  CCGCGCTGG  CACTCAGGAA  CAACAGCATT  AAAATTGAAA
851 CCGTCAACGG  CGCATTATCC  GCCGCGGCG  AATATGCCCG  ATGGGACGGT
901 TCGTTCAAGC  TCGACAAAGC  CAACCTGCAC  TCCGGCATCG  CCAACATCGG
951 CAACGCCGAA  ATCTCCGGCA  GCTTCAAAAC  ACCGCGCCAC  CAGACCAACT
1001 TCTCCCTCAA  TTCGCCGCTC  GTATGGACGG  AAAACAAAGG  GCTGGACGCG
1051 CCGCGCCTGT  ATGTATCGAC  CCTCAGGAT  ACCGTCAACC  GCCTGCCGCA
1101 ACCCCGTTTC  ATCAGCCGGC  TCGACGGTTC  GCTGTCCGTA  CCGAATCTGC
1151 AAAATTGGAA  TGCCGAATTA  AACGGACAT  TCGACCGCCA  AACCGTTGCC
1201 GCGAAATTCA  GATACACACA  TGAAGACGCA  CCGCATCTGG  AAGCCGCCGT
1251 CGCACTGCAA  AAATTGAACC  TGACCCCTTA  TCTTGACGAC  GTGCGGCAAC
1301 AAAACGGCAA  AATATTTCCT  GACCCCTCG  CCAAGCTGTC  CGGCGACATC
1351 GAGGCGCACC  TGAATTCG  AAAAGTCCAA  CTTCCCGGCC  TGCAACTGGA
1401 CGATATGGAA  ACCTACCTCC  ACGCCGACAA  AGGCCATATC  GCGCTCAGCC
1451 GTTTCAAGTC  AGGGCTTTAC  GCGGCCATA  CCGAAGGCGG  CATCAGCATC
1501 GCCAACACCC  GTCCCGCCAC  TTACCGCCTG  CAACAGAAAT  CAAGCAACAT
1551 CCAATCCAA  CCGCTGCTGC  AAGACCTGTT  CGGCTTCCAC  AGCTTCAGCG
1601 GCAACGGCGA  CGCGGTATC  GACCTGACCG  CGGCGGCGA  AACC CGAPAA
1651 GAGCTTATCC  GCTCGCTTCA  GGGCAGCCTG  TCGCTAAATA  TTTCCACGCG
1701 TGCAATGGCA  GGTATCGACA  TGGACAATAT  CCGTGAATAA  GGCATTTCCG
1751 GCAAACTGTC  CGACAATGCC  GCACCCAGCA  CACCCTTCCA  CCGATTACCG
1801 CTCACACGCG  AAATTTCAGA  CGGCATCAGC  CGCCACATCG  ATACCGAACT
1851 CTCTCCGAG  AGCCTCTATG  TTACCAGCAA  CGGCTATACC  AATCTGGATA
1901 CGCAGGAATT  GTCTGAAGAT  GTCCTTATCC  GCAACGCCGT  CCATCCGAAA
1951 AACAAACCGA  TTCCCTGAA  AATCAACGGC  ACGGTGGACA  AACCGTCCAT
2001 TACCGTCGAT  TACGGCAGGC  TGACC3GCGG  CATCAATTCC  CGCAAAGAGA
2051 AACAGAAAAT  CCTCGAAGAC  ACCCT3CTGG  AACAAATGGCA  GTGGCTCAAA
2101 CCTAAAGAAC  CGTA

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m771.pep
1 MDLLSVFHKY RLKYAVAVLT ILLLAAGVLH ASVYRTFTPE NIRSRLQOSI
51 AHTHRKISFD ADIQRRLLPR PTVILKNLTI TEPGGDQTAV SQVETKIGLS
101 WKNLWSDQIQ IEKVVVSSAE LALTRDGKGV WNIQDLIDSQ KROASVNRII
151 VENSTVRLNF LQEQLILKEI NNLQSPDSS GQPFESSGIL VWGLKLSVPWK
201 SRGLFLSNGI GPPEISPFHF EALSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLNLTAOI PALARNNISI KIETVNGAFT AGGEYARWNG
301 SFKLDKANLH SGLANIGNAE ISGSFKTPRH OTNFSLSNPL VWTENKGLDA
351 PRLYVSTLQD TVNRLPQPRF ISRLDGLSLV PNLQNNWNAEL NGTFDRQTV
401 AKF3RYTHEDA PLEAAVALQD KNLNLTPLYLD VRQQNGKIFL DTLAKLSGDI
451 EAHLKIGKGVQ LHLGLDDME TVLHADRGHI ALSRFKSGLY GGHTEGGISI
501 ANTRPATYRL QQNASNTQIQ PLLQDLFGFH SFGSGNDAVI DLTAGGETFRK
551 ELIRSLQGS LSNISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRTF
601 LNSEISDGIS RHIDTELFSD SLVYTSNGYT NLDTOELSED VLRINAWHPK
651 NKPPIPKITC TVDPKPSITVD YGRLTGGGINS RKEKQKILED TLLQEQWLK
701 PKP*
```

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 771 shows 90.3% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. gonorrhoeae*

m771/g771	90.3% identity in 704 aa overlap					
	10	20	30	40	50	60
g771.pep	MDLLSVFHKYRLKYAVAVLTMLLLAAVGLHASVYRTFTPENIRSRLLQQSIAHTRKRISFD					
m771	MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPENIRSRLLQQSIAHTRKRISFD					
	10	20	30	40	50	60
g771.pep	ADIRRRLLPRPTVILKNLTITEPGDGRGAVSVSKETKIGLSWKNLWSDRIQVEKWVVSGAD					
m771	ADIQRRLPRPTVILKNLTITEPGGDQTAVSVQETKIGLSWKNLWSDQIQIEKWVVSSAE					
	70	80	90	100	110	120
g771.pep	LALTRDRNGAWNIIQDLFDGAKHSASVNRIIVENSTVRLNFLQQQLILKEISLNLQSPDSS					
m771	LALTRDGKGVNNIIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQLILKEINLNLQSPDSS					
	130	140	150	160	170	180
g771.pep	GQGFESSGILVWRKLSVPWKSRLGLFLSDGIGTPEISPFHFEASTSLDGHGITISTTGSPS					
m771	GQGFESSGILVWGKLSVPWKSRLGLFLSNGIGPPEISPFHFEASTSLDGHGITISTTGSPS					
	190	200	210	220	230	240
g771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALKNNISIKTGTVNGTFTAGGEYARWDG					
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG					
	250	260	270	280	290	300
g771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRLQTNFSLGSPLVWSRDNGLEAPRLHISTLQD					
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLSPLVWTEKGLCAPRLYVSTLQD					
	310	320	330	340	350	360
g771.pep	TVDRLPQPRFISRLDGLSLIINLQNNWNAELNGTDFDRQVAAKFYTTREGAPHLEAAAAAQ					
m771	TVNRLPQPRFISRLDGLSLVSNLQNNWNAELNGTDFDRQTVAAKFRYTHEDAPHLEAAVALQ					
	370	380	390	400	410	420
g771.pep	KLNLAPVYLDEFROONGKIFPDILGRLSGNVEAHLKIGSIQLPGLQLDDMETYLHADKDH					
m771	KLNLTPVYLDVVRQONGKIFPDITLAKLSGDIKAHLKIGKVLPGLOLDDMETYLHADKGH					
	430	440	450	460	470	480

1258

	430	440	450	460	470	480
	490	500	510	520	530	540
g771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	
g771.pep	DLTASGENRKQLIRSLQGSLSLNISNGAWHGIDMDSILKNLSGKISG---STPFYRFT					
m771	DLTAGGETRKELIRSLQGSLSLNISNGAWHGIDMDNILKNISGKTADNAPSTPFHRFT					
	550	560	570	580	590	600
	600	610	620	630	640	650
g771.pep	LNSEISDGISRHIDTELFSDSLVYTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLVYTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	660	670	680	690	700	
g771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDITLLEQWQWLKPKEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDITLLEQWQWLKPKEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2655>:

a771.seq

```

1  ATGGATTAT  TATCGGTCTT  CCACAAATAC  CGTCTGAAAT  ATGCGGTAGC
51  CGTGTGACG  ATACTGCTTT  TGGCGGCAAT  CGGGCTGCAC  GCTTCCGTAT
101 ATCGCATCTT  CACACCTGAA  AACATCCGAA  GCCGCCTCCA  ACAAAGCATT
151 GCCCATACGC  ACCGGAATAA  CTCGTTTGAT  GCGGATATAC  AGCGCAGGCT
201 TCTGCCCGCG  CCGACCGTCA  TCCTGAAAAA  CCTGACCATT  ACCGAACCCG
251 GCGCGCACCG  GACTGCCGTT  TCCGTCCAAG  AAACCAAAAT  CGGATTGAGC
301 TGGAAAAACC  TGTGGTCGGA  TCAGATACAG  ATTGAAAAAT  GGGTGGTTTC
351 GAGTGGCGAA  CTTCGCCCTG  CGCGCGACCG  GAAAGGTGTT  TGGACATCC
401 AAGACCTGAT  CGACAGCCAA  AAACGCCAAG  CCTCAGTCAA  CCGCATTATC
451 GTCGAAACAA  GCACCGTCCG  CCTCAATTTC  CTGCAGGAAC  AGCTTATCCT
501 GAAGGAATTC  AACCTCAACC  TGCAATCCCC  CGATTCTGTC  GGGCAGCCGT
551 TTCAAAAGTTC  GGCATACTG  GTTTGGGGAA  AGCTGTCCGT  CCGTGGGAAA
601 AGCAGGGGGC  TGTTCCTTTC  AGACGGCATC  GGCACGCCCA  AAATCTCACC
651 GTTCCATTTT  GAAGCTTCCA  CTTCGCTGGA  CGGACACGGC  ATTACCATT
701 CCACCCACCG  CAGCCCTTCT  GTCGCTTCA  ACGCCGCGCG  AGCGGATGCC
751 GCGGCGCTCG  GCCTGCGTGC  AGACACTTCC  TTCGCAATCC  TCCACCTGAC
801 CGCCCAATAC  CCTACGCTGG  CACTCAGGAA  CAACAGCATT  AAAATTGAAA
851 CCGTCAACGG  CGCATTATAC  GCCGGCGCG  AATATGCCCA  ATGGGACGGT
901 TCGTTCAAAC  TCGACAAAGC  CAACCTGCAC  TCCGGCATCG  CCAACATCGG
951 CAACGCCGAA  ATCTCCGGCA  GCTTCAAAAC  ACCGCGCCAC  CAGACCAACT
1001 TCTCCCTCAA  TTCGCCGCTC  GTATGGACGG  AAAACAAAGG  GCTGGACGG
1051 CCGCGCTGTG  ATGTATCGAC  CCTCAGGAT  ACCGTCAACC  GCCTGCCGCA
1101 ACCCGCTTTC  ATCAGCCGGC  TCGACGGTTC  GCTGTCCGTA  CCGAATCTGC
1151 AAAATTGGAA  TGCCGAATTA  AACGGCACAT  TCGACCGCCA  AACCGTTGCC
1201 GCGAAATTC  GATACACACA  TGAAGACGCA  CCGCATCTGG  AAGCCGCCGT
1251 CGCACTGCAA  AATTTGAACC  TGACCCCTTA  TCTTGACGAC  GTGCGGCAAC
1301 AAAACGGCAA  AATATTTCCT  GACACCTCG  CCAAGCTGTC  CGGCGACATC
1351 GAGGCGCACC  TGAATACTCG  AAAAGTCCAA  CTTCCTCGCC  TGCAACTGGA
1401 CGATATGGAA  ACCTACCTCC  ACGCCGACAA  AGGCCATATC  GCGCTCAGCC
1451 GTTTCAGTTC  AGGCTTTAC  GCGGGCCATA  CCGAAGGCGG  CATCAGCATC
1501 GCCAACACCC  GTCCCGCCAC  TTACCGCTTG  CAACAGAATG  CAAGCAACAT
1551 CCAAAATCAA  CCGCTGCTGC  AAGACCTGTT  CGGCTTCCAC  AGCTTCAGCG
1601 GCAACGGCGA  CGCGGTATC  GACCTGACCG  CGGCGGCGCA  AACC CGAAAA
1651 GAGCTTATCC  GCTCGCTTCA  GGGCAGCCTG  TCGCTAAATA  TTTCCAAACG
1701 TGCATGGCAC  GGTATCGACA  TGGACAATAT  CCTGAAAAAC  GGCATTTCGG
1751 GCAAACTGTC  CGACAATGCC  GCACCCAGCA  CACCCTTCCA  CGATTTCACG
1801 CTCAACAGCG  AAATTTTACA  CGGCATCAGC  CGCCACATCG  ATACCGAACT
1851 CTCTCTCGAC  AGCCTCTATG  TTACCAGCAA  CGGCTATACC  AATCTGGATA
1901 CGCAGGAATT  GTCTGAAGAT  GTCCTTATCC  GCAACGCCGT  CCATCCGAAA
1951 AACAAACCGA  TTCCCTGAA  AATCACCAGT  ACGGTGGACA  AACCCTCCAT
2001 TACCGTCGAT  TACCGCAGGC  TGACCGGCGG  CATCAATTTC  CGCAAAGAGA
2051 AACAGAAAT  CCTCGAAGAC  ACCCTGCTGG  AACATGGCA  GTGGCTCAAA
2101 CCTAAAGAAC  CGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2656; ORF 771.a>:

1259

a771.pep
 1 MDLLSVFHKY RLKYAVAVLT ILLLAAGLH ASVYRIFTPE NIRSRLQOSI
 51 AHTRKISFD ADIQRRLPR PTVILKNLTI TEPGGDRTAV SVQETKIGLS
 101 WKNLWSDQIQ IEKWWVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
 151 VENSTVRLNF LQEQILILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
 201 SRGLFLSDGI GTPKISPFHF EASTSLDGHG ITISTTGSPTS VRFNAGGADA
 251 AGLGLRADTS FRNLHLTAQI PTLALRNNSI KIETVNGAFT AGGEYAQWDG
 301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH OTNFSLSPL VWTENKGLDA
 351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDROTVA
 401 AKERYTHEDA PHLEAAVALQ KNLNTPYLDV VRQONGKIFP DTLAKLSGDI
 451 EAHLKIGKVQ LPGLQLDDME TYLHADKGHI ALSRFKSGLY GGHTEGGISI
 501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFSNGDAVI DLTAGGETRK
 551 ELIRSLQGS LNLISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRFT
 601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDTOELSED VLIRNAVHPK
 651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEKQKILED TLLEQWQNLK
 701 PKEP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 771 shows 98.9% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. meningitidis*

m771/a771 98.9% identity in 704 aa overlap

	10	20	30	40	50	60
a771.pep	MDLLSVFHKYRLKYAVAVLTILLAAIGLHASVYRIFTPENIRSRLQOSIAHTRKISFD					
m771	MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPENIRSRLQOSIAHTRKISFD					
	10	20	30	40	50	60
	70	80	90	100	110	120
a771.pep	ADIQRRLPRPTVILKNLITIEPGGDRTAHSVQETKIGLSWKNLWSDQIQIEKWWVSSAE					
m771	ADIQRRLPRPTVILKNLITIEPGGDRTAHSVQETKIGLSWKNLWSDQIQIEKWWVSSAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a771.pep	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNQLQEQILILKEINNLQSPDSS					
m771	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNQLQEQILILKEINNLQSPDSS					
	130	140	150	160	170	180
	190	200	210	220	230	240
a771.pep	GQPFESSGILVWGKLSVPWKSRLFLSDGIGTPKISPFHFEASTSLDGHGITISTTGSPTS					
m771	GQPFESSGILVWGKLSVPWKSRLFLSNGIGPPEISPFHFEASTSLDGHGITISTTGSPTS					
	190	200	210	220	230	240
	250	260	270	280	290	300
a771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPTLALRNNSIKIETVNGAFTAGGEYAQWDG					
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG					
	250	260	270	280	290	300
	310	320	330	340	350	360
a771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD					
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD					
	310	320	330	340	350	360
	370	380	390	400	410	420
a771.pep	TVNRLPQPRFISRLDGSLSVSNLQNWNAELNGTFDROTVAAKFRYTHEDAPHLEAAVALQ					
m771	TVNRLPQPRFISRLDGSLSVSNLQNWNAELNGTFDROTVAAKFRYTHEDAPHLEAAVALQ					
	370	380	390	400	410	420
	430	440	450	460	470	480
a771.pep	KNLNTPLYLDDVRQONGKIFPDTLAKLSGDI EAHLKIGKVQLPGLQLDDMETYLHADKGHI					
m771	KNLNTPLYLDDVRQONGKIFPDTLAKLSGDI EAHLKIGKVQLPGLQLDDMETYLHADKGHI					
	430	440	450	460	470	480

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	490	500	510	520	530	540
a771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	600
a771.pep	DLTAGGETRKELIRSLQGSLSLNI SNGAWHGI DMDNILKNGI SGKTADNAAPSTPFHRET					
m771	DLTAGGETRKELIRSLQGSLSLNI SNGAWHGI DMDNILKNGI SGKTADNAAPSTPFHRET					
	550	560	570	580	590	600
	610	620	630	640	650	660
a771.pep	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	670	680	690	700		
a771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2657>:

```

g772.seq
1  GTGTTCCGCA CGGTCTTGCG GACTGATGCC GACTGCCTGC AAATCATCGT
51  CGTCGCAGAG TTCCTTCAGG TTGTTGCGTA TGGTTTTCGG GCGTTGGCGG
101 AAGGCGAGTT TCACCAAGTTT GCGGAAATGA TCGAAATCGT CCGCCTTGCC
151 GATACGGTGT TTCACCGGAA TCATGCGCAC CACTGCGGAA TCGATTTTCG
201 GCGCGGGATC GAACGATTCG GCGGCGACGT CAATCAGCAG CTCATATATC
251 AAAAAATATT GCAGCATCAC ACCCAAGCGA CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATGCGCTCGA CCACTTCTTT TTGCAACATA AAGTGCATAT
351 CGCGGACATC GTCCGCCACC TCCGCCAGTT TGAACAAAAG CGGCGTGGAG
401 ATGTTATACG GCAGGTTGCC GACGATTTTC TTTTTCCTG AGATGCCGTT
451 GAAATCAAAC TGCAACACGT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCAGCGT TTTCAGACGG CATACGATGT CGCGGTCGAT TTCGACAACG
551 TGCAGGCGGT TCAGCTTTTTC CGCCAAAGGT TCGGTAATTG CCGCCAAACC
601 CGGGCCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCC GATAATCCGC GTGTCCTGCA AAAAATTCTG CCCGAAACCG
701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTC CCTCTTCGGT TGAACCCCGT
751 CCGCTTAGGG CGGCAGGATC AGACTCTGTT TGGCGGGGCG GTAACCCCTT
801 CCAATCAGG ACGACACATA GGGCGGTGCT TTATGTGTCT TCCTGTGTGT
851 TGAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2658; ORF 772.ng>:

```

g772.pep
1  VEGTVLRDA DCLQIIVVGK FFOVVAYGFA ALAEGEFHOF GEMIEIVRLA
51  DTVFHRNHAH HCGIDFRRI ERFGRHVNQO LHIEKILQHH TOATVVVAFR
101 RGNHALDHFF LQHKVHIGDI VRHLRQFEQK RRGDVIRQVA DDFLFA*DAV
151 EIKLQHVAFV NHQFIRKROR FOTAYDVAVD FDNVQAVQLF RQREGNCRQT
201 RADFNHDIIR LRAHGVNDIA DNPRVLQKIL PETLAGFVFF HRVSSSVETP
251 PFRAAGSDSV WAGRNPFQIR TTHRAVLVVS SCVLEHKCVY SIRLMSAL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2659>:

```

m772.seq
1  ATGTTCCGCG CGGTCTTGCG GATTGATGCC GACTGCCTGC AAATCATCGT
51  CGCCTGCAAG CTCTTTCAGA TTGTTGCGTA TGGTTTTCGG GCGTTGGTGG
101 AAGGCGAGTT TCACCAAGTTT GCGGAAATGC TCGAAATCGT CCGCCTTGCC
151 GATGCGGTGT TTCACCGGAA TCATACGGAC GACGGCGGAA TCCACTTTCG
201 GCGCAGGATC GAACGATTCG GCGGCTACGT CAATCAGCAT TTCATATATC
251 AAAAAATATT GCAGCATCAC GCCCAAGCGG CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATACGCTCGA CCACTTCTTT TTGCAGCATA AAGTGCATAT
351 CGACGACATC GTCCGCCACC TCCGCCAGCT TGAACAAAAG CGGTGTGGAA
401 ATGTTGTACG GGAGGTTGCC GACGATTTTC TTTTTCCTG CGATGCCGTT
451 GAAATCAAAC TGCAATACAT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCAGCGT TTTCAGACGG CATACGATGT CGCGGTCGAT TTCGACAACG
551 TGCAGGCGGT TCAGCTTTTTC CGCCAAAGGT TCGGTAATCG CCGCCAAACC
601 CGGGCCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCT GATAATCCGC GTGTCCTGCA AAAAATTCTG CCCGAAACCG

```

1261

```

701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTT CCTTTTCGGT TGAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTTTT
801 CCAATCAGG ATGGCACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2660; ORF 772>:

```

m772.pep
1  MFGAVLRIDA DCLQIIVACK LFOIVAYGFA ALVEGEFHEF GKMLEIVRLA
51  DAVFHRNHTD DGGIHFRRRV ERFGRYVNHQ FHIEKILQHH AQAQVVAFR
101 RGNHTLDHFF LQHKVHIDDI VRHLRQLEQK RCGNVVREVA DDFLFACDAV
151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RADENHDIIR LRAHGVDNIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR MAHRAVLVVS SCVLKHKCVY SIRLMSAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 772 shows 85.2% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. gonorrhoeae*

```

m772/g772    85.2% identity in 298 aa overlap

          10      20      30      40      50      60
g772.pep    VFGTVLRTDADCLQIIVVGKFFQVYAGFAALAEGEFHQFGEMIEIVRLADTVFHRNHAH
              |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
m772         MFGAVLRIDADCLQIIVACKLFOIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD
              10      20      30      40      50      60

          70      80      90      100     110     120
g772.pep    HCGIDFRGIERFGRHVNQQLHIEKILQH:TOATVVVAFRRGNHALDHFFLQHKVHIGDI
              || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m772         DGGIHFRRRVERFGRYVNOHFHIEKILQHHAAQAAVVVAFRRGNHTLDHFFLQHKVHIDDI
              70      80      90      100     110     120

          130     140     150     160     170     180
g772.pep    VRHLRQFEQKRRGDVIRQVADDFLFXDAVEIKLQHVAFVNHQFIRKRQRQTAYDVAVD
              || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m772         VRHLRQLEQKRCGNVVREVADDFLFCDAVEIKLQYIAFVNHQFIRKRQRQTAYDVAVD
              130     140     150     160     170     180

          190     200     210     220     230     240
g772.pep    FDNVQAVQLFRQRFNGCRQTRADFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF
              || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m772         FDNVQAVQLFRQRFNGRRQTRADFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF
              190     200     210     220     230     240

          250     260     270     280     290     299
g772.pep    HRVSSSVETPPFRAAGSDSVWAGRNPFQIRTTTHRAVLVSSCVLEHKCVYSIRLMSALX
              || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m772         HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRAVLVSSCVLKHKCVYSIRLMSALX
              250     260     270     280     290

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2661>:

```

a772.seq
1  ATGTTTCGGCG CGGTCTTGCG GATTGATGCC GACTGCCTGC AAATCATCGT
51  CGCCTGCAAG CTCCTTCAGA TTGTTGCGTA TGGTTTTCGG GCGTTGGTGG
101 AAGGCGAGTT TCACGAGTTT GCGGAAATGC TCGAAATCGT CCGCCTTGCC
151 GATACGGTGT TTCACCGGAA TCATGCGGAC GACGGCCGAA TCCACTTTCG
201 GCGCGGGGTC GAACGATTCT GCGGCGACGT CAATCAGCAT TTCCATATCG
251 AAGAAATATT GCAGCATCAC GCCCAAGCGG CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATACGATCGA CCACTTCTTT TTGCAGCATA AAGTGCAAT
351 CACGACATC GTCCGCCACC TCCGCCAGCT TGAACAAAAG CGGCGTGGAA
401 ATGTTGTAGG GCAGGTGCCC GACGATTTC TTTTTCCTG CGATGCCGTT
451 GAAATCAAAC TGCAATACAT CGCCTTCGTG AATCACCAGT TTATCCGCA
501 ACGGCAGCGT TTTCAGACGG CACACGATGT CGCGGTCGAT TTCGACAACG
551 TGCAGGCGGT TCAGCTTTT CGCCAAAGGT TCGGTAATCG CCGCCAAACC
601 CCGACCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCT GATAATCCGC GTGTCTGCA AAAAATTCTG CCCGAACGC
701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTT CCTTTTCGGT TGAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAATCAGG ACGGCACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

1262

This corresponds to the amino acid sequence <SEQ ID 2662; ORF 772.a>:

```
a772.pep
1  MFGAVLRIDA DCLQIIVACK LFOIVAYGFA ALVEGEFHEF GEMLEIVRLA
51  DTVFHRNHAD DGRHFRRGV ERFGRHVNQH FHIEEILQHH AQAAVVVAFR
101 RGNHTIDHFF LQHKVHIDDI VRHLRQLEOK RRGNVVGQVA DDFLFACDAV
151 EIKLOYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RTDFNHDII RLAHGVNDIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR TAHRVLYVS SCVLKHKCVY SIRLMSAL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 772 shows 95.6% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. meningitidis*

```
m772/a772 95.6% identity in 298 aa overlap

a772.pep      10      20      30      40      50      60
MFGAVLRIDADCLQIIVACKLFOIVAYGFAALVEGEFHEFGEMLEIVRLADTVFHRNHAD
|||||
m772          10      20      30      40      50      60
MFGAVLRIDADCLQIIVACKLFOIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD

a772.pep      70      80      90      100     110     120
DGRHFRRGVVERFGRHVNQHFIIEILQHHAQAAVVVAFRGNHTIDHFFLQHKVHIDDI
|| |||||
m772          70      80      90      100     110     120
DGGIHFRRRRVERFGRYVNQHFIIEILQHHAQAAVVVAFRGNHTLDHFFLQHKVHIDDI

a772.pep      130     140     150     160     170     180
VRHLRQLEQKRGRNVVGQVADDFLFACDAVEIKLOYIAFVNHQFIRKRQRFQTAYDVAVD
|||||
m772          130     140     150     160     170     180
VRHLRQLEQKRGRNVVREVADDFLFACDAVEIKLOYIAFVNHQFIRKRQRFQTAYDVAVD

a772.pep      190     200     210     220     230     240
FDNVQAVQLFRQRFGNRRQTRTDFNHDIIRLAHGVNDIADNPRVLQKILPETLAGFVFF
|||||
m772          190     200     210     220     230     240
FDNVQAVQLFRQRFGNRRQTRADFNHDIIRLAHGVNDIADNPRVLQKILPETLAGFVFF

a772.pep      250     260     270     280     290     299
HRVSFSVETPPFRAVESDSIWEGRNSFQIRTAHRVLYVSSCVLKHKCVYSIRLMSALX
|||||
m772          250     260     270     280     290
HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRVLYVSSCVLKHKCVYSIRLMSALX
```

g773.seq not found yet

g773.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2663>:

```
m773.seq
1  ATGGGATTGG GTGCAACGAC TTTTGTGGT TCGGGTGCTA TAGGCGGAGG
51  TCTGTGCAGT ACCGGGATTG GCTGTGCGGC CGGTGGACTT ATTGCAACGG
101 CAGGTATGAC CGGTGGTTAT ACACAGGCCT CAGAAGGAAG CCGGCAATGG
151 TTTGGCACTT ACCAGTCCGA TTTTGGTAAA AAAGTTGTCC TATCTTTGGG
201 TACACCAATA GAATACGAAT CGCCGTTAGT ATCTGATGCG AAAAATCTAG
251 CCGTATGGGG ATTGGAACG CTGATTACGC GCAAATTGGG AAAC TTGGCA
301 ACGGGTGTGA AAAC TTCTCTT GACTCCGAAA ACTGCTGACG TACAGCGAAA
351 TATCTGTGCC CAATCCGAAG TCGGTATCAA CTGGGGCAAG GGGATTGAAG
401 GACAGGGAAT GCCTTGGGAG GATTATGTCG GTAAGGCCTT GTCTGCCAAT
451 GCAAGGTTAC CTAAAAATTT TAAAAACATT GATTATTTTG ATCGTGGTAC
501 AGGCACGGCA ATCAGTGCCA AACTCTGGA TACGCAAACT ACGGCACGCC
551 TGTCCAAACC CGAACAGCTT TACAGTACCA TGAAAGGGTA CATCGATAAG
601 ACGGCAAAAT TCAAAAGTTA TGAATTATCA GAAGTACCGT TAAGGGCAGA
651 CATGATCAAA CAGCGCGAAA TCCATCTGGC CATACCCGCA CAACTAATA
701 AGGAGCAAAG ATTGCAGTTG CAACGTGTGG TAGAGTATGG CAAAAGTCAA
751 AACATTACAG TCAAATTAC GGAGATCGAA TAA
```

1263

This corresponds to the amino acid sequence <SEQ ID 2664; ORF 773>:

```
m773.pep
  1  MGLGATTFVG  SGAIGGGLCS  TGIGCAAGGL  IATAGMTGGY  TQASEGSROL
51  FGTYQSDFGK  KVVLSLGTPI  EYESPLVSDA  KNLAVWGLET  LITRKIGNIA
101 TGVKTSLTPK  TADVORNILS  OSEVGIKWKG  GIEGQGPWE  DYVGKGLSAN
151 ARLPKNFKTF  DYFDRGTGTA  ISAKTLDTQT  TARLSKPEQL  YSTMKYIDK
201 TANFKSYELS  EVPLRADMIK  QREIHLAIPA  QTNKEQRLQL  QRVVEYKGSQ
251 NITVKITEIE *
```

a773.seq not found yet

a773.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2665>:

```
g774.seq
  1  ATGAAGACCA  AATTACCGCT  TTTTATCATT  TGGCTGTCTG  TGTCTGCCTC
51  CTGTGCTTCC  GTTTTACCCG  TTCCGGAGGG  CAGCCGAACC  GAAATGCCGA
101 CACAGGAAAA  TGCTTCAGAC  GGCATTCCCT  ATCCCGTTCC  CACTCTGCAA
151 GACCGTTTGG  ACTATCTGGA  AGGCAAAATC  GTCCGGCTGT  CGAACGAAGT
201 GGAATGTGTA  AACGGGAAAG  TCAAAGCATT  GGAGCATACG  AAAATACACC
251 CTTCCGGCAG  GACATACGTC  CAAAAACTCG  ACGACCGCAA  ATTGAAAGAG
301 CATTACCTCA  ATACCGAAGG  CGGCAGCGCA  TCCGCACATA  CCGTCGAAAC
351 CGCACAAAAC  CTCTACAATC  AGGCACTCAA  ACACTATCAA  AACGGCAGGT
401 TTTCTGCGCG  AGCCGCCCTG  TTGAAGGGGG  CGGACGGCGG  AGACGGCGGC
451 AGCATCGCGC  AACGCAGTAT  GTACCTGTTG  CTGCAAAGCA  GGGCGCGTAT
501 GGGGAACGTG  GAATCTGTCA  TCGAAATCGG  AGGGCGTTAC  GCCAACCGTT
551 TCAAAGACAG  CCCAACCGCG  CCCGAAGTCA  TATTCAAAAT  CGGCGAATGC
601 CAATACAGGC  TTCAGCAAAA  AGACATTGCA  AGGGCGACTT  GGCGCAGCCT
651 GATACAGACC  TATCCCGGCA  GCCCGCGCGC  AAAACGCGCC  GCCGCAGCGC
701 TACGCAACG  ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2666; ORF 774.ng>:

```
g774.pep
  1  MKTKLPLFII  WLSVSASCAS  VLPVPEGSRT  EMPTQENASD  GIPYPVPTLQ
51  DRLDYLEGKI  VRLSNEVEML  NGKVKALEHT  KIHPSGRITY  QKLDRLKLE
101 HYLNTEGGS  SAHTVETAQN  LYNQALKHYQ  NGRFSAAL  LKADGDCG
151 SIAQRSMYLL  LQSRARMGNC  ESVIEIGGRY  ANRFKDSPTA  PEVIFKIGEC
201 QYRLQKDIA  RATWRSLIQT  YPGSPAARKA  AAARVRKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2667>:

```
m774.seq
  1  ATGAAGATCA  AATTACCGCT  TTTTATCATT  TGGCTGTCTG  TGTCCGCCTC
51  CTGTGCTTCC  GTTTTACCCG  TTCCGGCAGG  CAGCCAAACC  GAAATGTGCA
101 CACGGGAAAA  TGCTTCAGAC  GGCATTCCCT  ATCCCGTTCC  GACCTTGCAA
151 GACCGTTTGG  ACTATCTGGA  AGGCAAAATC  GTCCGGCTGT  CGAACGAAGT
201 GGAACCTTAA  AACGGCAAAG  TCAAAGCACT  GGAACACGCA  AAAACACATT
251 CTTCCGGCAG  GGCATACGTC  CAAAAACTCG  ACGACCGCAA  GTTGAAGAG
301 CATTACCTCA  ATACCGAAGG  CGGCAGCGCA  TCCGCACATA  CTGTGCAAAC
351 CGCACAAAAC  CTCTACAATC  AGGCACTCAA  ACACTATAAA  AGCGGCAAGT
401 TTTCTGCGCG  TGCTCCCTG  TTGAAGGGCG  CGGACGGAGG  CGACGGCGGC
451 AGCATCGCGC  AACGCAGTAT  GTACCTGTTG  CTGCAAAGCA  GGGCGCGTAT
501 GGGCAACTGC  GAATCCGTCA  TCGAAATCGG  AGGGCGTTAC  GCCAACCGTT
551 TCAAAGACAG  CCCAACCGCG  CCTGAAGCCA  TGTTCAAAAT  CGGCGAATGC
601 CAATACAGGC  TTCAGCAAAA  AGACATTGCA  AGGGCGACTT  GGCGCAGCCT
651 GATACAGACC  TATCCCGGCA  GCCCGCGGCG  AAAACGCGCC  GCCGCAGCGC
701 TCGCAACG  ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2668; ORF 774>:

```
m774.pep
  1  MKIKLPLFII  WLSVSASCAS  VSPVPAGSQT  EMSTRENASD  GIPYPVPTLQ
51  DRLDYLEGKI  VRLSNEVETL  NGKVKALEHA  KTHSSGRAYV  QKLDRLKLE
101 HYLNTEGGS  SAHTVETAQN  LYNQALKHYK  SGKFSAAASL  LKADGDCG
151 SIAQRSMYLL  LQSRARMGNC  ESVIEIGGRY  ANRFKDSPTA  PEAMFKIGEC
201 QYRLQKDIA  RATWRSLIQT  YPGSPAARKA  AAARVRKR*
```

Computer analysis of this amino acid sequence gave the following results:

1264

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 774 shows 92.8% identity over a 237 aa overlap with a predicted ORF (ORF 774) from *N. gonorrhoeae*

m774/g774 92.8% identity in 237 aa overlap

	10	20	30	40	50	60
g774.pep	MKTKLPLFI	IWLSVSASCASVLPVPEGSRT	EMPTQENASDGI	PYPVPTLQDR	LCYLEGKI	
m774	MKIKLPLFI	IWLSVSASCASVSPV	PAGSQTEMSTRENASDGI	PYPVPTLQDR	LCYLEGKI	
	10	20	30	40	50	60
	70	80	90	100	110	120
g774.pep	VRLSNEVE	MLNGKVKALEHTKIHPSGR	TYVQKLD	DRKLKEHYLNTEGGS	ASAHTVETAQN	
m774	VRLSNEVE	TLNGKVKALEHAKTHSS	GRAYVQKLD	DRKLKEHYLNTEGGS	ASAHTVETAQN	
	70	80	90	100	110	120
	130	140	150	160	170	180
g774.pep	LYNQALKHY	QNGRFSAAAALLKGADGG	SGSIAQRSMYLLQSR	ARMGN	CESVIEIGGRY	
m774	LYNQALKHY	KSGKFSAAASLLKGADGG	SGSIAQRSMYLLQSR	ARMGN	CESVIEIGGRY	
	130	140	150	160	170	180
	190	200	210	220	230	
g774.pep	ANRFKDSPT	APEVIFKIGECQYRLQ	QKDIARATWRS	LIQTYPGSPA	KRAAAVRKR	
m774	ANRFKDSPT	APEAMFKIGECQYRLQ	QKDIARATWRS	LIQTYPGSPA	KRAAAVRKR	
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2669>:

a774.seq

```

1  ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCCG TATCCGCCGC
51  CTGTTCTTCC CCTGTTTCCC GCAATATTCA GGATATGCGG CTCGAACCGC
101 AGGCAGAGGC AGGTAGTTCG GACGCTATTC CCTATCCCGT TCCCACTCTG
151 CAAGACCGTT TGGATTATCT GGAAGGCACA CTCGTCCGCC TGTCGAACGA
201 AGTGGAAACC TTAACGGCA AAGTCAAAGC ACTGGAGCAT GCGAAACAC
251 ACCCTTCCAG CAGGGCATAC GTCCAAAAC TCGACGACCG CAAGTTGAAA
301 GAGCATTACC TCAATACCGA AGGCGGCAGC GCATCCGCAC ATACCGTCGA
351 AACCGCACAA AACCTCTACA ATCAGGCACT CAAACACTAT AAAAGCGGCA
401 GGTTTTCTGC CGCTGCCTCC CTGTTGAAAG GCGCGGACGG AGGCGACGGC
451 GGCAGCATCG CGCAACGCAG TATGTACCTG TTGCTGCAAA GCAGGGCGCG
501 TATGGGCAAC TGCGAATCCG TCATCGAAAT CGGAGGGCGT TACGCCAACC
551 GTTTCAAAGA CAGCCCAACC GCGCCTGAAG CCATGTTCAA AATCGGCGAA
601 TGCCAATACA GGCTTCAGCA AAAAGACATT GCAAGGGCGA CTTGGCGCAG
651 CCTGATACAG ACCTATCCCG GCAGCCCGGC GGCAAAACGC GCGGCCGCAG
701 CCGTGCACAA ACGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2670; ORF 774.a>:

a774.pep

```

1  MKTKLPLFII WLSVSAACSS PVSRIQDMR LEPQAEAGSS DAIPYPVPTL
51  QDRLDYLEGT LVRLSNEVET LNGKVKALEH AKTHPSSRAY VQKLDRLK
101 EHYLNTEGGS ASAHTVETAQ NLYNQALKHY KSGRFSAAAS LLKGADGGDG
151 GSIAQRSMYL LLQSRARMGN CESVIEIGGR YANRFKDSPT APEAMFKIGE
201 CQYRLQKDI ARATWRS LIQTYPGSPA AKRAAAVRKR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 774 shows 89.5% identity over a 238 aa overlap with a predicted ORF (ORF 774) from *N. meningitidis*

m774/a774 89.5% identity in 238 aa overlap

	10	20	30	40	50	60
a774.pep	MKTKLPLFII	WLSVSAACSSPVSRIQDMR	LEPQAEAGSSDAIPYPVPTL	QDRLDYLEGT		
m774	MKIKLPLFII	WLSVSASCAS-VSPV	PAGSQTEMSTRENASDGI	PYPVPTLQDR	LDYLEGK	
	10	20	30	40	50	

1265

		70	80	90	100	110	120
a774.pep		LVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKLD	DRKLKEHYLNT	EGGSASAHTV	ETAQ		
m774		LVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLD	DRKLKEHYLNT	EGGSASAHTV	ETAQ		
	60	70	80	90	100	110	
		130	140	150	160	170	180
a774.pep		NLYNQALKHYKSGRFSAAASLLKGADGGDGG	SGIAQRSMYLLQSR	RMGNCS	EVIEIGGR		
m774		NLYNQALKHYKSGKFSAAASLLKGADGGDGG	SGIAQRSMYLLQSR	RMGNCS	EVIEIGGR		
	120	130	140	150	160	170	
		190	200	210	220	230	239
a774.pep		YANRFKDSPTAPEAMFKIGECQYRLQQRDI	ARATWRS	LIQTYPGSPA	AKRAAAV	RRKRX	
m774		YANRFKDSPTAPEAMFKIGECQYRLQQRDI	ARATWRS	LIQTYPGSPA	AKRAAAV	RRKRX	
	180	190	200	210	220	230	

g790.seq not found yet

g790.pep not found vet

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2671>:

```
m790.seq
1   ATGGCAAGAA  GGTCAA AAAAC  ATTTGAAGAA  GCTGCTGCTG  AGGTTGAGGA
5   ACCGTTCCGT  CATCGTGCCA  TTAAGTTGGT  CGAGTTTGGAG  GGTACAGCCA
101  AGCCGTGTGT  AATCAACTGC  CCTAABACTG  GAAACCAAAC  CTGTTGCGGG
151  TACTCCAATG  TGTCATAGG  AAGTAGCTGG  GGTGGCCCTT  CTGTGTTGTA
201  TGAGCAAGCT  GCAAAGCCGC  GTATACGCGA  CCTTAGGAAG  AATCACATAG
251  CGTTAGAATG  GCTGAAACAG  GCTGTACACG  GTATGACCAA  CCAAGAGCGC
301  ATCACGACGC  AAGCTTCACA  TGAGATGACC  AATCCGTGG  CAGGTTCAA
351  CAGCATAGTC  CTTAACGATG  TCCAAGGCCA  TACGACCATT  AACAAACCAT
401  ATACGCATAC  GCACAACCA  ACGGATGCGG  ATGGCAAAGC  ATGTCGATGT
451  AGGCTCACAC  CCGGTCCTTT  GTGTGACAG  CGTCAGGCCG  CGGCTTTCCG
501  CCGTACAGGC  AAATCCACGG  GCAGTTTCGA  CCTGTTTGCT  TCGGTTGgTC
551  CCCCCTCGCA  GTACAGCTTT  GCGGTTGCCA  TGCCCGACAT  TGCATGTCTG
601  CCGGTTATCG  AAAAGGGAGA  CTGTGCTGGT  GTCGAGCCCG  GTATGTGCCC
651  TGCGGACCA  GACATCGCGC  TGATTGAAGT  GTCCGACAG  CGGCTGGTTC
701  TCGCGCATAT  TGTATTGAT  ATTCGCGGCA  GGATGCTGAT  TATACAGAG
751  GGCAGGCGCT  CTGAAGCCTT  TGACGTTGCC  GAAGCGACGA  CGATTTTAGG
801  TGTGGTGGTG  GAGTCAAAA  ACGGTTTATG  TCCGCGCAC  AGGCAAGAT
851  GCGTGTGTAT  TCGGATTACC  GCCCTFGATG  GTGTGACGCT  TGGTATGATT
901  TCCGCTTCCA  AAACGTCGTG  TACGCGCCCG  ACCGACGCCC  GGAATCAGC
951  CGTATGCTTT  CTTFCGATTT  GGCAGGCTAC  CGGTGGGATA  CCGAAAAACC
1001 GTTCGTGGCG  AAATCCGAAA  AACCGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2672; ORF 790>:

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2673>:

```

a790.seq
1  ATGGCAAGAA  GGTCAAAAAC  ATTGAAGAA  GCTGCTGCTG  AGGTTGAGGA
5  ACCTTTCCGT  CATCGTGGCA  TTAAGTTGTT  CGAGTTTGAG  GGTACAGCCA
101 AGCCCTGTGT  AATCAACATG  CCTAAACATG  GAAACCAAAC  CTGTTTCGAGG
151 TACTCCAATA  TGTTTCATAG  AAGTAGCTGG  GGGTGCCCT  CTTGTGGTAA
201 TGAGCAAGTA  GCAAAGCGG  GTATAGCGAC  CTTAGGAAG  AATCATATAG
251 CGTTAGAAGT  GCT'GAACAG  GCGTGAACAG  GTATGACCAA  GCAAGAGCGC
301 ATACACAGCG  AAGCTTACAA  TGAGATGACC  AAATCCGTGG  CAGGTTCAA
351 CAGCATAATC  CTTAACGATG  TCCAAGGCGA  TACGACCATC  AACAAACCATC
401 ATACGCATAC  GCACATCCAC  ACGCATGCGC  ACGGCAAAAG  ACTGTCGATG
451 AGGCTCACAC  CCGCTGCTTT  GTTGTCAGAC  CGTCAGCGGG  CCGCTTTCCG
501 CCGTACAGCA  AAATCATCGG  GCAGTTTGCA  CTTGTTTGCT  TCGGTGGTGC
551 CCGCTTACCA  ATATACGTTT  CCGCTTGCCA  TGCCGACAC  GTTCATGTCC
601 CCGGTTATCG  AAAAGGGGGA  TTTGCTGGTG  GTCGAGCCGC  GTATGCGCGT
651 TCGGCAAGCA  GACATCGTAT  TGATTGAATC  GTCCGACAAG  CCGGCTGGTC
701 TCGCGCACTT  TGTTATTCGAT  ATTGCGGGCA  GGATGCTGAT  TTATCAACA

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1266

```

751 GGCAGGCCGT CTGAAGCCCT CGACCTGCCC GAAGGCAGCG TGATTTTAGG
801 TGTGGTGCTG GAGTCAAAA ACGGTTTATG TCCGCCGCAC AGGCAAGAAG
851 GCGTGTGTAT TCGGATTACC GCCCCTGATG TGTGGACGGT TGGTACGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCAGCCC GGAATCAGC
951 CGTATGCTTT CTTGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGT

```

This corresponds to the amino acid sequence <SEQ ID 2674; ORF 790.a>:

```

a790.pep
1  MARRSKTFEE AAEEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCRS
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSII LNDVQGDFTI NNHHTHTNH SDADGKALSM
151 RLTPRPLLSD RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVVAHLVID IAGRMLIYOT
251 GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVNTVGTI
301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNPN NAC

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 790 shows 98.2% identity over a 342 aa overlap with a predicted ORF (ORF 790) from *N. meningitidis*

a790/m790 98.2% identity in 342 aa overlap

	10	20	30	40	50	60
a790.pep	MARRSKTFEEAAAEVEERFGHRGIKLVEFEGTAKPCVINC PKHGNQTCRSRYSNMFIGSSW					
m790	MARRSKTFEEAAAEVEERFGHRGIKLVEFEGTAKPCVINC PKHGNQTCRSRYSNMFIGSSW					
	10	20	30	40	50	60
	70	80	90	100	110	120
a790.pep	GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSII					
m790	GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSIV					
	70	80	90	100	110	120
	130	140	150	160	170	180
a790.pep	LNDVQGDFTI NNHHTHTNHSDADGKALSMRLTPRPLLSDRQAAAFARTGKLTGSFDLFA					
m790	LNDVQGDFTI NNHHTHTNHSDADGKALSMRLTPRPLLSDRQAAAFARTGKLTGSFDLFA					
	130	140	150	160	170	180
	190	200	210	220	230	240
a790.pep	SVVAPSQYTF AVAMPDTSMSPVIEKGDLLVVEPRMRPADE DIVLIELSDKRLVVAHLVID					
m790	SVVAPSQYTF AVAMPDTSMSPVIEKGDLLVVEPRMCPAEDIALIELSDKRLVVAHLVID					
	190	200	210	220	230	240
	250	260	270	280	290	300
a790.pep	IAGRMLIYOTGRPSEALDLPESVILGVVLESKNGLCPPHRQEGVLIRITAPDVNTVGTI					
m790	IAGRMLIYOTGRPSEAFDLPEGSTILGVVLESKNGLCPPHRQEGVLIRITAPDVNTVGM					
	250	260	270	280	290	300
	310	320	330	340		
a790.pep	SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNPN NAC					
m790	SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNPN NAX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2675>:

```

g791.seq
1  ATGGTAAATT ATTATTCAGC TATCATTTAA AAGATTTTAA CTACTTGTTT
51  TGCTTTGTTT TTTGGTTTTT GTGTATTTGG AGTGGGTCTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACGTCCGT CTTTGGATTC TTTGCAGCAT
151 TACCAGCCIA AAATGCCGTT GACTATTTAT TCGGCGGATG GAGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GGCAGCAATT TACAATAATC GGCATTTC
251 CCGAGGTGTT GCGGAATCGG GTTATTGCCG CCGAGGATAA ACGCTTTTAC
301 CCGCATTTGG GGGTGGATGT TTGGGGTGTG CCCCAGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACACAGCAGG

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1267

```

401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCCTA TAAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTTGAG TTGTATTTC AATCAGATTTA CCTCGGTGAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAAATG CCGAGATTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGC GGGA CTGCCAAGG CTCGCTGTC
651 CTATAATCCG ATTGTTAA TC CGAGCGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCCGAT
751 CAGGCATTGA ATGAGGAAC GCATTATGAG CGGTTGTTC GGAATACTGA
801 TCAGAGTGTG TTATATGTGG CGGAAATGGT GCGTCGGGAA CTGTATGAGA
851 AATATGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTA TACCACGGTC
901 CGCACCGATC ATCAGAAAGC GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTCGAT CGCGGCAGCA GCTACCGCGG TGCGGAAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCGC GTTGTGTGG ATGTTACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTGCCTTG
1151 ACAGCGCGCG CTGGGTTTT GCGGCCCGAG CGGTCGATAA TGAGAAAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTGGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTT TCTATTCGGC GGCATTATCT AAGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGTTTCCA
1601 TCCGTATTTT GATGTCATC GGTGTCGGT ACAGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGCGGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTT
1701 AGGTACGGGC GAGACGACGC CGTTGAAAGT GGCAGGAGCA TATAGTGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTCGCG ACGTGATCGA TAAGATTAT
1801 CACAGACAGC GCAGCTTCCG CCCCAAATG CAACCTTGG TGCGAGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTAGTCAGAA TGTGGTCCGT GTCGGTACGG CAAGGGGGGC AGTGCCTTG
1951 GGAAGAACGG ATATTGCCGG TAAACCGGT ACGACCAACG ACAATAAGA
2001 TGCGTGGTTT GTCGGTTTT ACCCTGATGT GGTACTGACC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGCGGTG CCGGCTACGG CGGTACGATT
2101 GCGTGCCGGT TTTGGGTGGA CTATATGCGT TTTGCGTGA AAGGAAAGCA
2151 GGGCAAAGGG ATGAAATGCT CTGAAGGTGT GGTGAGCAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAT GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCGACGG GCAAAAGAAG ATGATGAAGC
2301 GGCAGTAGAA AACGAACAGC AGGGAAGGTC TGACGAAACG CGTCAGGACG
2351 TACAGGAAAC GCCGGTGCTT CCGAGCAATA CGGATTCCAA ACAGCAGCAG
2401 TTGATTCCCT TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2676; ORF 791.ng>:

```

g791.pep
1 MVNYSAMIK KILTTCEGLF FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVVDVWG ARAAVGNVVS GSVQSGASTI TQVAKNFYL SSEKTETRFK
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR OKYILNMLE EKMITVQORD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRRE LYEKYGEDAY TQGFVYTTV
301 RTDHQKAATE ALRKALRNFD RGSSYRGAEN YIDLKSEDEV EETVSQYLSG
351 LYTVDKMVPA VVLDVTKKN VVIQLPGGRR VALDRRALGF AARAVDNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPLLQG ALVSLDAKTC AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTFPN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRPSELP ASLSMALGTG ETTPKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRRLRAQM QPLVAGQNAQ QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRIDIAAGTKT TTNDNKDAWF VGFPDVTVA VYIGFDKPKS MGRAGYGGTI
701 AVPVWVDYMR FALKGKQKKG MKMPEGVVSS NGEYYMKERM VTDPLMLDN
751 SGIAPOPSRR AKEDDEAAVE NEQQGRSDET RQDVQETPVL PSNTDSKQQQ
801 LDSL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2677>:

```

m791.seq
1 ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51 TGCTTTGGTT TTTGGGTTTT GTGTATTGAG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAAGTCCGCT CTTTGGATTC TTGTCAGCAT
151 TACCAAGCTA AAATGCCGTT GACTATTAT TCGGCGGATG GGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGAATT TACAAAAATC GCGGATTTC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGTGTT GCCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AACGTTTAC ACGCAAATTC

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1268

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451 AATGAGGTGT TGCTTGCCTA TAAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAAATG CCGAGATTTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTTGA ATGAGGAAC TGCATTACGAG CGGTTTGTTC GGAAAATCGA
801 TCAGAGTGGC TTATATGTGG CGGAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCGCGGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTCGAT CGCGGCAGCA GCTACCGCGG TCGGGAACAA TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCCTGCC GTTGTGTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTT GCGGCCCGCG CGGTCAATAA TGAAAAATG
1201 GGGGAGGACC GTATCCGCGG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGGTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGTGGTTCGG CGGTTATGAT
1351 TTTACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTGCGC GGCATTATCT AAGGGGATGA
1451 CCGGTCACAC AGTGGTTAAT GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTGCGTT ACGCCAAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGSATATAGG GTTCTTCCG ACGTAATCGA TAAGATTAT
1801 CAGACAGAGC GCAGGTTGCG CGCCCAATG CAACCTTTGG TGCTGGGCA
1851 AAATGCGCGT CAGGCAATCG ATCCGCGCAA TGCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACCGGT ACGACCAATG ACAATAAGGA
2001 TGCCTGGTTT GTCGGTTTAA ACCCTGATGT GGTACTGCGG GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAATGTC CTGAAGGTGT GGTACAGAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CGCGGCAGAA GCGGACGGC AGGCGGCGGA TGACGAAGTC CGCCAAGATA
2351 TGCAGGAAAC GCCGGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGGATTCTC TGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2678; ORF 791>:

m791.pep

```
1 MVNYYSAMIR KILTTFCGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPKMPLTIY SADGEVIGMY GEORREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLILAYKIE QSLSKDKILE LYFNQIYLGO RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVKYVTTV
301 RADHOKVATE ALRKALRNFD RGSSYRGAEN YIDLKSESDV EETVSQYLSG
351 LYTVDKMVPV VVLDVTKKKN VVIQLPGGRR VTLDRLALGF ARAVNNNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPQLQG ALGSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAAIS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGRIRSEL P ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKLY
601 DRDGLRAQM OPLVAGQNAQ QAIIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRIDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRVGYGGTI
701 AVEFVVDYMR FALKGQCKG MKMPEGVVS NGEYMKERM VTDPLGLTLDN
751 SGIAPQPSRR AKEDDGGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*
```

g791/m791 97.3% identity in 805 aa overlap

```
10 20 30 40 50 60
g791.pep MVNYYSAMIRKILTTFCGLFFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
|||||
m791 MVNYYSAMIRKILTTFCGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
10 20 30 40 50 60
70 80 90 100 110 120
g791.pep SADGEVIGMYGEORREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVVS
|||||
m791 SADGEVIGMYGEORREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVVS
70 80 90 100 110 120
```

1269

	130	140	150	160	170	180
g791.pep	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
g791.pep	RAYGFASAAQIYFNKNVRDLTLAEAAAGLPGKAPSAYNPVNERAKLRQKYILNNMLE					
m791	RAYGFASAAQIYFNKNVRDLTLAEAAAGLPGKAPSAYNPVNERAKLRQKYILNNMLE					
	190	200	210	220	230	240
	250	260	270	280	290	300
g791.pep	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKYGEDAYTQGFVYTTV					
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKYGEDAYTQGFVYTTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
g791.pep	RTDHQKAATEALRKALRNFDGSSSYRGAENYIDLKSEDEETVSQYLSGLYTVDKMVP					
m791	RADHQQVATEALRKALRNFDGSSSYRGAENYIDLKSEDEETVSQYLSGLYTVDKMVP					
	310	320	330	340	350	360
	370	380	390	400	410	420
g791.pep	VVLDTVTKKKNVVIQLPGGRRVALDRRALGFAARAVDNEKMGEDRIIRGAVIRVKNNGGRW					
m791	VVLDTVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIIRGAVIRVKNNGGRW					
	370	380	390	400	410	420
	430	440	450	460	470	480
g791.pep	AVVQEPQLLQGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
m791	AVVQEPQLLQGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
	430	440	450	460	470	480
	490	500	510	520	530	540
g791.pep	KGMTASTVVNDAPISLPKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
m791	KGMTASTVVNDAPISLPKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
	490	500	510	520	530	540
	550	560	570	580	590	600
g791.pep	GVGYAQQYIRRFGRFSELPAISLMSALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
m791	GVGYAQQYIRRFGRFSELPAISLMSALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
	550	560	570	580	590	600
	610	620	630	640	650	660
g791.pep	DRDGRRLRAQMPLVAGQNAPOAIDERNAYIMYKIMQDVVRVGTARGAAALGRTDIACKTG					
m791	DRDGRRLRAQMPLVAGQNAPOAIDERNAYIMYKIMQDVVRVGTARGAAALGRTDIACKTG					
	610	620	630	640	650	660
	670	680	690	700	710	720
g791.pep	TTNDNKDAWFVGFNPDVVTAVYIGFDKPKSMGRAGYGGTIAVPVWVDYMRFALKGKGK					
m791	TTNDNKDAWFVGFNPDVVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKGK					
	670	680	690	700	710	720
	730	740	750	760	770	780
g791.pep	MKMPEGVVSSNGEYYMKERMVTDPLGLDLSGIAQPQSRRAKEDDEAAVENEQQGRSDET					
m791	MKMPEGVVSSNGEYYMKERMVTDPLGLDLSGIAQPQSRRAKEDDGGAAEGGQAADDEV					
	730	740	750	760	770	780
	790	800				
g791.pep	RQDVQETPVLPSNTDSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2679>:

1270

a791.seq

```
1 ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTC
51 TGGTTTGGTT TTTGGGTTTT GTGTATTTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACGCGCGT CTTTGGATTC TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGCAATT TACAAAAATC GGCATTTC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CCGCATTTGG GGGTGGATGT TTGGGGTGTG GCCCGCGCTG CCGTCGGCAA
351 TGTCTGTGTC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTGTC AGCAGTGAAG AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCCTA TAAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCTCGAGC TTGTATTTCA ATCAGATTTA CCTCGGTGAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCGAGATTTC
601 ACTTTGGCCG AAGCCGCCAT GCTTGCGGGA CTGCCCAAGG CTCCGCTGTC
651 CTATATATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAATGTA TTACCGTGCA ACAGCGCGAT
751 CAGCGGTTGA ATGAGGAACT GCATTACGAG CGGTTTGTTC GGAAAAATCGA
801 TCAGAGTGCT TTATATGTGG CCGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCACCGGAG GCATTGCGCA AGGCTCTACG
951 GAATTTCCGAT CGCGGCAGCA GCTACCGCGG TCGCGAAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCGC GTTGTGTGGT ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGCGCG GTTACGCTTG
1151 ACAGGCGCGC CTGCGGTTTT GCGGCCCGCG CGGTCAATAA TGAAAAAATG
1201 GGGGAGGACC GTATCCGCGG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CCGGCGTTGG GCGGTGCTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTACACAGA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGCG GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAT GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCGGG
1551 CTACATTACT TTGAGACAGG CTCTGACGCG TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGITTCGGCT TCAGGTGCTC CGAGCTGCGG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAGT GCGGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTCGCG ACGTAATCGA TAAGATTAT
1801 GACAGAGAGC GCAGGTTGCG CGCCCAATG CAACCTTGG TGGCCGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAAACGGGT ACGACCAATG ACAATAAGGA
2001 TGCGTGGTTT GTCGGTTTFA ACCCTGATGT GGTACTGCGG GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCGCG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAAAATG CTGAAGGTGT GGTACAGCAG AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 AGCCGTATTG CGCCGCAACC TTCCCGACGG GCAAAAAGAG ATGACGGGGG
2301 CGCGGCAGAA GCGGACGGGC AGGCGGCGGA TGACGAAGTC CGCCAAGATA
2351 TGCAAGGAAC GCCGGTGCCT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGATTCTC TGTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2680; ORF 791.a>:

a791.pep

```
1 MVNYSAMIK KILTTCFGLV FGFCVFGVGL VAIALVITYP KLPSLDSLQH
51 YQPKMPLTIY SADGEVIGMY GEORREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNEYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVKYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLKSEDEV EETVSQYLSG
351 LYTVDKMPVA VVLDVTKKN VVIQLPGRR VILDRRALGF ARAAVNNEKM
401 GEDRIRRAV IRVKNNGRW AVVQEPLLOQ ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAAIS KGMTASTVVN DAPISLPGKG
501 PNGSVWTFKN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGYAQYYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGLRAQM QPLVAGQNAQ QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFPDVTVA VYIGFDKPKS MGRVGYGGTI
701 AVPVWVDYMR FALKGQKQKG MKMPEGVVSS NGEYYMKERM VTDPLGLTDN
751 SGIAPQPSRR AKEDDGGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*
```

a791/m791 99.9% identity in 805 aa overlap

10 20 30 40 50 60

1271

a791.pep	MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLOHYQPKMPLTIY
m791	
	10 20 30 40 50 60
a791.pep	70 80 90 100 110 120
m791	SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGVNVVS
	70 80 90 100 110 120
a791.pep	130 140 150 160 170 180
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
	130 140 150 160 170 180
a791.pep	190 200 210 220 230 240
m791	RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPIVNERAKLRQKYILNNMLE
	190 200 210 220 230 240
a791.pep	250 260 270 280 290 300
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGEKVYTTV
	250 260 270 280 290 300
a791.pep	310 320 330 340 350 360
m791	RADHQKVATEALRKALRNFDRGSSYRGAENYIDLKSEDEVEETVSQYLSGLYTVDKMVPA
	310 320 330 340 350 360
a791.pep	370 380 390 400 410 420
m791	VVLDVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
	370 380 390 400 410 420
a791.pep	430 440 450 460 470 480
m791	AVVQEPPLQGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS
	430 440 450 460 470 480
a791.pep	490 500 510 520 530 540
m791	KGMTASTVVNDAPISLPKGKPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIIRILMSI
	490 500 510 520 530 540
a791.pep	550 560 570 580 590 600
m791	GVGYAQYIIRFGFRSSELPAISLMAALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
	550 560 570 580 590 600
a791.pep	610 620 630 640 650 660
m791	DRDGRRAQMPLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRDIAAGTG
	610 620 630 640 650 660
a791.pep	670 680 690 700 710 720
m791	TTNDNKDAWVGFNPDVVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKQGGK
	670 680 690 700 710 720
a791.pep	730 740 750 760 770 780
m791	MKMPEGVSSNGEYYMKERMVTDPSGLTLDNSGIAPQPSRRAKEDDGGAAEGGRQAADDEV
	MKMPEGVSSNGEYYMKERMVTDPSGLTLDNSGIAPQPSRRAKEDDGGAAEGGRQAADDEV

1272

	730	740	750	760	770	780
	790	800				
a791.pep	RQDMQETPVLPSNTGSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2681>:

g792.seq

1	ATGTTCCGCA	TCGTCAAATG	GCTGATTGCC	CTGCCCGTCG	GCATCTTTAT
51	CTTTTCAAT	GCCTATGTGT	ACGGCAACAT	CATCACCTAC	CGCGCCGTCG
101	CGCCCCATCG	GACTGCCTTT	ATGTCGATGC	GGATGAAGCA	GTTTGAACAA
151	GAAGGTCGCG	ATGTCGCACT	GGATTACCGC	TGGGTGCCCT	ACAACCGCAT
201	TTCCACCAAC	CTGAAAAAAG	CCCTGATTGC	TTCGGAAGAT	GTCGTTTGTG
251	CCggacacgg	gggcttcGat	GGGGACGGCa	tTCAAAACGC	CATCAGCGCG
301	AACCGGAACA	GCGGCGAAGT	GAAGGCGGGC	GGATCGACCA	TCAGCCAGCA
351	GCTTGCCAAA	AACCTCTTCC	TCAACGAAAG	CCGCAACTAT	CTGCGCAAAAG
401	GGGAAGAGGC	GGCCATTACG	GCAATGATGG	AAGCTGTTAC	CGACAAAAC
451	AGGATTTTCG	AACTGTATTT	AAACTCAATC	GAATGGCACT	ACGGCGtTTT
501	CGGCGCGGAA	GCTGCGTCCC	GgtatTttTA	TAAAAAACCG	GcgcgaGACC
551	TGACCAACA	GCAggcggcG	aaactgacgg	tactcgtccc	cgccccgttt
601	tactactctg	accatccaaa	aagcaaacgg	ctgcgcaaca	aaaccaatal
651	cgtgctcaga	cgcattgggtt	cggcaaatTA	ccccaaagcg	aaacgggactg
701	attgttcag	atatggaaat	gccgcctgaa	ctgggggttcg	aacggcatat
751	gtttctctggg	acttataa			

This corresponds to the amino acid sequence <SEQ ID 2682; ORF 792.ng>:

g792.pep

1	MFRIVKWLIA	LPVGIFIFFN	AYVYGNIIITY	RAVAPHRTAF	MSMRMKQFEQ
51	EGRDVALDYR	WVPYNRISTN	LKKALIASED	VRFAGHGGFD	GDGIQNAIRR
101	NRNSGEVKAG	GSTISQQLAK	NLFLNESRNY	LRKGEEAAIT	AMMEAVTDKN
151	RIFELYLNSI	EWHYGVFGAE	AASRYFYKKP	AADLTQQA	KLTVLVPAPF
201	YYSDFPKSKR	LRNKTNIVLR	RMGSANYPKA	KRTDCSRYGN	AA*TGVRTAY
251	VFWDL*				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2683>:

m792.seq

1	ATGTTCCGCA	TCATCAAATG	GCTGATTGCC	CTGCCCGTCG	GCATCTTTAT
51	CTTTTCAAT	GCCTATGTGT	ACGGCAACAT	CATTACCTAC	CGCGCCGTCG
101	CGCCCCATCG	GACTGCCTTT	ATGTCGATGC	GGATGAAGCA	GTTTGAACAG
151	GAAGGTCGCG	ATGTCGCACT	GGATTACCGC	TGGATGCCCT	ACAAACGCAT
201	TTCCACCAAC	CTGAAAAAAG	CCCTGATTGC	TTCGGAAGAT	GCCGTTTTCG
251	CGGGGCACGG	CGGCTTCGAT	TGGGGCGGCA	TCAAAACGC	CATCAGGCGC
301	AACCGGAACA	GCGGCGAAGT	GAAGGCGGGC	GGCTCGACCA	TCAGCCAGCA
351	GCTTGCCAAA	AACCTGTTTT	TAAACGAAAG	CCGCACTAT	ATCCGCAAAG
401	GCGAAGAAGC	GGCGATTACC	GCGATGATGG	AAGCCGTTAC	CGACAAGAC
451	AGGATTTTTC	AACTGTATTT	AAACTCAATC	GAATGGCACT	ACGGCGTTTT
501	CGGCGCGGAA	GCCGCGTCCC	GGTATTTTTA	TCAAATACCC	GCCGCCAAGC
551	TGACCAACA	GCAGGCGGCA	AAACTGACGG	CGCGCGTCCC	CGCCCCGCTC
601	TACTACGCCG	ACCATCCGAA	AAGCAAAACGG	CTCCGCAACA	AAACCAATAT
651	CGTGCTCAAA	CGCATGGGTT	CGGCAGAGTT	GCCTGAAAGC	GACACGGACT
701	GA				

This corresponds to the amino acid sequence <SEQ ID 2684; ORF 792>:

m792.pep

1	MFRIVKWLIA	LPVGIFIFFN	AYVYGNIIITY	RAVAPHRTAF	MSMRMKQFEQ
51	EGRDVALDYR	WNPYKRISTN	LKKALIASED	ARFAGHGGFD	WGDIQNAIRR
101	NRNSGKVKAG	GSTISQQLAK	NLFLNESRSY	IRKGEEAAIT	AMMEAVTDKD
151	RIFELYLNSI	EWHYGVFGAE	AASRYFYQIP	AAKLTQQA	KLTARVPAPL
201	YYADHPKSKR	LRNKTNIVLK	RMGSAELPES	DTD*	

g792 / m792 90.4% identity in 230 aa overlap

	10	20	30	40	50	60
g792.pep	MFRIVKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR					
m792	MFRIVKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR					
	10	20	30	40	50	60
	70	80	90	100	110	120
g792.pep	WVPYNRISTNLKKALIASEDVRFAGHGGFDGDGIQNAIRNRNSGEVKAGGSTISQQLAK					

1273

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	52
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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2685>:

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a792.seq
1  ATGTTCCGCA  TCATCAATG  GCTGATTGCC  CTGCCCGTCG  GCATCTTTAT
51  CTTTTTCAAT  GCCTATGTGT  ACGGCAACAT  CATTACCTAC  CGCGCCGTCG
101  CGAGGTCATCG  GACTGCCTTT  ATGTGCGATGC  GGATGAAGCA  GTTTGAACAG
151  GAAGGTCGCG  ATGTGCGACT  GCGATTACCG  TGGATGCCCT  ACAAAAGCAT
201  TTCCACCAAC  CTGAAAAGAAG  CCGTATGTGC  TTCCGAAGAT  GCCCGTTTCG
251  CGGGGACGCG  CGGCTTCGAT  TGGGGCGGCA  TTCAAAACGC  CATCAGGCGC
301  AACCGBAACA  CGCGCAAAAT  GAAGGCGGGC  GGCTGCAGCA  TCAGCCAGCA
351  GCTTGCCAAA  AACCTGTTTT  TAAACGAAAG  CCGCAGCTAT  ATCCGCAAAG
401  CGGAAGAAGC  GCGGATPACC  GCGATGATGG  AAGCCGCTTAC  CGCAAAAGAC
451  AGGATTTTTG  AACTGTATTT  AAACCTCAAT  GAATGGCATC  ACGCGCTTTT
501  CGCGCGGGAA  GCGCGTCCCG  GGTATTTTTA  TCAAATACCC  GCCGCCAAGC
551  TGACCAACA  CAGGGCGGCA  AAACCTGACG  CGCGCGTCCC  CGCCCCCGTC
601  TACTACGCG  ACCATCCGAA  AAGCAAAACG  CTCGCAACA  AAACCAATAT
651  CGTGCTCAGA  CGCATGGGTT  CGGCAGAGTT  GCCTGAAAGC  GATCGGACT
701  GA
```

This corresponds to the amino acid sequence <SEQ ID 2686; ORF 792.a>:

```
a792.pep
1  MFRIIKWLI1 LPVGIFIFFN2 AYVYGNII3TV RAVAPHRTAF4 MSMRMKQFEQ5
51  EGRDVALDYR6 WMPYKRISTN7 LKKALIAS8ED ARFAGHG9GFD WGGIQN10AI11RR
101 NRNSGKVKAG12 GSTISQQLAK13 NLFNLN14ESRSY IRKGEEAAIT15 AMMEAVTD16DKD
151 RIFELYLN17SI ERHWYGVFGA18 AASRYF19YQIP AAKLTQKQAA20 KLTARVPA21PL
201 YYADHPK22SK23 L24RNKNTYV25LR26 AMSGAE27PL28ES DTD*
```

m792/a792 99.6% identity in 233 aa overlap

	10	20	30	40	50	60
a792.pep	MFRIIKWLLIALPVGIFIFNAYVYGNII	TYRAVAPHRTAFMSMRMKQFEQGRDVALDYR				
m792	MFRIIKWLLIALPVGIFIFNAYVYGNII	TYRAVAPHRTAFMSMRMKQFEQGRDVALDYR				
	10	20	30	40	50	60
	70	80	90	100	110	120
a792.pep	WMPYKRISTNLKKALIASEDARFAGHG	GGFDWGGIQNAIRNRNSGKVKAGGSTISQQLAK				
m792	WMPYKRISTNLKKALIASEDARFAGHG	GGFDWGGIQNAIRNRNSGKVKAGGSTISQQLAK				
	70	80	90	100	110	120
	130	140	150	160	170	180
a792.pep	NLFLNESRSYIRKGEEAAITAMMEAVTDKDRIFEL	YLSNIEWHYGVFGAEAAASRYFYQIP				
m792	NLFLNESRSYIRKGEEAAITAMMEAVTDKDRIFEL	YLSNIEWHYGVFGAEAAASRYFYQIP				
	130	140	150	160	170	180
	190	200	210	220	230	
a792.pep	AAKLTQQAAKLTARVPAPLYADHPKSKRLRNKTNIVLRRMGS	AELPESD	TDX			
m792	AAKLTQQAAKLTARVPAPLYADHPKSKRLRNKTNIVLRRMGS	AELPESD	TDX			
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 2687>:

q793.seq

1274

```

1  ATGTTGATTA AAAGCGAATA TAAGCCCCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATTAGCTTC GTCCTGATGG
101 CAATGGCGGT CTTGTTTGCC TGTCTGATTG CCCGCGGGCT GTATCTGCAG
151 ACGGTAACGT ATAACCTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAGCA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTGGC GTTGAGCGCG CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GATATGAAGG AAATGCCGTC TGCCGCCCAA TTGGAACGCC TGTCCGAGCT
351 TGTCGATGTG CCGGTCGATG TTTTGAGGAA CAAACTCGAA CAGAAAGGCA
401 AGTCGTTTAT TTGGATCAAG CCGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAAGCCT TGGGTTTGGG AAACCTTTGTA TTTGAAAAAG AATTAAAAAG
501 CCATTACCCG ATGGGCAACC TGTTTGACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTGCTTGA AGACAGCCTG
601 TATGGCGAAG ACGGCGCGGA AGTTGTTTGG CCGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATA AGCACCGCAA AACGGCAAG
701 ACATCATCCT TTCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTCGAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACATATCCAA CAGACCGGCG CGGCGAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCTGGTTCG GCAATCAAAC CGTTCGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TCGCGATGA TACCCATGTT
1051 TACCCCTCTT TGGATGTGCG CGGCATTATG CAGAAATCGT CCAACGTCGG
1101 CACAAGCAAA CTGTCTGCGC GTTTCGGCGC CGAAGAAATG TATGACTTCT
1151 ATCATGAATT GGGCATCGGT GTGCGIATGC ACTCGGCCTT TCCGGGGGAA
1201 ACTGCAGGTT TGTGAGAAA TTGGCGCAGG TGGCGGCCCA TCGAACAGGC
1251 GACGATGTCT TTCGGTTACG GTCTGCAATT GAGCCTGCTG CAATTGGCGC
1301 GCGCCTATAC CGCACTGACG CACGACGGCG TTTTGCTGCC GCTCAGCTTT
1351 GAGAAGCAGG CGGTTGCGCC GCAAGSCAAA CGCATATCA AAGAATCGAC
1401 CGCGCGCGAG GTACGCAATC TGATGGTTTC CGTAACCGAG CCGGGCGGCA
1451 CCGGTACGGC GGGTGCAGTG GACGGTTTCG ATGTCGCGCG TAAACCGGCG
1501 ACGGCGCGCA AGTTCGTCAA CGGCGTTAT GCGGACAACA AACACGTCGC
1551 TACCTTTATC GGTTTTGGCC CGGCCAAAAA CCCCCGTGTG ATTGTGGCGG
1601 TAACCATCGA CGAACCGACT GCCACGGCT ATTACGCGCG CGTAGTGCCA
1651 GGGCCGCCCT TCAAAAAAAT TATGGGCGGC AGCCTGAACA TCTTGGGCAT
1701 TTCCCGGACC AAGCCACTGA CCGCGCGAGC CGTCAAAACA CCGTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2688; ORF 793.ng>:

g793.pep

```

1  MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMAMAVLFA CLIARGLYLQ
51  TVTYNFKLEQ GDNRIVRTQA LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 DMKEMPAAQ LERLSELVDV PVDVLRNKLE QKGSFIWIK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYP MGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 YGEDGAEVFL RDRQGNIVDS LDSPRNKAPQ NGKDIILSLD QRIOTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPG RADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
351 YPSLDVRGIM QKSSNVGTSK LSARFGAEM YDFYHELIGI VRNHSGFPE
401 TAGLLRNWRR WRPIEQATMS FGYGLQLSLL QLARAYTALT HDGVLLPLSF
451 EKQAVAPQKG RIFKESTARE VRNLMVSVTE PGGTGTAGAV DGFVDVGAKTG
501 TARKFVNGRY ADNKHVATFI GFAPAKNPRV IAVVTIDEPT AHGYGGVVA
551 GPFFKIMGG SLNILGISPT KPLTAAAVKT PS*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2689>:

m793.seq

```

1  ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACCTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAAACA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTGGC GTTGAGTGC GCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCCGAGCT
351 TGTCGATGTG CCGGTTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAAG CCGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAAGCCT TGGGTTTGGG AAACCTTTGTA TTTGAAAAAG AATTAAAAAG
501 CCATTACCCG ATGGGCAACC TGTTTGACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTGG CCGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTCGAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACATATCCAA CAGGCCCGGC CGGCGAGACA GCGAACAGCG GCGCAACCGT
901 GCGGTAACCG ATATGATCGA ACCCGGTTTC GCAATCAAAC CGTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA

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1275

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1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TCGCGGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACCTG TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 GATGTCCTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAAACGC ATATTCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GCGCGCACCG
1451 GTACGGCGGG TCGCGTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTTGCCCCCG CCAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGTTATT ACGGCGCGGT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGCATTTC
1701 CCCGACCAAG CCACTGACCG CCGCAGCCGT CAAACACCG TCTTAA

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This corresponds to the amino acid sequence <SEQ ID 2690; ORF 793>:

m793.pep

```

1  MLIKSEYKPR MLPKEEQVK PMTSNGRISF VLMAI AVLFA GLIARGLYLQ
51  TVTYNLFKEQ GDNRIVRTQT LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 EMKEMPSSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHPY MGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 HGEDGAEEVL RDRQGNIVDS LDSPRNKAPK NGKDIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPGRADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPKYIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEMY DFYHELIGIV RMHSGFPGET
401 AGLLRNWRW RPIEQATMSF GYGLQLSLQ LARAYTALH DGVLLPVSE
451 KQAVAPQGRK IFKESTAREV RNLMSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNGRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYGGVVVAG
551 PPFKKIMGGS LNILGISPTK PLTAAAVKTP S*

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g793/m793 98.5% identity in 582 aa overlap

	10	20	30	40	50	60
g793.pep	MLIKSEYKPRMLPKEEQVKPMTSNGRISFVLMAMAVLFACLIARGLYLQTVTYNLFKEQ					
m793	MLIKSEYKPRMLPKEEQVKPMTSNGRISFVLMIAVLFAGLIARGLYLQTVTYNLFKEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
g793.pep	GDNRIVRTQALPATRGTVSDRNGAVLALSAPTESLFAVPKMDKEMPSSAAQLERLSELVDV					
m793	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKMDKEMPSSAAQLERLSELVDV					
	70	80	90	100	110	120
	130	140	150	160	170	180
g793.pep	PVDVLRNKLEQKGKSFIIWKRLDPKVAEEVKALGLENFVFEKELKRHPYPMGNLFAHVIG					
m793	PVDVLRNKLEQKGKSFIIWKRLDPKVAEEVKALGLENFVFEKELKRHPYPMGNLFAHVIG					
	130	140	150	160	170	180
	190	200	210	220	230	240
g793.pep	FTDIDGKGQEGLELSLEDSLYGEDGAEEVLDRQGNIVDSLDSPRNKAFQNGKDIILSLD					
m793	FTDIDGKGQEGLELSLEDSLHGEDGAEEVLDRQGNIVDSLDSPRNKAFKNGKDIILSLD					
	190	200	210	220	230	240
	250	260	270	280	290	300
g793.pep	QRIQTLAYEELNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPGRADSEQRNR					
m793	QRIQTLAYEELNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPGRADSEQRNR					
	250	260	270	280	290	300
	310	320	330	340	350	360
g793.pep	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPKYIGPSPVRDDTHVYPSLDVRGIM					
m793	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPKYIGPSPVRD-THVYPSLDVRGIM					
	310	320	330	340	350	
	370	380	390	400	410	420
g793.pep	QKSSNVGTSKLSARFGAEMYDFYHELIGIVRMHSGFPGETAGLLRNWRWRPIEQATMS					
m793	QKSSNVGTSKLSARFGAEMYDFYHELIGIVRMHSGFPGETAGLLRNWRWRPIEQATMS					
	360	370	380	390	400	410

1276

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          430      440      450      460      470      480
g793.pep  FGYGLQLSLLQLARAYTALTHDGVLLPLSF EKQAVAPQ GKRI FKESTAREVRNLMVSVTE
          |||||
m793      FGYGLQLSLLQLARAYTALTHDGVLLPV SF EKQAVAPQ GKRI FKESTAREVRNLMVSVTE
          420      430      440      450      460      470

          490      500      510      520      530      540
g793.pep  PGGTGTAGAVDGFVGA KTGTARKFVN GR YADNKH VATFI GFAPAKNPRVIVAVTIDEPT
          |||||
m793      PGGTGTAGAVDGFVGA KTGTARKFVN GR YADNKH VATFI GFAPAKNPRVIVAVTIDEPT
          480      490      500      510      520      530

          550      560      570      580
g793.pep  AHGYGGVVAGPPFKKIMG GSLN ILGISPTKPLTAAAVKTPSX
          |||||
m793      AHGYGGVVAGPPFKKIMG GSLN ILGISPTKPLTAAAVKTPSX
          540      550      560      570      580

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2691>:

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a793.seq
1  ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCIGATCG
101 CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACTTTTT GAAAGAACAG GCGACAACCC GGATTGTGCG
201 GACTCAACA TTGCCGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTGGC GTTGAGTGGC CCGACGGAGT CCCTGTTTGC CGTGCTTAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCCGAGCT
351 TGTCGATGTG CCGGTTGATG TTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAA GCGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAAGCCT TGGGTTTGA AACTTTGTA TTGAAAAAG AATTAAACG
501 CCATTACCCG ATGGGCAACC TGTTCGACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTCGAAC TTTCGTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTGG CGGACCGCGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTGCAATA CCATCAGGCA AAAGCCGGA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACATGCCCAA CAGGCCCGGC CGGCGAGACA GCGAACAGCG GCGCAACCGT
901 GCGGTAACCG ATATGATCGA ACCCGGTTCC GCAATCAACG CTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TCGCGGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACTG TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCASGTTTGT TGAGAAATTG GCGCAGGTGG CGGCTATCG AACAGGCGAC
1251 GATGTCTTTC GGTACGGCC TGCAATTGAG CCGTGTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAACGCG ATATTCAAAG AATCGACCGC
1401 CGCGGAGGTA CGCAATCTGA TGGTTCCCGT AACCGAGCCG GCGCGCACCG
1451 GTACGGCGGG TCGGTGGAC GGTTCGATG TCGGCGCGAA AACCGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTTGCCCCCG CCAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACGGACTGCC CACGGTTATT ACGGCGCGGT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 CCGGACCAAG CCACTGACCG CCGCAGCCGT CAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2692; ORF 793.a>:

```

a793.pep
1  MLIKSEYKPR MLFKEEQVKK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNFKLEQ GDNRIVRTQT LPATRCTVSD RRGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLK QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYF MGNLFHVVIG FTDIDGKQGE GLELSLEDSL
201 HGEDGAEVVL RDRQGNIVDS LDSPRNKAPK NGKDIIISLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPG RADSEQRNR
301 AVTDMLEPGS AIKPFVIAKA LDAGKTDLNE RLNTOPYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEMY DFIHELIGIV RMHSGFPGET
401 AGLLRNWRW RPIEQATMSF GYGLQLSLLQ LARAYTALTI DGVLLPVSTF
451 KQAVAPQGKR IFKESTAREV RNLMSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNGRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYGGVVAG
551 PPFKKIMGGS LNILGISPTK PLTAAAVKTP S*

```

a793/m793 100.0% identity in 581 aa overlap

1277

	10	20	30	40	50	60
a793.pep	MLIKSEYKPRMLPKEEQVKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ					
m793	MLIKSEYKPRMLPKEEQVKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
a793.pep	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
m793	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
	70	80	90	100	110	120
	130	140	150	160	170	180
a793.pep	PVDVLRNKLEQKGKFSFIWIKRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
m793	PVDVLRNKLEQKGKFSFIWIKRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
	130	140	150	160	170	180
	190	200	210	220	230	240
a793.pep	FTDIDGKGQEGLELSLEDSLHGEGDAEVVLRDRQGNIVDSLDSFRNKAPKNGKDIILSLD					
m793	FTDIDGKGQEGLELSLEDSLHGEGDAEVVLRDRQGNIVDSLDSFRNKAPKNGKDIILSLD					
	190	200	210	220	230	240
	250	260	270	280	290	300
a793.pep	QRIQTLAYEELNKAVEYHQAKAGTVVVLARTGEILALANTPAYDPNRPGRADSEQRNR					
m793	QRIQTLAYEELNKAVEYHQAKAGTVVVLARTGEILALANTPAYDPNRPGRADSEQRNR					
	250	260	270	280	290	300
	310	320	330	340	350	360
a793.pep	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGSPVVRDTHVYPSLDVRGIMQ					
m793	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGSPVVRDTHVYPSLDVRGIMQ					
	310	320	330	340	350	360
	370	380	390	400	410	420
a793.pep	KSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
m793	KSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
	370	380	390	400	410	420
	430	440	450	460	470	480
a793.pep	GYGLQLSLLQLARAYTALHDGVLLPVSFQKQAVAPQKRIKKESTAREVRNLMVSVTEP					
m793	GYGLQLSLLQLARAYTALHDGVLLPVSFQKQAVAPQKRIKKESTAREVRNLMVSVTEP					
	430	440	450	460	470	480
	490	500	510	520	530	540
a793.pep	GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
m793	GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
	490	500	510	520	530	540
	550	560	570	580		
a793.pep	HGYYGUVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX					
m793	HGYYGUVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX					
	550	560	570	580		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2693>:

g794.seq

```

1  gtgcgtttca ATCATTTCAT AATGGTAACG ATTATTATAT ATGTGATTC
51  CCCTGCAAAC AAGCCGGTCC GCCGCCCGG CGTCCCACT TATCCGGCTT
101 TGCCCTTATA TTGCTTTTTT TATGTAACAG ATTCACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAAACGA AATCGCTGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGTGCCGG CATACCCGTC
301 AATCCCGCGT CCACGATGAA GCTCGTTACC GCGTTGCCG CCTTCAAAC
351 CTTCGGCAGC AATTACCGCT GGGCGACCGA GTTTAAAGC AACGGTACCG
401 TAAACGACGG CACGCTTGAC GGAAACCTGT ATGGGCGGG CAGCGCGAC
451 CCCGTTTCCA ATCAGGAAAA CCTGCTTGCC GTCCACGCC AGTTGCGCGA
501 CAAAGGCATC CGCAATATCA CGGGGCGCCT SATGCTCGAC CACAGCCTGT

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1278

```

551 GGGGCGAAGT CGGCAGTCCC GACCATTITG AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCAATCC GACTATGCTG TCTGCCGTA TGGTTATGGT
651 GC CGCGCGGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGGCCGCA TATTTTGGCC CAAAACAAC TGAAAATTAC CGCCTCCCA
751 GCTGCTGACC CTTGCGTCAA AAAACTGATG CGCGCATCTT TTTGCGGCAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA AAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTGCGG CTTGACGAAC TGATCCGCCA AAGTTTACC
901 AACCGCTGSC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATAGC
951 CGACACACCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTGATTGCG
1051 CGTTCCTCTC TCCTCAAAC CCGCGCGGAC GGCAAACTGC CCGCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGAGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CGGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGGCAATG TTGGAACCGG CTTATTTTCA
1251 CCGTTTGCA CAAGATTCA TCGACACGCT GCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAAGCG CGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT CGAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA AAAACATCAT CTCGGCGCGC
1501 GACGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2694; ORF 794.ng>:

g794.pep

```

1 VRFNHFIMVT IIIYVISPAN KPVRRPGVPT YPALPYNCFF YVTDSPMNEP
51 KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRAGIPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLN GNLYWAGSGD
151 VFNQENLLA VQRQLRDKGI RNITGRLMLD HSLWGEVSGP DHFEADSGSP
201 FMTPPNPTML SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSVKKLM RASFSGNLTK LRGNIPESCL GKPVGVMFMA LDELIRQSFT
301 NRWLLGGRI SDGIGIADTP EGAOTLAVAH SKPMKEILD MNKRSNLLIA
351 RSVFLKLGSD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVFARMMAQM LETAYFSFPA QDFIDTLPIA GTDGLTRNRF KQSGLLRLK
451 TGTLLNVRL AGYWLGDKPM AVVVIINSR AVSLLPDLN FVAKNIISGG
501 DGWLDKLMC KERRA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2695>:

m794.seq

```

1 GTGCGTCTCA ATCATTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51 CCTGTCAAAC AAGCCGCGCC GCCGCCACAG CGTTCCCACT TATCCGGCTT
101 TGCCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAAACGA AATCGCCGTA TATGTCGAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCGTTC
301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTGCGCG CCTTCAAAC
351 CTTCCGCAGC AATTACCGCT GGGCGACCGA GTTTAAAGC AACGTTACGG
401 TAAACGACGG CACGCTTGAC GGAACCTAT ATTGGCGGG CAGCGCGCAG
451 CCGGTTTTCA ATCAGGAAAA CCTGCTGAT GCTCAAAAC AGTTGCGCGA
501 ACAAGGCATA CTCAATATCA CGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTCG AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGGCCGCA TATTTTCGCC CAAAACAAC TGAAAATTAC CGCCTCCCAA
751 GCTGCTGACC CTTGATCAA AAAACTGATG CGTGATCTT TTTGCGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCCG CTTACGAAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGTA TCGGCATAGC
951 CGACACGCGG GAAGGCGCGC AGACACTTGC CGTTGCACAC GCCAAACCGA
1001 TGAAGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCGTCTC TCCTCAAAC CCGCGCGGAC GGCAAACTGC CCGCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGCGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CGGGCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGGCAATG TTGGAACCGG CTTATTTTCA
1251 CCGTTTGCA CAAGATTCA TCGACACGCT ACCCATCGCC GGCACAGACG
1301 GAACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT SCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCAGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCGGCGCGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2696; ORF 794>:

m794.pep

```

1 VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCFF YVTDLPMNEP
51 KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRSVPEV

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1279

101 NPASTMKLV T AFAAFKTFGS NYRWATEFKS NGTVNDGTLD GNLWAGSGD
 151 PVFNQENLLD AQKQLREQGI LNITGHLMLD HSLWGEVGS DFEADSGSP
 201 FMTPPNPTML SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
 251 AACPSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
 301 NHWLLGGGRI SDGIGIADTP EGAQTLAVAH AKPMKEILTD MNKRSNLI
 351 RSVFLKLGSD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
 401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGLRNRF KQSGGLRLK
 451 TGTNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLDN FVANNIISGG
 501 DGWLDKLMC KERRA*

g794/m794 95.5% identity in 515 aa overlap

	10	20	30	40	50	60
g794.pep	VRFNHFIMVTIIIVIS	PANKPVR	RGVPTYP	ALPYNCF	FYVTDSP	MNFKTAASLLLLL
m794	VRLNHFIMIAIIIVIS	PANKPARRH	SVPTYP	ALPYNCF	FYVTDLP	MNFKTAASLLLLL
	10	20	30	40	50	60
g794.pep	ASLAHAHALDTGRIP	QNEIAVY	VOELDSG	KVIIIDHR	AGIPVN	PASTMKLVTAFAAFKTFGS
m794	ASLAHAHALDTGRIP	QNEIAVY	VOELDSG	KVIIIDHR	SDVPVN	PASTMKLVTAFAAFKTFGS
	70	80	90	100	110	120
g794.pep	NYRWATEFKSNGTV	NDGTLDG	NLWAGSG	DPVFNQ	ENLLAV	QRLDRKGIRNITGRMLD
m794	NYRWATEFKSNGTV	NDGTLDG	NLWAGSG	DPVFNQ	ENLLDA	QQLREQGILNITGHLMLD
	130	140	150	160	170	180
g794.pep	HSLWGEVGS	PDHFEADSG	SPFMTPP	NPNTMLS	SAGMVM	VRAERNAAGSTDILTDPPLPHIFA
m794	HSLWGEVGS	PDHFEADSG	SPFMTPP	NPNTMLS	SAGMVM	VRAERNAAGSTDILTDPPLPHIFA
	190	200	210	220	230	240
g794.pep	QNNLKITASQA	ACPSVK	KLMRAS	FSGNTL	KLRGNI	PESCLGKPVGVRMFALDELIRQSFT
m794	QNNLKITASQA	ACPSVK	KLMRAS	FSGNTL	KLRGNI	PESCLGKPVGVRMFALDELIRQSFT
	250	260	270	280	290	300
g794.pep	NRWLLGGGRIS	DGIGIAD	TPEGAQ	TAVAH	SKPMKE	ILTD MNKRSNLIARSVFLKLGSD
m794	NHWLLGGGRIS	DGIGIAD	TPEGAQ	TAVAH	AKPMKE	ILTD MNKRSNLIARSVFLKLGSD
	310	320	330	340	350	360
g794.pep	GKLPVSEQA	ASAVRRE	LAVSGI	DVADLV	LENGSG	LSRKERV TARMMAQMLETAYFSPFA
m794	GKLPVSEQA	ASAVRRE	LAVSGI	DVADLV	LENGSG	LSRKERV TARMMAQMLETAYFSPFA
	370	380	390	400	410	420
g794.pep	QDFIDTLPIA	GTDTL	RNRFKQ	SGGLRL	KTGTL	NNVRALAGYWLGDKPM
m794	QDFIDTLPIA	GTDTL	RNRFKQ	SGGLRL	KTGTL	NNVRALAGYWLGDKPM
	430	440	450	460	470	480
g794.pep	AVSLLPDLDN	FAKNIIS	GGDGW	LDAKLM	CKERRAX	
m794	AVSLLPDLDN	FAKNIIS	GGDGW	LDAKLM	CKERRAX	
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2697>:

a794.seq

1 GTGCGTCTCA ATCATTTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
 51 CCCTGCAAAC AAGCCGGCCC GCCGCCACAG CGTTCCTTAT TATCCGGCTT
 101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTCCTCC
 151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
 201 GCTCGATACA GGTCCGATTC CGCAAAACGA AATCGCCGTA TATGTCCAAAG
 251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCGTTC

1280

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301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CTTCAAAC
351 CTTCCGCGAGC AATTACCGCT GGGCGACCGA GTTTAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAACCTGT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTCA ATCAGGAAAA CTTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 ACAAGGCATA CGCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGCGGAAGT CGGCAGCCCC GACGATTTCG AAGCCGACAG CGGTTCCCGG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCGCGCGGAA CGCAATGCCG CCGACAGTAC CGACATCCTC ACCGATCCCG
701 CTTTGCGGCA TATTTTCGCC CAAAACAAC TGAATAATAC CGCCTCCCAA
751 GCTGCCTGCC CTTGCATCAA AAAACTGATG CGTGCATCTT TTTCGGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCGG CTTGACGAAC TGATCCGSCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CCGACGGATT TCAGACGGCA TCGGCATATC
951 CGACACGCGG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCAAAGCCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATGCG
1051 CGTTCCGTCT TCCTCAAAC TCGCGCGGAC GGCAAACTGC CCGCGTTTC
1101 CGAACAGGCA GCGTCTGCCG TCGGCGGTGA ACTTGCCGTG TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTTG GAAAACGTT CAGGCTGTG CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGGCAATG TTGGAACGG CTTATTTCAG
1251 CCGGTTTGCA CAAGATTCA TCGATACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCAGCG TCAACAATGT CCGCGCCCTT GCAGGTATT GGCTGGGCGA
1401 CAACCGCATG GCGGTGGTGC TCATCATCAA CAGCGGCGCG GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCGCGCGGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC CAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2698; ORF 794.a>:

a794.pep

```

1 VRLNHFIMIA IIIYVISPA KPARHSVPT YPALPYNCF YVTDLPMNFP
51 KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRSDVPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLG GNLVWAGSGD
151 PVFNOENLLA VOROLREOGI RNITGHLMLD HSLWGEVGSF DDFEADSGSP
201 FMTPPNPTML SAGVMVRAE RNAADSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSLKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGISDTP EGAQTLAVAH SKPMKEILD MNKRSDNLIA
351 RSVFLKGGD GKLPAVSEQA ASAVRRELAV SGIDVADLVI ENGSGLSRKE
401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGLRNRK KQSGGLRLK
451 TGTLLNVRL AGYWLGDKPM AVVVIINSR AVSLLPDLN FVANNIISGG
501 DGWLDAKLMC KERRA*

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a794/m794 98.6% identity in 515 aa overlap

	10	20	30	40	50	60
a794.pep	VRLNHFIMIA	IIIYVISPA	KPARHSVPT	YPALPYNCF	YVTDLPMNFP	KTAASLLLLL
m794	VRLNHFIMIA	IIIYVISPA	KPARHSVPT	YPALPYNCF	YVTDLPMNFP	KTAASLLLLL
	10	20	30	40	50	60
a794.pep	ASLAHALDT	GRIPQNEIA	VYVQELDSG	KVIIIDHRSD	VPVNPASTM	KLVTAFAAF
m794	ASLAHALDT	GRIPQNEIA	VYVQELDSG	KVIIIDHRSD	VPVNPASTM	KLVTAFAAF
	70	80	90	100	110	120
a794.pep	ASLAHALDT	GRIPQNEIA	VYVQELDSG	KVIIIDHRSD	VPVNPASTM	KLVTAFAAF
m794	ASLAHALDT	GRIPQNEIA	VYVQELDSG	KVIIIDHRSD	VPVNPASTM	KLVTAFAAF
	70	80	90	100	110	120
a794.pep	NYRWATEFK	SNGTVNDG	TLGDNLYW	AGSGDPVF	NOENLLAV	QRLREQGIR
m794	NYRWATEFK	SNGTVNDG	TLGDNLYW	AGSGDPVF	NOENLLAV	QRLREQGIR
	130	140	150	160	170	180
a794.pep	NYRWATEFK	SNGTVNDG	TLGDNLYW	AGSGDPVF	NOENLLAV	QRLREQGIR
m794	NYRWATEFK	SNGTVNDG	TLGDNLYW	AGSGDPVF	NOENLLAV	QRLREQGIR
	130	140	150	160	170	180
a794.pep	HSLWGEVGS	PDDFEADSG	SPFMTPPN	PTMLSAGM	VMVRAER	NAADSTDIL
m794	HSLWGEVGS	PDDFEADSG	SPFMTPPN	PTMLSAGM	VMVRAER	NAADSTDIL
	190	200	210	220	230	240
a794.pep	HSLWGEVGS	PDDFEADSG	SPFMTPPN	PTMLSAGM	VMVRAER	NAADSTDIL
m794	HSLWGEVGS	PDDFEADSG	SPFMTPPN	PTMLSAGM	VMVRAER	NAADSTDIL
	190	200	210	220	230	240
a794.pep	QNNLKITAS	QAACPSIK	KLMRASFS	DNTLKL	LRGNIPES	CLGKPVGVR
m794	QNNLKITAS	QAACPSIK	KLMRASFS	DNTLKL	LRGNIPES	CLGKPVGVR
	250	260	270	280	290	300
a794.pep	QNNLKITAS	QAACPSIK	KLMRASFS	DNTLKL	LRGNIPES	CLGKPVGVR
m794	QNNLKITAS	QAACPSIK	KLMRASFS	DNTLKL	LRGNIPES	CLGKPVGVR
	250	260	270	280	290	300
a794.pep	NHWLLGGGR	ISDGI	SDTPEGAQ	TAVAH	SKPMKEIL	TDMNKRSDN
m794	NHWLLGGGR	ISDGI	SDTPEGAQ	TAVAH	SKPMKEIL	TDMNKRSDN
	310	320	330	340	350	360
a794.pep	NHWLLGGGR	ISDGI	SDTPEGAQ	TAVAH	SKPMKEIL	TDMNKRSDN
m794	NHWLLGGGR	ISDGI	SDTPEGAQ	TAVAH	SKPMKEIL	TDMNKRSDN

1281

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|||||
m794 NHWLLGGGRISDGIGIADTPEGACTLAVAHAKPMKEILTDMNKRSDNLARSVFLKLGGD
      310      320      330      340      350      360
a794.pep GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAOMLETAYFSPFA
      370      380      390      400      410      420
m794 GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAOMLETAYFSPFA
      370      380      390      400      410      420
a794.pep QDFIDTLPIAGTDGTLRNRFKQSGGLRLKLTGT LNNVRALAGYWLGDKPMV VVIINSGR
      430      440      450      460      470      480
m794 QDFIDTLPIAGTDGTLRNRFKQSGGLRLKLTGT LNNVRALAGYWLGDKPMV VVIINSGR
      430      440      450      460      470      480
a794.pep AVSLLPDLDNFVANNIISGGDGWLD AKLMCKERRAX
      490      500      510
m794 AVSLLPDLDNFVANNIISGGDGWLD AKLMCKERRAX
      490      500      510

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2699>:

```

g900.seq
1   ATGccgTCTG AAATGCCGTC TGAACGTGG CAGGCGEAGG TTCGACGGC
51  ATTGGGTTTA TTTCAACGGG CGGATGCCGA CCGCATCGCG TACTTTATCC
101 AACAAATTCGC GCGCTTCTTT GCGCGCTTTT TGCGCGcctg cctGCAAAAT
151 CTCTTCGATT TGCGAAGGAT TAGAGGTCAA TGCGTGTAG CGTTCGCGCA
201 GTTCTGCCAA TTCGGCGTTG ATTTTCGCCG CCGAAAGTTT TTTCGCCTCG
251 CCCCAAGCCA AGCCGTCGGC AAGCATTTGC GTAAATTCCG CCGTTTCAGA
301 CGGCGTGGAG AAGGCTTTAT AGATTTCAAA CAAAGGGCTT TCGTCGGGCT
351 GTTTCGGCTC GCCCGGCTCT TTCATGTTGG TAATGATTTT GTTGACCGAT
401 TTTTGGGTTT TTTTGTGCTT TTCCCAAAGC GGAATGGTAT TGCCGTAGGA
451 TTTGGACATT TTGCGTCCGT CCAAACCGAC CAAGAGTTTCG ACGTTTTCGT
501 CGATTTTCAC TTCGGGCagg GTGaagagtt cTTGGAaacc gtgggtgaag
551 cggccggcAa tgcgcgcgc cATTTCgacg tgttgGATTT GGTGCGGCC
601 GACGGGGA CTGTTGGCGT TGAACATCAA AATGTCGCA GTCATCAGAA
651 TCGGATAACT GAACAAACCC ATTTCCACAC CGAAATCGGG GTCTTCCTGC
701 CCGTTTTCCG CATTGGCTTG AACGGCGGCT TTGTAGGCGT GGGCGCGGTT
751 CATCAAACCC TTGGCGGTGA TGCAGGTCAG AATCCAGTTC AACTCCATCA
801 CTTCGGGAAT GTCGCTTTGG CGGTAGAAGG TGGTGCCTC GGGGTCGAGT
851 CCGCAGGCAA GCCAAGTGGC GGCAACGGCt tggGTGGATT GGTGAATCAT
901 CTCCTGCTCG TGGCATTGTA TGATGCCGTG GTAATCGCG AGGAAGAGGA
951 AGGATTCGGT ATCGGGGTTT TGCGCGCGC GGACGGCGGG GCGGATGGCG
1001 CCGACGTAGT TGCCAGATG CGGGGTGCC GTGGTGGTTA CGCCGTCAG
1051 AACTCGTTTT TTGCTCATAA AAATGTCCTT ACGGCAGCAA TGCCGTCTGA
1101 AAGGAAAa. gatgcgCCGA TTATACCCGA TTTGCCACAT ACATCCAGCC
1151 GacaACagaC TTTTCCATAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2700; ORF 900.ng>:

```

g900.pep
1   MPSEMPSETW QAEVRTALGL FQRADADRIA YFIQQFARFF ARFLRACLQN
51  LFDLRRIRGQ CVVAFQFCQ FGVDFFFFKF FRLAPSQAVG KHLRKFRFRF
101 RRGEFIDFK QRAFVGLFRL ARLFHVGNDF VDRFLGFFV FPKRNGIAGV
151 FGHFASVQTD QEFDVFDVFH FGQGEFLET VGEAAGNVAR HFDVLDLVAP
201 DGDFVGVHEQ NVGSHQNRIT EQTHFTEIG VFPLPVFRIGL NGGFVGVGAV
251 QTLGGDAGQ NPVQLHHFGN VALAVEGGAL GVESAGKPSG GNLGGLVNH
301 LLLVAFDDAV VIGEEEGFG IGVLRRADG ADGADVVAQM RGAGGGYAGQ
351 NSFFAHKNVL TAAMPSEK DAPIIPDLPH TSSRQOTFPY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2701>:

```

m900.seq
1   ATGCCGCTCTG AAACGCGGCA GGCGGAGGTT CGGACGGCAT CGGGTTCATT
51  TCAACGGGCG GATGcCGACC GCATCgG.TA CTTTGTCCAA TAATTCGCGT
101 GCTTCCTTAC GCGCTTTCGC CGCGCCTGCC TGCAAAATCT CTTGATTTG

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1282

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151 CGAAGGGTCG GCGGTCAGCT CGTTGTAGCG TTCGCGCGGT TCGGCGAGTT
201 CCGCGTTGAT TTTCGCGGCC AAAAGTTTTT TGGCTTCACC CCACGCCAAG
251 CCGTCGGCAA GCATTTTCGT AAATTCACC GTTTCAGACG GCGTGGAGAA
301 GGCTTTGTAG ATTTCAAACA ATGGGCTTTC GTCGGGCTGT TTCGGCTCGC
351 CCGGCTCTTT CATATTGGTG ATGATTTGT TGACCGATT TTGGGTTTTT
401 CTGTCTGTTT CCCAAAGCGG AATGGTGTG CCGTAGGATT TGGACATTTT
451 GCGTCCGTCC AAACCGACCA AGAGTTCGAC GTTTTCATCG ATTTTCACTT
501 CCGGCAGGGT GAAGAGTTC CGGAAGCGGT GGTGGAAGCG GCCGGCGATG
551 TCGCGCGCCA TTTCGACGTG TTGGATTGTG TCGCGCCCGA CgGGCaCTTC
601 GTTGGCGTTG AACATCAGAA TATCGGCGAT CATCAGAATC GGATAACTGA
651 ACAAACCCAT TTCCACACCG AAATCAGGGT CTTCTGCCC GTTTTCTGCA
701 TTTGCCTGCA CGGCGGCTTT GTAGGCATGG GCGCGGTTCA TCAAACCTT
751 GGCAGTGATG CAGGTAGAA TCCAGTCAA TTCCATCACT TCgGGAGTGT
801 CGCTTTGGCG GTAGAAGGTG GTGCGCTCGG GGTGAGTCC GCAGCAAGC
851 CAAGTGGCGG CAACGGCTTG GGTGGATTGG TGAATCATCT CCGGCTCGTG
901 GCATTTGATG ATACCGTGGT AATCGGCGAG GAAGAGGAAG GATTGCGTAT
951 CGAGGTTTTG CGCCGCGCGG ACGGCGGGGC GGATGGCGCC GACGTAGTTG
1001 CCCAGATGCG GGATGCCGCT GGTGGTTACG CCGGTCAGAA CTCGTTTTTT
1051 GCTCATAAAA ATGTCCTTGC GGCATCAATG CCGTCTGAAA GGGAAAAAGA
1101 TGTGCCGATT ATACCGATT TGCCACCTAC ATCCAGCCGA CAACAGACTT
1151 TTCCATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2702; ORF 900>:

m900.pep

```

1 MPSETRQAEV RTASGSFQRA DADRIXFYVQ *FACFFTRFR RACLQNLFDL
51 RRVGGQLVVA FARFGEFGVD FRRQKFFGFT PRQAVGKHFR KFHRFRRRGE
101 GFVDFKQWAF VGLFRLARLF HIGDDFVDRF LGFFVVFPRK NGVAVGPGHF
151 ASVQTDQEFV VFIDFHFGQG EEFPEAVVEA AGDVARHFDV LDLVAPDGHF
201 VGVEHQNIGS HQNRITEQTH FHTEIRVFLP VFCICLHGGF VGMGAHVQTL
251 GSDAGQNPVQ FHHFGSVALA VEGGALGVES AGKPSGGNGL GGLVNHLRLV
301 AFDDTVVIGE EEEFGFIEVL RRDAGGADGA DVVAQMRDAG GYGAGQNSFF
351 AHKNVLAASM PSEREKDVPI IPDLPTSSR QQTFPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 900 shows 87.0% identity over a 386 aa overlap with a predicted ORF (ORF 900.ng) from *N. gonorrhoeae*:

m900/g900

```

          10      20      30      40      50
m900.pep  MPSETRQAEVRTASGSFQRADADRIGYFVQXFACFFTRFRRAACLQNLFDLRRVGGQ
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g900      MPSEMPSETWQAEVRTALGLFQRADADRIAYFIQQFARFFARFLRACLQNLFDLRRIRGQ
          10      20      30      40      50      60

          60      70      80      90      100     110
m900.pep  LVVAFARFGEFGVDFRRQKFFGFTPRQAVGKHFRKFHRFRRRGEGFVDFKQWAFVGLFRL
          ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g900      CVVAFAPQFCQFGVDFRRRKFFRLAPSQAVGKHLRKFRFRRRRGEGFIDFKQRAFVGLFRL
          70      80      90      100     110     120

          120     130     140     150     160     170
m900.pep  ARLFHIGDDFVDRFLGFFVVFPRKNGVAVGFGHFASVQTDQEFVDFIDFHFGQGEFPEA
          ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g900      ARLFHVGNDFVDRFLGFFVVFPRKNGIAVGFGHFASVQTDQEFVDFVDFHFGQGEFLET
          130     140     150     160     170     180

          180     190     200     210     220     230
m900.pep  VVEAAGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTEIRVFLPVFCICL
          ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g900      VGEAAGNVARHFDVLDLVAPDGHFVGVEHQNVGSHQNRITEQTHFHTEIGVFLPVFRIGL
          190     200     210     220     230     240

```

1283

	240	250	260	270	280	290
m900.pep	HGGFVGMGAVHOTLGSDAGQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNH					
	: : : : : : :					
g900	NGGFVGVGAVHQTLGGDAGQNPVQLHHFGNVALAVEGGALGVESAGKPSGGNGLGGLVNH					
	250	260	270	280	290	300
	300	310	320	330	340	350
m900.pep	LRLVAFDDTVVIGEEEEFGFIEVLRRADGGADGVVAQMRDAGGGYAGQNSFFAHKNVL					
	: : : : : : :					
g900	LLLVAFDDAVVIGEEEEFGFIEVLRRADGGADGVVAQMRGAGGGYAGQNSFFAHKNVL					
	310	320	330	340	350	360
	360	370	380			
m900.pep	AASMPSEREKDVPIIPDLPTSSRQQTFFPYX					
	: : : : : :					
g900	TAAMPSEEREKDAPIIPDLPTSSRQQTFFPYX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2703>:

a900.seq (partial)

```

1   GAGGTTCCGA CGGCATTGGG TTTATTTCAA CGGGCGGATA CCGACCGCAT
51  CACGTACTTT GCCCAATAAT TCGCGTGCCT CTTTACGCGC TTTTTCGCGC
101 CCTGCCTGCA AAATCTCTTC GATTTCGCAA GGGTCGGCGG TCAGCTCGTT
151 GTAGCGTTTCG CGCGGTTTCGG CGAGTTCGGC GTTGATTTCG GCCGCCAAAA
201 GTTTTTTTGTC CTGCCCCCAA GCCAAGCCGT CGGCAAGCAT TTTCGTAAAT
251 TCTGCCGTTT CAGACGGCGT GGAGAAAGCT TTGTAGATT CAAACAGAGG
301 GCTTTCGTCG GGTTCCTTCG GCTCGCCCGG CTCTTTCATA TTGGTGATGA
351 TTTTGTGAC  CGATTTTGGT GTTTTTTTGT CGTTTTCCCA AAGCGGAATG
401 GTGTTGCCGT AGGATTTGGA CATTTTGCCT CCGTCCAAAC CAACCAAGAG
451 TTCGACGTTT TCGTCGATTT TCACTTCGGG CAGTGTGAAG AGTTCCTCGG
501 AGCGGTGGTT GAAGCGGCCG GCAATATCGC GTGCCATTTC AACGTGTTGG
551 ATTTGGTTCG GACCGACTGG AACTTCATGG GCATTGAACA TGAGAATGTC
601 GGCACTCATG AGGATAGGGT AGCTGTACAA ACCCATTTC ACGCCGAAAT
651 CGGGGTCTTC CTGCCCGTTT TCCGCATTG CCTGCACGGC GGCTTTGTAG
701 GCGTGGGCGC GGTTCATCAA ACCCTTGCGG GTGATGCAGG TCAGAATCCA
751 GTTCAATTCC ATCACTTCGG GAATGTCGCT TTGACGGTAG AAGGTGGTGC
801 GCTCGGGGTC GAGTCCGCAG GCAAGCCAAG TGGCGGCAAC GGCTTGGGTG
851 GATTGGTGAA TCATCTCCGG CTCGTGGCAT TTGATGATAC CGTGGTAATC
901 GCGGAGGAAG AGGAAGGATT CGGTATCAGG GTTTTGGCCC GCGCGGACGG
951 CGGGGCGGAT AGCACCAGC TAGTTGCCCA GATGCGGGAT GCCGGTGGTG
1001 GTTACGCCGG TCAGAACTCG TTTTGTGCTC ATAAAAATGT CCTTGCGGCA
1051 TCAATGCCGT CTGAAAGGGA AAAAGATGCG CCGATTATAC CCGATTGGCC
1101 ACCTACATCC AGCCGACAAC AGACTTTTCC ATATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2704; ORF 900.a>:

a900.pep (partial)

```

1   EVRTALGLEFQ RADTDRTYF AQ*FACFFTR FLRAQLQNLF DLRRVGGQLV
51  VAFARFGEFG VDFRRQKEFC LAPSQAVGKH FRKFCRFRRR GESFVDFKQR
101 AFVGLLRLAR LFHIGDDFVD RFLGFFVFP KRNGVAVGFG HFASVQTNQE
151 FDFVDFHFG QCEEFPEAVV EAAGNIACHF NVLDLVATDW NFMGIEHENV
201 GSHEDRVAVQ THEHAEIGVF LPVFRICLHG GFVGVGAVHQ TLGGDAGQNP
251 VQFHHFGNVA LTVEGGALGV ESAGKPSGGN GLGGLVNH LR LVAFDDTVVI
301 GEEEEFGIR VLRRADGGAD STDVVAQMRD AGGGYAGQNS FFAHKNVLAA
351 SMPSEREKDA PIIPDLPTS SRQQTFFPY*

```

m900/a900 88.4% identity in 378 aa overlap

	10	20	30	40	50	60
m900.pep	MPSETRQAEVVRTASGSFQRADADRIXFYVQXFACFFTRFRRAQLQNLFDLRRVGGQLVVA					
	: : : : : :					
a900	EVRTALGLFQRADTDRTYFAQXFACFFTRFLRAQLQNLFDLRRVGGQLVVA					
	10	20	30	40	50	
	70	80	90	100	110	120

1284

```

m900.pep    FARFGEFGVDFRRQKFFGFTPRQAVGKHFRKFHRRRGEGFVDFKQWAFVGLFRLARLF
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900        FARFGEFGVDFRRQKFFCLAPSAQVAGKHFRKFHRRRGESFVDFKQRAVGLRLRLARLF
             60      70      80      90      100     110

             130     140     150     160     170     180
m900.pep    HIGDDFVDRFLGFFVFPKRNGVAVGFGHFASVQTDQEFDFIDFHFQGEFFPEAVVEA
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900        HIGDDFVDRFLGFFVFPKRNGVAVGFGHFASVQTNQEFDFVDFHFQCEEFPEAVVEA
             120     130     140     150     160     170

             190     200     210     220     230     240
m900.pep    AGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTAIRVFLPVFCICLHGGF
             ||::| ||:||||| |::|:||||:||||:||||: ||||:| ||||| |||||
a900        AGNIACHFNVLDLVATDWNFMGIEHENVGSHEDRVAVQTHFAEIGVFLPVFRICLHGGF
             180     190     200     210     220     230

             250     260     270     280     290     300
m900.pep    VGMGAVHQTLGSDAGQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNHRLRV
             ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900        VGVGAVHQTLGSDAGQNPVQFHHFGNVALTVEGGALGVESAGKPSGGNGLGGLVNHRLRV
             240     250     260     270     280     290

             310     320     330     340     350     360
m900.pep    AFDDTVVIGEEEEGFGIEVLRADGGADGADVVAQMRDAGGGYAGQNSFFAHKNVLAASM
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900        AFDDTVVIGEEEEGFGIRVLRADGGADSTDVVAQMRDAGGGYAGQNSFFAHKNVLAASM
             300     310     320     330     340     350

             370     380
m900.pep    PSEREKDVPIIPDLPTSSRQQTFFPYX
             |||||:|||||:|||||:|||||:|||||
a900        PSEREKDAPIIPDLPTSSRQQTFFPYX
             360     370

```

g901.seq not found yet

g901.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2705>:

```

m901.seq
1  ATGCCCGATT TTTCGATGTC CAATTTGGCC GTTGCCTTTT CCATCACATT
51  GGCTGCCGGT TTGTTTACCG TATTAKyAG TGGCTTGGTG ATGTTTTCCT
101 AAACGCCCAA TCCGCGTGTG TTGTCGTTTG GTTTGGCGTT TGCCGCGCGT
151 GCGATGGTAT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTGCGCGC GCGACCATGG
251 CATTTTTGGC CGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
301 AACCCGCATG AAACCTTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA
351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGGCGGTTT GCGATTACTG
401 CGCACAAATT CCCCGAAGGC TTGGCGACGT TTTTGGCCAC ATTGGAAAAT
451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTC
501 GGAGGGCATT TCCATCGCCG CGCCGGTTTA TTTTGCCACC CGCAGCCGTA
551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGGCCGA GCCGTGGGG
601 GCGGCTTTGG GCTATTGGT TTGCAGCCG TTTTGTGCG CTGCCGTGTT
651 TGSTTCGGTA TTCGGCGTGA TAGCCGCGT GATGGTGTT TTGGCGTTGG
701 ACGAGCTGnt GCCGGCTGCC AAACGCTATT CAGACGCCA TGAAACCGTT
751 TACGGCTGA CAACGGGTAT GCGGTGATT GCCGTCAGCC TGGTATTGTT
801 CCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2706; ORF 901>:

```

m901.pep
1  MPDFSMNL A VAFSITLAAG LFTVLXGLV MFSKTPNPRV LSFGLAFAGG
51  AMVYVSLTEI FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP

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1285

101 NPHETLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWAC LLSGLAEPLG
 201 AALGYLVLPQ FLSPAVFGSV FGVAGVMVF LALDELXPAA KRYSDGHETV
 251 YGLTTGMAVI AVSLVLFHF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2707>:

a901.seq
 1 ATGCCCCGATT TTTGATGTC CAATTTGGCC GTTGCCCTTT CCATTACGTT
 51 GGCTGCCGGT TTGTTTACCG TATTAGGCAG CGGCTTGGTG ATGTTTTCCT
 101 AAACCGCCAA TCCGCGCGTG TTGTCGTTTG GTTGGCATT TGCCGGCGGT
 151 GCGATGGTGT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
 201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTGCGGCG GCGACCATGG
 251 CATTTTTGGC AGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
 301 AACCCGCATG AAACCTTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA
 351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGGCGGTTT GCGATTACTG
 401 CGCACAATT CCCCGAAGGC TTGGCGACGT TTTTGCCAC ATTGGAATAT
 451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTC
 501 GGAGGGCATT TCCATCGCCG CGCGGTTTA TTTGCCACC CGCAGCCGTA
 551 AGAAACCGGT GTGGGCGTGT CTGCTATCCG GCTTGGCCGA GCCGTTGGGG
 601 GCGGCTTTGG GCTATTTGGT TTTGCAGCG TTTTGTGCG CTGCCGTGTT
 651 TGGTTCGGTA TTCGGCGTGA TAGCCGGTGT GATGGTGTG TTGGCGTTGG
 701 ACGAGCTGCT GCCGCTGCC AAACGCTATT CAGACGGCA TGAAACCGTT
 751 TACGGCCTGA CAATGGGCAT GCGGTGATT GCCGTCAGCC TGGTATTGTT
 801 CCATTTTAA

This corresponds to the amino acid sequence <SEQ ID 2708; ORF 901.a>:

a901.pep
 1 MPDFSMSNLA VAFSITLAAG LETVLGSGLV MFSKTPNPRV LSFGLAFAGG
 51 AMVYVSLTEI FSKSSEAFAE IYDKDHAFAA ATMAFLAGMG GIALIDRLVP
 101 NPHETLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWAC LLSGLAEPLG
 201 AALGYLVLPQ FLSPAVFGSV FGVAGVMVF LALDELLPAA KRYSDGHETV
 251 YGLTMGMAVI AVSLVLFHF*

m901/a901 98.9% identity in 269 aa overlap

m901.pep	10	20	30	40	50	60
	MPDFSMSNLA	VAFSITLAAG	LETVLGSGLV	MFSKTPNPRV	LSFGLAFAGG	AMVYVSLTEI
a901	10	20	30	40	50	60
	MPDFSMSNLA	VAFSITLAAG	LETVLGSGLV	MFSKTPNPRV	LSFGLAFAGG	AMVYVSLTEI
m901.pep	70	80	90	100	110	120
	FSKSSEAFAE	IYDKDHAFAA	ATMAFLAGMG	GIALIDRLVP	NPHETLDAQD	PSFQESKRRH
a901	70	80	90	100	110	120
	FSKSSEAFAE	IYDKDHAFAA	ATMAFLAGMG	GIALIDRLVP	NPHETLDAQD	PSFQESKRRH
m901.pep	130	140	150	160	170	180
	IARVGMMAAF	AITAHNFPEG	LATFFATLEN	PAVGMPLALA	IAIHNIPEGI	SIAAPVYFAT
a901	130	140	150	160	170	180
	IARVGMMAAF	AITAHNFPEG	LATFFATLEN	PAVGMPLALA	IAIHNIPEGI	SIAAPVYFAT
m901.pep	190	200	210	220	230	240
	RSRKKTWAC	LLSGLAEPLG	AALGYLVLPQ	FLSPAVFGSV	FGVAGVMVF	LALDELXPAA
a901	190	200	210	220	230	240
	RSRKKTWAC	LLSGLAEPLG	AALGYLVLPQ	FLSPAVFGSV	FGVAGVMVF	LALDELLPAA
m901.pep	250	260	270			
	KRYSDGHETV	YGLTTGMAVI	AVSLVLFHF			
a901	250	260	270			
	KRYSDGHETV	YGLTTGMAVI	AVSLVLFHF			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2709>:

g902.seq

```

1  ATGCCGTCCG AACCCGAACG GCGGCATGGC AATACTGCCC TACCCTTCCC
51  GATAGCCGCA CGCCCAACGG TCGTTTTTTC CGGCAAGCCT TTCAAGATAA
101 CCGGCAAGTG TGTCGTATTG CGCCGCCGCA TTGTCCAAGC GGTTGATTTT
151 ACGCCGCGCC TGTTGCGCGT CGGGCATTTC GCCGATGTAC CAGCCTATGT
201 GTTTGCGTGC GATGCGCACA CCGACGGTCT CACCATAAAA CGCGTGCATG
251 GCGCGGATGT GGTTCAAAAT GGCGGCTCTG CATTCTGCCA AACTCAAGGC
301 AGGCGGTAAA ACGCCGTGTT CGGCATAATG CTTCAAATCG CGGAAAAACC
351 ACGGCCTGCC TTGCGCGCCG CGCCCTATCA TGATGCCGTC GGCGGCGGTT
401 TGTTTGAGGA cggCGGCGGC TTTTgcggc GAagtGATGT CGCCGTTGac
451 cCaggCCGGG ATGTTCAgAc ggCTTTTGGT CTCGgcatg agttCGTAAC
501 gcGCCTCGCC TTTGTACATT TGCGTGcgCG CGcgccgtg aacgcaagGg
551 gcggaatgc cgcaatcttc ggcgattttg gcgacggcgG gcaggttttg
601 atcgctcgctg tgccaaccca AacggGTTTT GaggGTAAAG GGTAcgcCCG
651 CCGCCTTgac caccgcctcc aAAatggcGg caaccagcgg CTCGTCTGTC
701 ATCagcGCGC TACCGGCTTG GACGTTGCAC ACTTTCTtgg cgggGCAGCC
751 CATAttgATG TCGATGACCT GCGCCCGAG TCCGACGTTg taacgcgCG
801 catCCGCCAT CtgttcggGG TCGTGCCGG CAATCTGCAC GGCAACGATG
851 CCGccttcac cggcaAAAtc actgcggtgc aGGGTTTTTC CGGTATTCTT
901 GAGCGTCGGA TCGCTGGCCA GCATTTCGCA CACCGCCCAA CCTGCGCCAA
951 ACGCCCGACA GAGGCGCGCG AAGGGTTTGT CGGCAATGCC CGCCATCGGC
1001 GCAAGTGCga TGGGGTGTTC GATAAAATAA CCGCCGATGT GCATAATGGG
1051 CCCGCGTTTC AAAAAAGTGC GCCATTGTAC ATTTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2710; ORF 902.ng>:

g902.pep

```

1  MPSEPERRHG NTALPFPIAA RPTVGFSGKP FKITGKCVVL RRRIVQAVDF
51  TPRLFAVGHF ADVPAYVFAC DAHTDGLTIK RVHGADVQN GGSAPCQTQ
101 RR*NAVFGIM LQIAEKPRPA LRAAPYHDAV GGGLFEDGG FLRRSDVAVD
151 PGRDVQTAFG LGDEFVTRLA FVHLRARAPV NGKGGNAIF GDFGDDGQVL
201 IVVVPTQTGF EGNGYARRLD HRLQNGGNQR LVLHORATGL DVAHFLGGAA
251 HIDVDLRLPE SDVVTRRIRH LFGVAAGNLH GNDAAFIGKI TAVQFSGIP
301 ERRIAGQHFA HRPTCAKRPT EAAEGFVGNA RHRRKCDGVV DKITADVHNG
351 PAFQKSAPLY IF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2711>:

m902.seq

```

1  TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATT TGGCGGTAGG
51  CGCACGCCCC ACTGTCGGTT TTTTCGGCAA GTCTTTCAAG ATAACTGCA
101 AGCATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTACGACG
151 TgTCTgTTTC CCGTcGGGCA TTTCTGCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTGCGCGT AAAACGCGTG TATGGCGCGG
251 ATGTGTTTCA AAATAGCGGC GGCGCATTCT GCCAACTCA AGGCAGGCGG
301 CAAAACACCG TGTTGCGCAT AATGTTTCAA ATCGCGGAAG AACCACGGCC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCGGCGGC GGTGTGTTTG
401 AGGACGGCTT GGGCTTTTTG CGGCGAAGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGTTTCGGC GATGAGTTG TAACGCGCTT
501 CGCCTTTGTA CATTTGCGTA CGCGTGCGTC CGTGGACGGC AAGGGCGCGG
551 ATGCCGCAAT CTTCGCGCAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCTGCCGCAC
651 GGACGACGGC TTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACA'T GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAAACG GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCCT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTTGAGCGT
901 CGGGTCGCTG GTCAGCATT TGCACACCGC CCAACCTGCG CCAAAATCTC
951 GGGAAAGTCG GCGGAACGGT TTGTGCGTAA TGCCCGCAT CGGcGCaAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCGG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2712; ORF 902>:

1287

m902.pep

```

1  LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT
51  CLFAVGHFVD VPAYVFACDA HTGGVAVKRV YGADVQNSG GAFQCQTQGRR
101 QNTVFGIMFQ IAEEPRPALR AAPYHNAVGG GLFEDGLGFL RRSNVAVDPD
151 RDVQTAFGFG DEFVTRFAFV HLRTRASVDG KGGDAAIFGD FGDDGOVLMV
201 VVPTQTGFEG NGYACRTDDG FQNGGNQRLV LHQRATGLDI ADFFSGTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFAGR PTCAKISAKS AERFVGNAH RRCDCGVVDK IAADVHNGSA
351 FQKSTPLYIF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 902 shows 80.9% identity over a 345 aa overlap with a predicted ORF (ORF 902.ng) from *N. gonorrhoeae*:

m902/g902

m902.pep	10	20	30	40	50
	LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT CLFAVGHF				
g902	MPSEPERRHGNTALPFPIAARPTVGFSKGPKITGKCVLRRRIQAVDFTPRLFAVGHF				
	10	20	30	40	50
m902.pep	60	70	80	90	100
	VDVPAYVFACDAHTGGVAVKRVYGADVQNSG GAFQCQTQGRRQNTVFGIMFQIAEEPRPA				
g902	ADVPAYVFACDAHTDGLTIKRVHGADVQNGGS AFCQTQGRRXNAVFGIMLQIAEKPRPA				
	70	80	90	100	110
m902.pep	120	130	140	150	160
	LRAAPYHNAVGGGLFEDGLGFLRRSNVAVDPDRDVQTAFGFGDEFVTRFAFVHLRTRASV				
g902	LRAAPYHDAVGGGLFEDGGGFLRRSDVAVDPGRDVQTAFGLGDEFVTRLAFVHLRARAPV				
	130	140	150	160	170
m902.pep	180	190	200	210	220
	DGKGGDAAIFGDFGDDGOVLMVVVPTQTGFEGNGYACRTDDG FQNGGNQRLVLHQRATGL				
g902	NGKGGNAAIFGDFGDDGOVLIVVVPTQTGFEGNGYARRLDHRLQNGGNQRLVLHQRATGL				
	190	200	210	220	230
m902.pep	240	250	260	270	280
	DIADFFSGTAHVVDVDKLRPKADVVTTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSIS				
g902	DVAHFLGGAHIDVDDL RPESDVVTRRIRHLFGVAAGNLHGNDAAFIGKITAVQGFSGIP				
	250	260	270	280	290
m902.pep	300	310	320	330	340
	ERRVAGQHFAGRPTCAKISAKSAERFVGNAHRRRKCDCGVVDKIAADVHNGSAFQKSTPLY				
g902	ERRIAGQHFAGRPTCAKRPTAAEGFVGNAHRRRKCDCGVVDKIADVHNGPAFQKSAPLY				
	310	320	330	340	350
m902.pep	360				
	IFX				
g902	IFX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2713>:

a902.seq

```

1  TTGCACTTTC AAAGGATAAT CAAGTGTCA GAAGGCATTT GGGCGGTAGG
51  CGCACGCCCA ACTGTCGTT TTTTCGGCAA GTCTTCAAG ATAACCTGCA

```


1288

```

101 AACATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTACGACG
151 TGTCTGTTTCG CCGTCGGGCA TTTCTGTCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTGCGCGT AAAACGCGTG CATGGCTCGG
251 ATGTGTTTCA AAATAGTGGC GGTACATTCT GCCAACTCA AGGCAGGCGG
301 TAAAACACCG TGTTGCGCGT AATGTTTCAA ATCGCGGAAG AACCACGGTC
351 TGCTTTCGCG GCCGCGCCT ATCATAATGC CGTCTGCGGC GGTGTTTGTG
401 AGGACGGCTT GGGCTTTTTG CGGCGAGGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC AATCAGGTCG TAAGCCGCTT
501 CGCCTTTGTA CATTGCGTG CGCGTGGTC CCGGACGGC AAGGGCGGCA
551 ATGCCGCAAT CTTCGGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCCGCCGCTT
651 TGACCACCGC CTCCAAAATG GCGCAACCA GCGGCTCGT CTGCATCAGC
701 CGCCTTACCG CTGGACATT GCAGACTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC CGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGCAATCT GCACGGCAAC AATGCCGCCT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGT TTTCTAGTAT TTCTGAGCGT
901 GGGTGGCTG GTCAGCATT CGCACACCG CCAACCTGCG CCAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CGGCGCAAGT
1001 GCGATGGGGT TGTGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2714; ORF 902.a>:

a902.pep

```

1 LHFQRIKCS EGIWAVGARP TVGFFGKSFK ITCKHVLRRTVQAVDFTT
51 CLFAVGHFVD VPAYVFACDA HTGGVAVKRV HGSDVVQNSG GTFCQTQGRR
101 *NTVFGVMFQ IAEPRPSALR AAPYHNAVCG GLFEDGLGFL RRGNVAVDPD
151 RDVQTAFGFG NQVVSRAFAV HLRARASVDG KGNAAIFGD FGDDGQVLMV
201 VVPTQTGFEG NGYARRFDHR LQNGGNQRLV LHQRATGLDI ADFFSGTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFHHR PTCAKISAKS AERFVGNAHR RRCDCGVVDK TAAVDHNGSA
351 FQKSTPLYIF *

```

m902/a902 94.7% identity in 360 aa overlap

	10	20	30	40	50	60
m902.pep	LHFQRIKCS	EGIWAVGARPT	TVGFFGKSFK	ITCKHVLRRTV	QAVDFTTCL	FAVGHFVD
a902	LHFQRIKCS	EGIWAVGARPT	TVGFFGKSFK	ITCKHVLRRTV	QAVDFTTCL	FAVGHFVD
	10	20	30	40	50	60
m902.pep	VPAYVFACDA	HTGGVAVKRV	GADVQNSG	AFQCQTQGR	RQNTVFGIM	FQIAEPRPALR
a902	VPAYVFACDA	HTGGVAVKRV	HGSDVVQNSG	TFCQTQGR	RXNTVFGVM	FQIAEPRPSALR
	70	80	90	100	110	120
m902.pep	AAAPYHNAV	GGGLFEDGL	FLRRSNVAV	DPDRDVQT	AFGFGDEF	VTFRFAFVHLRTRASVDG
a902	AAAPYHNAV	CGGLFEDGL	FLRRGNVAV	DPDRDVQT	AFGFGNQV	SRAFAFVHLRARASVDG
	130	140	150	160	170	180
m902.pep	KGGDAAI	FGDFGDDG	QVLMVVVPT	QTGFEGNG	YACRTDDG	FQNGGNQRLV
a902	KGNAAI	FGDFGDDG	QVLMVVVPT	QTGFEGNG	YARRFDHRL	QNGGNQRLV
	190	200	210	220	230	240
m902.pep	ADFFSGTA	HVDVDKLR	PKADVVT	TRGIRHLL	RIASGNLH	GNNAFIGKIAA
a902	ADFFSGTA	HVDVDKLR	PKADVVT	TRGIRHLL	RIASGNLH	GNNAFIGKIAA
	250	260	270	280	290	300
m902.pep	RVAGQHFA	HRRPTCAK	ISAKSAER	FVGNARH	RRKCDGV	VDKIAADVH
a902	RVAGQHFA	HRRPTCAK	ISAKSAER	FVGNARH	RRKCDGV	VDKIAADVH
	310	320	330	340	350	360
m902.pep	RVAGQHFA	HRRPTCAK	ISAKSAER	FVGNARH	RRKCDGV	VDKIAADVH
a902	RVAGQHFA	HRRPTCAK	ISAKSAER	FVGNARH	RRKCDGV	VDKIAADVH

1289

```

|||||
a902      RVAGQHFHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF
              310      320      330      340      350      360

m902.pep    X
              |
a902        X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2715>:

```

g903.seq
1  ATGGCAACAC AGGTAGGCGG TGCAAattcG gatgaggCAA GCCCCTGCTT
51 TCCTATTTCT GAGGTGGAA TGGTGGGTGA aGaaacggct aaATTCCGgt
101 tTGCCTcaaa ccaTGCCTTG tgccAAACAC ATTTTGtttc cGgcaagtgt
151 CTGcATGcgg gcgacatTAA TCAAAtcaTG TCCTTAGCAC AAAATGCTTT
201 GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG CCACAGGATT
251 TGAATAGTGG caaGCTTCAA TTAaccctga tgccggGCTA TCtgcgctcC
301 ATAcgaATCG atcggtccaa cgatgatcaa ACCCATgcAG GACGTATTGC
351 AGCATTCCAA AACAAATTTC CCACCCGCTC GAACGATCTG TTGAATCTGC
401 GTGATTTGGA ACAAGGACTG GAAAATCTCA AATGTCTCCC GACTGCGGAA
451 GCCGATCTCC AAATCgttcc cgtAGAGAGA GAACcAAACC AAAGTGATGT
501 CGTGGTGCAA TGGCGGTAAC GTCTGCTGCC CTA CTGTGTG AGTGTGGGGA
551 TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG AAATATCACT
601 TTCTCTGCGG ACAATCCTTT TggactgAGT GATATGTTCT ATGTAAATTA
651 TGGACGTTCA ATTGGCGGTA CGcccgATGA GGAAAATTTT GACGGCCATC
701 GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC AGCCCCTTTC
751 GGTAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT ACCATCAGGC
801 GGTTCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA AGTTACAACA
851 CTGATTTGGG CTCAACCGC CTGTTGTATC GTGATGCCAA ACGCAAAACC
901 TATCTCAGTG TAAAACGTG GACGAGGGAA ACAAAAAGTT ACATTGATGA
951 TGCCGAAC TGCTGACAAC GGCCTAAAC CACAGGTTGG TTGGCAGAAC
1001 TTTCCCAAA AGGATATATC GGTCGCAGTA CGGCAGATT TAAGTTGAAA
1051 TATAACACG GCACCGGCAT GAAAGATGCT CTGCGCGCGC CTGAAGAAGC
1101 CTTTGCGGAA GGCACGTCAC GTATGAAAT TTGGACGGCA TCGGCTGATG
1151 TAAATACTCC TTTTCAAATC GGTAAACAGC TATTTGCCTA TGACACATCC
1201 GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG ACAAACTGGC
1251 TATCGGCGGA CACCACCCG TACGTGGCTT CGACGGTGAA ATGAGTTTGC
1301 CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG GCAATTAA
1351 CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG TTTCAAGACA
1401 ATCCGCCAAA TGGTTATCGG GCCAACTCT AGCCGGCACA GCAATTGGGA
1451 TACGCGGGCA GATAAAGCTT GCGCGCAACC TGCATTACGA TATATTACC
1501 GGCCGTGCAT TGA AAAAGCC cgaatat ttt cAGACGAAGA Aatgggtaac
1551 ggggtTCAG gtgggttatt cgTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2716; ORF 903.ng>:

```

g903.pep
1  MATQVGANS DEASPCFPIS EVELVGEETA KFRFALNHAL CQTHFVSGKC
51 LHAGDINQIM SLAQNALIGR GYTTTRILAA PDLNSGKLQ LTLMPGYLRS
101 IRIDRSNDQ THAGRIAAFQ NKFPTRNDL LNLRDLEQGL ENLKCLPTAE
151 ADLQIVPVER EPNQSDVVVQ WRXRLPYCV SVGMDNSGSE ATGKYQGNIT
201 FSADNPFGLS DMFYVNYGRS IGGTPDEENF DHRKEGGSN NYAVHYSAPF
251 GKWTWAFNHN GYRYHQA VSG LSEVYDNGK SYNTDFGFNR LLYRDAKRKT
301 YLSVKLWTR TKS YIDDAEL TVQRRKTGW LAELSHKGYI GRSTADFKLK
351 YKHGTGMKDA LRAPEEAFGE GTSRMKIWTA SADVNTPFQI GKQLFAYDTS
401 VHAQWNKTPL TSQDKLAI GG HHTVRGFDGE MSLPAERG WY WRNDSWQFK
451 PGHQLYLGAD VGHVSGQSAK WLSGQTLAGT AIGIRGQIKL GGNLHYDIPT
501 GRALKKPEYF QTKKWTGFPQ VGYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2717>:

```

m903.seq
1  ATGCAGCGTC AGCAGCACAT AGATGCTGAA TTGTTAACTG ATGCAAATGT
51 CCGTTTTGAG CAACCATGG AGAAGAACAA TTATGTCCTG ACTGAAGATG
101 AAACACCGTG TACTCGGTA AATTACATTA GTTTAGATGA TAAGACGGTG

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1290

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151 CGCAAATTTT CTTTCTTCC TTCTGTGCTC ATGAAAGAAA CAGCTTTTAA
201 AACTGGGATG TGTTAGGTT CCAATAATTT GAGCAGGCTA CAAAAAGCCG
251 CGCAACAGAT ACTGATCGTG CGTGGCTACC TCACTTCCCA AGCTATTATC
301 CAaCCACAGA ATATGGATTC GGAATTCTG AAATTACGGG TATCAGCAGG
351 CGAAATAGGG GATATCCGCT ATGAAGAAAA ACGGGATGGG AAGTCTGCCG
401 AGGGCAGTAT TAGTGCAATC AATAACAAAT TTCCCTTATA TAGGAACAAA
451 ATTCTCAATC TTCGCGATGT AGAGCAGGGC TTGGAACC TGCGTCGTTT
501 GCCGAGTGT AAAACAGATA TTCAGATTAT ACCGTCCGAA GAAGAAGGCA
551 AAAGCGATTT ACAGATCAAA TGGCAGCAGA ATAAACCCAT ACGGTTCACT
601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTGCGTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTtTATG
701 TTTTCATATGG ACGCGGTTTG GCGCACAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAA CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCCGGT
801 GCCCGTAAAA AAATGGCTGT TTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAACAAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGACTTCA
951 TAAAACTTCA GTCGAATGA AATTATGGAC ACGCCAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTACAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTAGT CCTGCACCGG
1151 AAGAAAACGG CGGCGATATT CTTCAGGTA CATCTCGTAT GAAAATCATT
1201 ACTGCCAGTT TGGACGCAGC CGCCCCATTT AyTTTAGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCGTTGGTTG
1301 CCCAAGATAA ATGTGCAATC GGCAGCCGCT ACACCGTTCG CGGATTTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTGCGCGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TCAACTTGA ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2718; ORF 903>:

```

m903.pep
1  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTV
51  RKFSFLPSVL MKETAFKTGM CLGSNNLSRL OKAAQQILIV RGYLTSQAI
101 QPONMDSGIL KLRVSAGEIG DIRYEKRDG KSAEGSISAF NKNFPLYRNN
151 ILNLRDVEQG LENLRLPSV KTDIQUIPSE BEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL AHKTDLTDAT
251 GTETESGSR S YSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKQ
301 YQSSLAERM LWRNRLHKTS VGMKLWTRQT YKYIDDABIE VQRRRSAGWE
351 AELRHAYLN RWOLDGKLSY KRGTMRQSM PAPEENGDDI LPGTSRMKII
401 TASLDAAFP XLGKQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYL ADYGRVSGES AQYVSGKQLM
501 GAVVGRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 903 shows 48.9% identity over a 519 aa overlap with a predicted ORF (ORF 903.ng) from *N. gonorrhoeae*:

```

m903/g903
          10      20      30      40      50      60
m903.pep  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTV RKFSFLPSVL
                                     |:::| |:::| |:::| |:::|
g903      MATQVGGANSDEASPCFP ISEVELVGEETAKFRFALNHA
                                     10      20      30
          70      80      90      100     110     120
m903.pep  MKETAFKTGM CLGSNNLSRL QKAAQQILIV RGYLTSQAI QPONMDSGIL KLRVSAGEIG
          : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g903      LCQTHFVSGKCLHAGDINQIMSLAQNALIGRGYTTTRILAAPQDLNSGKQLQLTLMPGYLR
          40      50      60      70      80      90

```

[illegible]

a903.seq

1	ATGCAGCGTC	AGCAGCACAT	AGATGCTGAA	TTGTAACTG	ATGCAAATGT
51	CCGTTTCGAG	CAACCATTGG	AGAAGAACAA	TTATGTCCTG	AGTGAAGATG
101	AAACACCGTG	TACTCGGGTA	AATTACATTA	GTTTAGATGA	TAAGACGGCG
151	CGCAAATTTT	CTTTTCTTCC	TTCTGTGCTC	ATGAAAGAAA	CAGCTTTTAA
201	AAC TGGGATG	TGTTTAGGTT	CCAATAATTT	GAGCAGGCTA	CAAAAAGCCG
251	CGCAACAGAT	ACTGATTGTG	CGTGCTACC	TCACTTCCCA	AGCTATTATC
301	CAACCACAGA	ATATGGATTG	GGGAATTCTG	AAATTACGGG	TATCAGCAGG
351	CGAAATAGGG	GATATCCGCT	ATGAAGAAAA	ACGGGATGGG	AAGTCTGCCG
401	AGGGCAGTAT	TAGTCGATTG	AATAACAAAT	TTCCCTTATA	TAGGAACAAA
451	ATTCTCAATC	TTCGCGATGT	AGAGCAGGGC	TTGGAAAACC	TGCGTCGGTT
501	GCGGAGTGTT	AAAACAGATA	TTTCAGATTAT	ACCGTCCGAA	GAAGAAGGCA
551	AAAGCGATTT	ACAGATCAAA	TGGCAGCAGA	ATAAACCCAT	ACGGTTCAGT

1292

```

601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTCGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTTTATG
701 TTTCATATGG ACGCGGTTTG GTGCACAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAA CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCGGT
801 GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAAACAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGGTTTCA
951 TAAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTGCAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCCGCACCTG
1151 AAGAAAACCG CGCGGCTACT ATTCCAGGCA CATCCCGTAT GAAAATCATA
1201 ACCGCGGAT TGGATGCAGC GGCCCCGTTT ATGTTGGGCA AACAGCAGTT
1251 TTTCTACGA ACCGCCATTC AAGCTCAATG GAACAAAACG CCTTTGGTTG
1301 CCAAGACAA GTTGTCTATC GGCAGCCGCT ACACCGTTNG CGGATTTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGNTTCAG AGGAGGNCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTGCGCGGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2720; ORF 903.a>:

a903.pep

```

1  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTA
51  RKFSFLPSVL MKETAFTKGM CLGSNNLSRL QKAAQQILIV RGYLTSQAI
101 QPNMDSGIL KLRVSAGEIG DIRYEKRDG KSAEGSISAF NKFPLYRNK
151 ILNLRDVEQG LENLRLPSV KTDIQUIPSE EEGKSDLQIK WQNKPIRFS
201 IGIDTAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL VHKTDLTDAT
251 GTETESGSR SSVHYSPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ
301 YQSSLAERM LWRNRFHKT VGMKLWTRQT KYIDDAEIE VQRRRSAGWE
351 AELRHAYLN RWQLDGKLSY KRGTGMRQSM PAPEENGSGT IPGTSRMKII
401 TAGLDAAAF MLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVXGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRRGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

m903/a903 98.4% identity in 547 aa overlap

	10	20	30	40	50	60
m903.pep	MQRQQHIDAE	LLTDANVRFE	QPLEKNNYVL	SEDETPCTRV	NYISLDDKTV	RKFSFLPSVL
a903	MQRQQHIDAE	LLTDANVRFE	QPLEKNNYVL	SEDETPCTRV	NYISLDDKTAR	KFSFLPSVL
	10	20	30	40	50	60
m903.pep	70	80	90	100	110	120
a903	MKETAFTKGM	CLGSNNLSRL	QKAAQQILIV	RGYLTSAIIQ	PNMDSGILK	LRVSAEIG
	70	80	90	100	110	120
m903.pep	130	140	150	160	170	180
a903	DIRYEKRDG	KSAEGSISAF	NKFPLYRNK	ILNLRDVEQ	LENLRLPSV	KTDIQUIPSE
	130	140	150	160	170	180
m903.pep	190	200	210	220	230	240
a903	EEGKSDLQIK	WQNKPIRFS	IGIDTAGGKT	TGKYQGNVAL	SFDNPLGLSD	LFYVSYGRGL
	190	200	210	220	230	240
m903.pep	250	260	270	280	290	300
a903	AHKTDLTDAT	GTETESGSR	SSVHYSPVK	KWLFSFNHNG	HRHYHEATEG	SVNYDYNKGQ

1293

	250	260	270	280	290	300
	310	320	330	340	350	360
m903.pep	YQSSSLAAERMLWRNRLHKT SVGMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHRLAYLN					
a903	YQSSSLAAERMLWRNRFHKT SVGMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHRLAYLN					
	310	320	330	340	350	360
	370	380	390	400	410	420
m903.pep	RWQLDGKLSYKRGTGMRQSMPEENG DILPGTSRMKIITASLDAAAPFXLGKQQFFYA					
a903	RWQLDGKLSYKRGTGMRQSMPEENG GTIPGTSRMKIITAGLDAAAPFMLGKQQFFYA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m903.pep	TAIQAQWNKTPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYL					
a903	TAIQAQWNKTPLVAQDKLSIGSRYTVXGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYL					
	430	440	450	460	470	480
	490	500	510	520	530	540
m903.pep	ADYGRVSGESAQYVSGKQLMGAVVGFRRGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
a903	ADYGRVSGESAQYVSGKQLMGAVVGFRRGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
	490	500	510	520	530	540
m903.pep	FNLNYSFX					
a903	FNLNYSFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2721>:

g904.seq

```

1  ATGATGCAGC ACAATCGTTT CTTCGCGGTC GGGGCCGGTg gaGACGATGG
51  CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGCA ATGCGTCGTA GCTTTTCACG CCGACAGTCG ATTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGTTTGCA GGTTCACACC GCATCCGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGC CTGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATGCA
301 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACAGGCC GCAGCGGCGC GCGCGGCCGG TTACCGAACC GAATTTCGTG
401 CCGCGCTCCG CCAAACCTGC GCCTACTTCG TCGAACAAAT CGGTCCGGAA
451 CGGGCCCGAA CCGACGCCCG TGGTATAGGC TTGACGATG CCCAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC CGCGCCGGCG
551 AGACAGTTGG ACGAGGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGCGCGCCTT CAAACAGCAG TTTTTCGCCG TTTTGTGTTT
651 TTTGCTTCAA CACGCgggaC acgtcgGCAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGGTCCGGC
751 GTTATGCAGG TATTGGAGTT GGACGTTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTTCAG CAGTTTTTCA GGATGCAGCA AATCGCGCGC GCGAATGGCG
851 CCGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGTCGT
901 GCCGATTTTG CCTTTGCCGC GCGATGCTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGg gaaacgAcaa cGCCCCAACC gatGAAGCAA TCCAATCCTT
1101 CGTGCAAGAT ACCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCGCGCG
1151 ACGACCAAGG TATGGCCCGC ATTGTGGCCG CTTTGAAGC GCACgacGct
1201 gCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTgc gccGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGatatTA A

```

This corresponds to the amino acid sequence <SEQ ID 2722; ORF 904.ng>:

g904.pep

```

1  MMQHNRFfAV GAGGDDGDRR AADFFNPFQI CFGIGRQCVV AFHADSRFAP

```

1294

```

51  AGHGFVNRFA GFHRIARTARQ DVGFAAAWQF VADADIDGFN AVHYIEFGNA
101 HTGNAVDLDG AFQGGGKPA AAARAAGYRT EFVSALRQTC AYFVEQFGRE
151 RARTDARGIG FDDAQNI IQH LRTYARACRS RAGETVGRGN EGVS AVVDVQ
201 QRTLRAFQKQ FFAVFVFFVQ HAGHVGNHRR NARRDFFDNR HHVFRFNRSR
251 VMQVLELDV IGKDGIOFFT QFFRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFARCF AGLVERDVVR QDQAGRRDF QTAFDVFHAC RVQLVDFAQQ
351 GFGGNDNART DEAIQSFVQD TARNQAQNGF FAADDQGMAR IVAALEAHDA
401 AGFFRQPVND FTFTLVAPLC ADYYNIFSHS HITYRY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2723>:

m904 .seq

```

1  ATGATGCAGC ACAATCGTTT CTTCTCGGTC GGGGCCGgTG GAGACGATGG
51  CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTCAAATA TGCTTTGGCG
101 TTTTCGGGCA ATGCGCCGTA GTCCTTCACG CCGAAAGTGG ATTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGCTTGCA GGTTCACACC GCATCGGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCGT CGGGCAATTC ATAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TAGTAATACA
301 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACAGACC GCAGCGGCGT GCGCGTCCG TTACCGAACC GAATTCGTGT
401 CCGCGTTCTG CCAAACCTAC GCCTACTTCG TCGAACAAAT CGGTCCGGAA
451 CGGGCCCCGA CCGACGCGCG TGGTATAGGC TTGACGATG CCCAAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCCAAGC TGCGCCCGCC
551 AGACAGTTGG ACGAGGTAAC GAAGGGATAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGCGCGCCTT CAAACAGCAG TTTTTCGCCG TTTTGTGTTT
651 TCTCGTTCAA CACGCGGGAC ACGTCGGTAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTAA CCGGCTCGGC
751 ATTGTGCAGA TGTGTCAGTT GGACATTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTCACG CAGTTTtTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTGTCTTTC GTAGGCAGGG CCGATGCCGC GGCCGTCGT
901 GCCGATTTTG CCTTGCCGCG GCG.ATcTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCACGTTTTC TCACGCTTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGG GAGACGACAA CGCCCAAGC GATGAAGCAG TCCAACTTT
1101 CATGCAGGAT GCGCTCGGA ATCAGGCGCA AAATGGTTT TTTGCCGCGC
1151 ACAACCAAGG TATGGCCGCG ATTGTGGCCG CCTTGGAAAG GCACCAAGCC
1201 GCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTast ACAACATTT TAGCCATAGC CATATAACCT
1301 ATCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2724; ORF 904>:

m904 .pep

```

1  MMQHNRFVSFV GAGGDDGDRR AADFFNPFI CFCGVFGQCAV VLHAESGFAP
51  AGHGFVNRFA GFHRIARTARQ DVGFAAVGQF IADADIDGFN AVHYIEFSNT
101 HTGNAVDLDG AFQGGGKPA AAACASGYRT BFVSAPCQTY AYFVEQFGRE
151 RARTDARGIG FDDAQNI IQH LRTYARACRS CARQTVGRGN EGISAVVDVQ
201 QRTLRAFQKQ FFAVFVFLVQ HAGHVGNHRR NARRDFFDNR HHVFRFNRLG
251 IVQMLQLDIV IGKDGIOFFT QFXRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAXIF AGLVERDVVR QDQAGRRDF QTAFDVFHAC RVQLVDFAQQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQGMR IVAALEAHHA
401 AGFFRQPVND FTFTLVAPLC ADXYNIFSHS HITYRY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 904 shows 90.4% identity over a 436 aa overlap with a predicted ORF (ORF 904.ng) from *N. gonorrhoeae*:

m904/g904

	10	20	30	40	50	60
m904 .pep	MMQHNRFVSFV GAGGDDGDRRAADFFNPFI CFCGVFGQCAV VLHAESGFAPAGHGFVNRFA					
	: : : : : : : :					
g904	MMQHNRFVAVGAGGDDGDRRAADFFNPFI CFCGIGRQCVVAFHADS RFAPAGHGFVNRFA					
	10	20	30	40	50	60
	70	80	90	100	110	120

1295

m904 . pep	GFHRIGTARQDVGF	AAVGGQFIADAD	IDGFN	AVHYIEFSN	THTGNA	VDLDGAFQGGGI	KPA
g904	GFHRIR	TARQDVGF	AAAWQFVADAD	IDGFN	AVHYIEFGNA	H	TGNAVDLDGAFQGGGIKPA
	70	80	90	100	110	120	
m904 . pep	AAACASGYRTEFV	SAFCQTYAYFVEQ	FGRE	RARTDARG	IGFDDAQNI	IQHLRTYARACRS	
g904	AAAAAAGYRTEFV	SALRQTCAYFVEQ	FGRE	RARTDARG	IGFDDAQNI	IQHLRTYARACRS	
	130	140	150	160	170	180	
m904 . pep	CARQTVGRGNEG	ISAVVDVQQR	TLRAFKQ	QFFAVFVFLV	QHAGHVGNHRR	NARRDFFDNR	
g904	RAGETVGRGNEG	VS	AVVDVQQR	TLRAFKQ	QFFAVFVFFV	QHAGHVGNHRRNARRDFFDNR	
	190	200	210	220	230	240	
m904 . pep	HHVFRFNRLG	IVQMLQLDIV	IGKDG	IQFF	TQFXRMQ	QIGGANGAACHFV	FVGRADAAAGR
g904	HHVFRFN	RS	GMQVLELDV	VIGKDG	IQFF	TQFFRMQ	QIGGANGAACHFV
	250	260	270	280	290	300	
m904 . pep	ADFAFAAR	IFAGLVERD	VVRQD	RAGRRD	FQTA	FDV	FHACRVQLVDF
g904	ADFAFAAR	CFAGLVERD	VVRQD	RAGRRD	FQTA	FDV	FHACRVQLVDF
	310	320	330	340	350	360	
m904 . pep	DEAVQTFMQDA	ARNQAQNGFF	AA	DNQGMAR	IVAAL	EAHHAAGFF	RQPVNDFTFTLV
g904	DEAIQSFVQD	TARNQAQNGFF	AA	DDQGMAR	IVAAL	EAHDAAGFF	RQPVNDFTFTLV
	370	380	390	400	410	420	
m904 . pep	ADXYNIF	SHSHITYRYX					
g904	ADXYNIF	SHSHITYRYX					
	430						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2725>:

a904 . seq

```

1  ATGATGCAGC ACAATCGTTT CTTCGCGGTC GGGGCCGGTG GAGACGATGG
51  CGACCGGCGC ACCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101  TGGCAGGTA ATGCGTCGTA GCTTTTCACG CCGAAAGTGG ATTCGCTCCA
151  ACCGGGCATG GTTTCGTAAA TCGGCTTGCA GGCTTCTACC GCATCAGAGC
201  CGCAAGGCAG GATGTCGGTT TTGCCGCCGT CGGGCAATTC GTAGCCGACG
251  CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATACA
301  CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351  CAAACCAGCC GCAGCGGCGT GCGCGTCCGG TTACCGAACC GAATTCGTGT
401  CCGCGTTCCTG CCAAACCTGC TCCGACTTCG TCGAACAAAT CGGTCGGGAA
451  CGGGCCCCGAA CCGACGCGCG TGGTATAGGC TTTGACGATG CCCAAACAT
501  AATCCAGCAT TTGAGGCGCT ACGCCCGCGC CTGCCGAAGC CGCGCCGGCG
551  AGGCAGTTGG ACGAAGTAAC GAAGGGGTAA CTGCCGTAGT CGATGTCCAA
601  CAACGCACCT TGCGCGCCTT CAAACAGCAG TTTTTCGCGG TTTTGTGTTT
651  TTTCGTTCAA CACGCGGGAC ACGTCGGTAA TCATCGGCGT AATGCGCGGC
701  GCGACTTTT CGATAACCGC CATCACGTCT TCCGCTTCA CCGACTCGGC
751  ATTGTGCAGA TGTGTCAGTT GGACGTTGTA ATAAGCAAAG ACGGCATCCA
801  GTTTTTCACG CAGTTTTCAT GCATGCAGCA AATCGCGCGC CGGAATGGCG
851  CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
901  GCCGATTTTG CCTTTCGCCG GCGATGCTTC TCGGCTTGG TCGAGCGCGA

```


1296

```

951 TGTGATAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGG GAGACGACAA CGCCCGAACC GATGAAGCAG TCCAGACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACAACCAAGG TATGACCCGC ATTGTGGCCG CCTTGAAGC GCACCACGCC
1201 TCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 .TCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2726; ORF 904.a>:

a904.pep

```

1  MMOHNRFFAV GAGGDDGDRR TADFFNPFI CFIGR*CVV AFHAESGFAP
51  TGHGFVNRLA GFYRIRARQ DVGFVAVGQF VADADIDGFN AVHYIEFGNT
101 HTGNAVLDL AFQGGGKPA AACASGYRT EFVSAFCQTC SDFVEQFGRE
151 RARTDARGIG FDDAQNIIQH LRAYARACRS RAGEAVGRSN EGVSAVVDVQ
201 QRTLRAFKQQ FFAVFVFFVQ HAGHVGNHRR NARRDFFDNR HHVFRFHLG
251 IVQMLQLDVV ISKDGIOFFT QFFRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAARCF SGLVERDVIR QDQAGRRDF QTAFDVFHAC RVQLVDFQQ
351 GFGDDNART DEAVQTFMQD AARNQAQNGF FAADNQGMR IVAALEAHHA
401 SGFRQPVND FTFTLVAPLC ADYYNIFSHS HITXRY*

```

m904/a904 91.3% identity in 436 aa overlap

m904.pep	10	20	30	40	50	60
	MMQHNRFFSVGAGGDDGDRRAADFFNPFIQCFGVFGQCAVVLHAESGFAPAGHGFVNRLA					
a904	MMQHNRFFAVGAGGDDGDRRTADFFNPFIQCFGIGRXCVVAFHAESGFAPTGHGFVNRLA					
	10	20	30	40	50	60
m904.pep	70	80	90	100	110	120
	GFHRIGTARQDVGFVAVGQFIADADIDGFNAVHYIEFSNTHGTGNAVLDLGAFOGGGKPA					
a904	GFYRIRARQDVGFVAVGQFVADADIDGFNAVHYIEFGNTHGTGNAVLDLGAFOGGGKPA					
	70	80	90	100	110	120
m904.pep	130	140	150	160	170	180
	AAACASGYRTEFVSAFCQTYAYFVEQFGRERARTDARGIGFDDAQNIIQHLRYARACRS					
a904	AAACASGYRTEFVSAFCQTCSDVEQFGRERARTDARGIGFDDAQNIIQHLRAYARACRS					
	130	140	150	160	170	180
m904.pep	190	200	210	220	230	240
	CARQTVGRGNEGISAVVDVQORTLRAFKQQFFAVFVQVHAGHVGNHRRNARRDFFDNR					
a904	RAGEAVGRSNEGVS AVVDVQORTLRAFKQQFFAVFVQVHAGHVGNHRRNARRDFFDNR					
	190	200	210	220	230	240
m904.pep	250	260	270	280	290	300
	HHVFRFNLGIVQMLQLDIVIGKDGIOFFTQFXRMQQIGGANGACHFVFVGRADAAAGR					
a904	HHVFRFHLGIVQMLQLDVVISKDGIOFFTQFFRMQQIGGANGACHFVFVGRADAAAGR					
	250	260	270	280	290	300
m904.pep	310	320	330	340	350	360
	ADFAFAAXIFAGLVERDVVRQDQAGRRDFQTAFDVFHACRVQLVDFQQGFGDDNART					
a904	ADFAFAARCFSGLVERDVIRQDQAGRRDFQTAFDVFHACRVQLVDFQQGFGDDNART					
	310	320	330	340	350	360
m904.pep	370	380	390	400	410	420
	DEAVQTFMQDAARNQAQNGFFAADNQGMRIVAALAHHAAGFFRQPVNDFTFTLVAPLC					
a904	DEAVQTFMQDAARNQAQNGFFAADNQMTRIVAALAHHAAGFFRQPVNDFTFTLVAPLC					
	370	380	390	400	410	420

430

1297

```

m904.pep      ADXYNIFSHSHITYRYX
               || ||||| |||| |||
a904          ADYYNIFSHSHITXRYX
               430

```

g906.seq not found yet
g906.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2727>:

```

m906.seq
1  ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
51 GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
101 TGAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCATTGAC
151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAAACAA
301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2728; ORF 906>:

```

m906.pep
1  MKYIVSISLA MGLAACSFEG FKNPWAAS FWELKNYANP YPGSASAALD
51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDPPYPENK
101 KYEWPREEGK TK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2729>:

```

g907.seq (partial)
1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTGcaAC GCCGCCGCCT
51 GCTGTGTGCC GCCGGCGCGC TGTGTATCAG CCCGCTGCGC CACGCCGGCG
101 CGCAACGTGA AGAAACGctt gCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTGACA ATCCGAAAGA
201 GGGCGAACGT TGGTTGTCCG CGATGTCGGC ACGTTTGGCA AGATTGCTCC
251 CCGACGAGGG GGAGCGGCGC AGGCTGCTGG TCAATATCCA ATACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGa ttgaagtgga
351 aagcgggtac cgagctcgaa tcatatca..

```

This corresponds to the amino acid sequence <SEQ ID 2730; ORF 907.ng>:

```

g907.pep (partial)
1  MKKPTDTLPV NLQRRRLCA AGALLISPLA HAGAQREETL ADDVASVMRS
51 SVGSVNPPRL VFDNPKEGER WLSAMSARLA RFVPDEGERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESGY RARIIS...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2731>:

```

m907.seq
1  ATGAGAAAAC CGACCGATAC CCTACCCGTT AATCTGCAAC GCCGCCGCCT
51 GTTGTGTGCC GCCGTGCGT TGTGTCTCAG TCCTCTGGCG CACGCCGGCG
101 CGCAACGTGA GGAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTTGACA ATCCGAAAGA
201 GGGCGAGCGT TGGTTGTCTG CCATGTCGGC ACGTTTGGCA AGGTTCTGTC
251 CCGAGGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
401 TGCAGGTTAT GCCGTTktGG AAAAActACA TCGGCAAACC GGCGCACAAc
451 CTGTTGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCGCTT GCCGCTTTA
551 ACGGCAGCTT GGGCAGCAAT AAATATCCGA ACGCCGTTTT GGgCGCGTGG
601 CGCAACCGCT GGCAGTGGCG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2732; ORF 907>:

```

m907.pep
1  MKKPTDTLPV NLQRRRLCA AGALLLSPLA HAGAQREETL ADDVASVMRS
51 SVGSVNPPRL VFDNPKEGER WLSAMSARLA RFVPEEEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYAISGVGA RGLMQVMPXW KNYIGKPAHN

```

1298

151 LFDIRTNLRY GCTILRHYRN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW
201 RNRWQWR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 907 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 907.ng) from *N. gonorrhoeae*:

g907/m907

	10	20	30	40	50	60
g907.pep	MKKPTDTLPVNLQRRRLCAAGALLISPLAHAGAQREETLADDVASVMRSSVGSVNPRL					
	: :					
m907	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQREETLADDVASVMRSSVGSVNPRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
g907.pep	VFDNPKEGERWLSAMSARLARFVPEDEGERRRLLVNIQYESSRAGLDTQIVLGLIEVESGY					
	: :					
m907	VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
	70	80	90	100	110	120
	130	140	150	160	170	180
g907.pep	RARIIS					
m907	RQYAIISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2733>:

a907.seq

```

1  ATGAAAAAAC  CGACCGATAC  CCTACCCGTC  AATCTGCAAC  GCCGCCGCTT
51  ATGTGTGCT  GCCGGCGCGC  TGTGTGCTCAG  CCCGCTGGCA  CAAGCCGGCG
101 CGCAACGTGA  AGAAACGCTT  GCCGACGATG  TGGCTTCCGT  GATGAGGAGC
151 TCTGTCGGCA  GCATAATCC  GCCGAGGCTG  GTGTTTCGACA  ATCCGAAAGA
201 GGGCGAGCGT  TGGCTGTCCG  CGATGTCTGC  TCGGTTGGCA  AGGTTTCGTCC
251 CCGATGAGGA  GGAGCGGCGC  AGGCTGCTGG  TCAATATCCA  GTACGAAAGC
301 AGCCGGGCGC  GTTTGGATAC  GCAGATTGTG  TTGGGGCTGA  TTGAGGTGGA
351 AAGCGCGTTC  CGCCAGTATG  CAATCAGCGG  TGTCGGCGCG  CGCGGCCTGA
401 TGCAGGTAT  GCCGTTTIGG  AAAAACTACA  TCGGCAAACC  GGCGCACAAC
451 CTGTTTCGACA  TCCGCACCAA  CCTGCGTTAC  GGCTGTACCA  TCCTGCGCCA
501 TTACCGGAAT  CTTGAAAAAG  GCAACATCGT  CCGCGCACTC  GCCCGTTTTA
551 ACGGTAGCCT  CGGCAGCAAT  AAATATCCGA  ACGCCGTTTT  GGGCGCGTGG
601 CGCAACCGCT  GGCAGTGGCG  TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2734; ORF 907.a>:

a907.pep

```

1  MKKPTDTLPV  NLQRRRLCA  AGALLSPLA  QAGAQREETL  ADDVASVMRS
51  SVGSINPRL  VFDNPKEGER  WLSAMSARLA  RFVPDEEERR  RLLVNIQYES
101 SRAGLDTQIV  LGLIEVESAF  RQYAIISGVA  RGLMQVMPFW  KNYIGKPAHN
151 LFDIRTNLRY  GCTILRHYRN  LEKGNIVRAL  ARFNGSLGSN  KYPNAVLGAW
201 RNRWQWR*

```

m907/a907 97.6% identity in 207 aa overlap

	10	20	30	40	50	60
m907.pep	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQREETLADDVASVMRSSVGSVNPRL					
	: :					
a907	MKKPTDTLPVNLQRRRLCAAGALLSPLAQAGAQREETLADDVASVMRSSVGSINPRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m907.pep	VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
	: :					
a907	VFDNPKEGERWLSAMSARLARFVPEDEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					

1299

	70	80	90	100	110	120
	130	140	150	160	170	180
m907 . pep	RQYAISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
a907	RQYAISGVGARGLMQVMPFWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
	130	140	150	160	170	180
	190	200				
m907 . pep	ARFNGSLGSNKYPNAVLGAWRNRWQWRX					
a907	ARFNGSLGSNKYPNAVLGAWRNRWQWRX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2735>:

```

g908 . seq
1  ATGAG .AAAA GCCGTCTAAG CCGGTATAAA CAAAATAAAC TCATTGGGCT
51  ATTTGTCGCA GGTGTAAC TG CAAGAACAGC GGCAGAGTTG GTAGGCATTA
101 ATAAAAATAC CGCAGCCTAT GATTTTCATC GTTTACGATG ACTGATTTAT
151 CAAAACGGTC CGCATTTAGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTTCCCTA TTATCCGTGA
351 acaagtgaac cctgacagta ttgtttatac ggattgttat CgTAGCTATG
401 ATGTATTAGA Tgtgagcgaa tttagccatT TTagcttcgc tgaaacttcg
451 ttttcgtaTC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2736; ORF 908.ng>:

```

g908 . pep
1  MXKSRLSRYK QNKLIGLFVA GVTARTAAEL VGINKNTAAY DFHRLR*LIY
51  QNGPHLEMF D GEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTVPNTQTAT LFPPIREQVK PDSIVYTD CY RSYDVL DVSE FSHFSFAETS
151 FSYQSQTFC RTTKPY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2737>:

```

m908 . seq
1  ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAmTAAAC TCATTGAACT
51  GTTTGTCACA GGTGTAAC TG CAAGAACGCC AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTTGGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTTCCCTA TTATCCGTGA
351 ACAAGTGAAA CCTGACAGCA TTTTTTATAC GGATTGTTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2738; ORF 908>:

```

m908 . pep
1  MRKSRLSRYK QXKLIELFVT GVTARTAAEL VGVNKN TAAY YFHRLRLLIY
51  QNSPHLEMF D GEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTVPNTQTAT LFPPIREQVK PDSIFYTD CY RSYDVL DVRE FSHFSFAETS
151 FSYQSQTFC RTTKPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 908 shows 93.4% identity over a 166 aa overlap with a predicted ORF (ORF 908.ng) from *N. gonorrhoeae*:

```

g908/m908
10      20      30      40      50      60
g908 . pep  MXKSRLSRYKQNKLIGLFVAGVTARTAAELVGINKNTAAYDFHRLRLXIYQNGPHLEMF D

```

1300

```

      |||||:|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m908  MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNNTAAYYFHLRLLLIYQNSPHLEMPD
      10      20      30      40      50      60
      70      80      90      100     110     120
g908.pep GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPPIIREQVK
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m908  GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPPIIREQVK
      70      80      90      100     110     120
      130     140     150     160
g908.pep PDSIVYTD CYRSYDVLVDVSEFSHFSFAETSFSYSQSHTF CRTTKPYX
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m908  PDSIFYTDCYRSYDVLVDVREFSHFSFAETSFSYSQSHTF CRTTKPYX
      130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2739>:

```

a908.seq
1  ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAATAAAC TCATTGAGCT
51  ATTTGTCGCA GGTGTAAC TG CAAGAACGGC AGCAGAGTTA CTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTTACGATT ACTTATTAT
151 CAAAACAGTC CGCATTTGGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GCGGACAAAC GCAAAGGCAA ACGCGGTGCG GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTTCCTA TTATCCGTGA
351 ACAAGTGAAG CCTGACAGCA TTGTTTATAC GGATTGTTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2740; ORF 908.a>:

```

a908.pep
1  MRKSRLSQYK QNKLIELFVA GVTARTAAEL VGVNKNNTAAY YFHLRLLLIY
51  QNSPHLEMPD GEVEADESYF GGQRKGKRG GR GAAGKVAVFG LLKRNGKVYT
101 VTPNTQTAT LFPIIREQVK PDSIVYTD CY RSYDVLVDVRE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

m908/a908 98.2% identity in 166 aa overlap

```

      10      20      30      40      50      60
m908.pep MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNNTAAYYFHLRLLLIYQNSPHLEMPD
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a908  MRKSRLSQYKQNKLIELFVAGVTARTAAELVGVNKNNTAAYYFHLRLLLIYQNSPHLEMPD
      10      20      30      40      50      60
      70      80      90      100     110     120
m908.pep GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPPIIREQVK
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a908  GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPPIIREQVK
      70      80      90      100     110     120
      130     140     150     160
m908.pep PDSIFYTDCYRSYDVLVDVREFSHFSFAETSFSYSQSHTF CRTTKPYX
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a908  PDSIVYTD CYRSYDVLVDVREFSHFSFAETSFSYSQSHTF CRTTKPYX
      130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2741>:

```

g909.seq (partial)
1  atgcgtaaaa ccgtacttat cCTgaccatc tccgcgcgcc ttttgcgagg
51  ctgcacatgG gaaacttatc aagacggcag cggcaaaacc gccgtccgtg
101 caaatgttc caccggcacg ccgctgtgtt ggcaagacgg gcgcggctcg

```

1301

151 aaaaaggtgg actgcgacga gtacgggtggc gaacgccggg ccgtgttgcg
 201 caaccaaaag cgggggaagc ccgcgacgag gagagccgca acgctgggga
 251 aaccgagttt ccgggcgagg gacggggggg ggcgggtgaa cagggcagaa
 301 acgggggagg ggaagcgatc ggcgagg..

This corresponds to the amino acid sequence <SEQ ID 2742; ORF 909.ng>:

g909.pep (partial)

1 MRKTVLILTI SAALLSGCTW ETYQDGSGKT AVRACSTGT PLCWQDGRGS
 51 KKVDCDEYGG ERRAVLNRNQK RGKPATRRAA TLGKPSFRAR DGGGRVNRAE
 101 TGEGRKSAR..

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2743>:

m909.seq

1 ATGCGTAAAA CCTTCCTCTT CTGACCGCT GCCGCCGCC TTTGTCTGGG
 51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
 101 AAAAATATCC CGCCGGCACG CCCGTTTATT ACCAAGACGG CAGCTACTCG
 151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTACC
 201 CAATCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
 251 AACCAGAGTT TCAAAACCGA TAA

This corresponds to the amino acid sequence <SEQ ID 2744; ORF 909>:

m909.pep

1 MRKTFLEFLTA AAALLSGCAW ETYQDGNGKT AVRQKYPAGT PVYYQDGSYS
 51 KNNMNYQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 909 shows 53.3% identity over a 90 aa overlap with a predicted ORF (ORF 909.ng) from *N. gonorrhoeae*:

m909/g909

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTAALLSGCAWETYQDGNGKTAVRQKYPAGTPVYYQDGSYSKNNMNYQYRP					
	: : : : : : : : :					
g909	MRKTVLILTI SAALLSGCTWETYQDGSGKTAVRAKSTGTPLCWQDGRGSKKVDCEYGG					
	10	20	30	40	50	60
	70	80	90			
m909.pep	ERHAVLPNQTGNNADEEHRQHWQKPKFQNRX					
	: : : : : : : : : :					
g909	ERRAVLRNQKRGKPATRRAATLGKPSFRARDGGGRVNRAETGEGKRSAR					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2745>:

a909.seq

1 ATGCGTAAAA CCTTCCTTAT CCGATGACT GCCGCCGCC TTTGTCTGGG
 51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
 101 AAAAATATCC CGCCGGCACG CCCGTTTATT ACCAAGACGG CAGCTACTCG
 151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTACC
 201 CAACCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
 251 AGCCCAAATT TCAAAACCGA TAA

This corresponds to the amino acid sequence <SEQ ID 2746; ORF 909.a>:

a909.pep

1 MRKTFILILMT AAALLSGCAW ETYQDGNGKT AVRQKYPAGT PVYYQDGSYS
 51 KNNMNYQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *

m909/a909 96.7% identity in 90 aa overlap

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTAALLSGCAWETYQDGNGKTAVRQKYPAGTPVYYQDGSYSKNNMNYQYRP					
	: : : : : : : : :					
a909	MRKTFILILMTAAALLSGCAWETYQDGNGKTAVRQKYPAGTPVYYQDGSYSKNNMNYQYRP					
	10	20	30	40	50	60

1302

	70	80	90
m909 . pep	ERHAVLPNQTGNNADEEHRQHWQKPKFQNRX		
a909	ERHAVLPNQTGNNADEEHRQHWQKPKFQNRX		
	70	80	90

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2747>:

```

g910 . seq
1  ATGAAAAAAC TGTATTGGC CGCGTTGTT TCCTAAATG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAATGT TGAACAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACTACTGG GGCAAACCTG TTTTGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2748; ORF 910.ng>:

```

g910 . pep
1  MKKLLLAADV SLNAATAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDYW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2749>:

```

m910 . seq
1  ATGAAAAAAC TGTATTGGC TGCCGTTGTT TCTCTGAGTG CCGCTGCCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCT GTGAAATGT TGGAGCAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACCATGG GGTAAGCCTG TGCTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2750; ORF 910>:

```

m910 . pep
1  MKKLLLAADV SLSAAAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 910 shows 96.8% identity over a 94 aa overlap with a predicted ORF (ORF 910.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
g910 . pep	MKKLLLAADVSLNAATAFAGDS	SAERQIYGD	PHFEQNRTKAV	KMLEQRGYQ	VYDVDADDYW	
m910	MKKLLLAADVSLSAAAFAGDS	SAERQIYGD	PHFEQNRTKAV	KMLEQRGYQ	VYDVDADDHW	
	10	20	30	40	50	60
	70	80	90			
g910 . pep	GKPVLEVEAYKDGREYDIVLS	SYPDLKIIKE	QLDRX			
m910	GKPVLEVEAYKDGREYDIVLS	SYPDLKIIKE	QLDRX			
	70	80	90			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2751>:

```

a910 . seq
1  ATGAAAAAAC TGTATTGGT CGCCGTTGTT TCCTTGAGTG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCTATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAATGT TGAACAGCG CGGTTATCAG
151 GTTCACGATG TCGATGCCGA CGACCATGG GGCAAACCTG TTTTGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATTGTGTTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2752; ORF 910.a>:

```

a910 . pep

```

1 MKKLLLVAVV SLSAATAFAG DSAERQIYGD PYFEQNRTKA VKMLEQRGYQ
51 VHDVDADDDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

      10      20      30      40      50      60
m910.pep  MKKLLLAVVVLSAAAAFAGDSAEERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDDHW
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a910      MKKLLLVAVVLSAATAFAGDSAEERQIYGDPYFEQNRTKAVKMLEQRGYQVHDVDADDDHW
          10      20      30      40      50      60

      70      80      90
m910.pep  GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a910      GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
          70      80      90

```

g911.seq

```
1  ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCC TCTTGATCGG
51  CGCGGCGGCG GTTGCCCTTTC TCGCTTTCGG CGTGGCGGGC GGCGCGGCGT
101 TCGGCGGGTTC GGACAAAATC TACCGCGTTT ATGCGGATTT CGGCGACATC
151 GCGCGTTTGA AGGTCAAATG CCCCGTCAAA TCCGCAAGGT TATTGTTCGG
201 GCGCGTCGGC GCTATCGGGC TTGACCCGAA ATCCTATCAG GCGAGGTGTC
251 GCCTTGATTT GGACGGCAAG TATCAGTTCA GCAGTGACGT TTCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAACAG TACATCGGGC TGCAGCAGGG
351 CGCGGATACG GAAACCTTTC CTGCGGCGCA CACCATCTCC GTAACCACTT
401 CTGCAATGGT TCTGAAAAAC CTGATCGGTA AATTCTAGAC CAGCTTCGCC
451 GAGAAAAACG CTGAGGGCGG CAATGCGGAA AAGCCGCaq aAtaa
```

g911.pep

1	MKKNILEFPWV	GLFVLIGAAA	VAFLAFRVAG	GAAFGGSDKT	YAVYADFGDI
51	GGLKVNAPVK	SAGVLVGRVG	AIGLDPKSYQ	ARVRLDLDGK	YQFSSEVSAQ
101	ILTSGLLGEQ	YIGLQQGDT	ENLAAGDTIS	VTSSAMVLEN	LIGKFMTSFA
151	EKNAEGGNAE	KAEE*			

```
m911.seq
1  ATGAAGAAGA ACATATTGGA ATTTTGGGTC GGAAGTGTTC TCTTGATTGG
51  CGCGGCGGCG GTTGCCCTTTC TCGCTTTCGC CGTGGCCGGC GGTGCGCGCGT
101 TCGGCGGGTTC GGACAAAATC TACGCCGTTT ATGCCGATTG CGGCGACATC
151 GCGCGTTTGA AGGTCAATGC CCCCGTCAAA TCCGCAAGTG TATTGGTTCG
201 GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATTT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCGCGCGAA
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
351 CGGCGACAGC GAATAACCTT CTGCCGGCGA CACCATCTCC GTAACCAAGT
401 CTGCAATGGT TCTGGAAAAA TTATCGGCA AATTCTATGAC GAGTTTGTGC
451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAGTCGCGCG AATAA
```

```
m911.pep
      1  MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
     51  GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSQA
    101  ILTSGLLGEQ YIGLQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
    151  EKNADGGNAE KAAE*
```

ORF 911 shows 99.4% identity over a 164 aa overlap with a predicted ORF (ORF_911.ng) from *N. gonorrhoeae*:

10 20 30 40 50 60

1304

```

g911.pep  MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAPGSDKTYAVYADFGDIGGLKVNAPVK
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
m911      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAPGSDKTYAVYADFGDIGGLKVNAPVK
          10      20      30      40      50      60

          70      80      90      100     110     120
g911.pep  SAGVLVGRVGAIGLDPKSYQARVRLLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
m911      SAGVLVGRVGAIGLDPKSYQARVRLLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          70      80      90      100     110     120

          130     140     150     160
g911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNAEGGNAEKAEX
          ||||||||||||||||||||||||||||||||||||||||:|||||||
m911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2757>:

```

a911.seq
1  ATGAAAAAGA ACATATTGGA ATTTGGGTC GGA CTGTTTCG TCCTGATTGG
51 CGCGCGGCGC GTTGCCCTTC TCGCTTCCG CGTGGCCGCG GGTGCGGCGT
101 TCGGCGGTTT GGACAAACT TACGCCGTT ATGCCGATT CGGCGACATC
151 GCGCGTTTGA AGTCAATGC CCCCGTCAA TCCGCAGGC TATTGGTCGG
201 GCGCGTCGGC GCTATCGGAC TTGACCGGA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATTT GGACGGCAAG TATCAGTTCA GCAGCGACG TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGC TGCAGCAGGG
351 CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAATT
401 CTGCAATGGT TCTGGAAC CTTATCGGCA AATTCATGAC GAGTTTTGCC
451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCGG AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2758; ORF 911.a>:

```

a911.pep
1  MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLLDLGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

```

m911/a911 100.0% identity in 164 aa overlap

```

m911.pep  MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAPGSDKTYAVYADFGDIGGLKVNAPVK
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a911      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAAPGSDKTYAVYADFGDIGGLKVNAPVK
          10      20      30      40      50      60

          70      80      90      100     110     120
m911.pep  SAGVLVGRVGAIGLDPKSYQARVRLLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a911      SAGVLVGRVGAIGLDPKSYQARVRLLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          70      80      90      100     110     120

          130     140     150     160
m911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
          ||||||||||||||||||||||||||||||||||||||||
a911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2759>:

```

g912.seq
1  gtgAAAAaat cctcctTcat cagcGCATTG GGCATCGgtA TTTTGAGCAT
51 CGGCATGGCA TTTGCCTCCC CGGCCGACGC AGTGGGACAA ATCCGCCAAA
101 ACGCCACACA GGTTTTGACC ATCCTCAAAA GCGGCGACGC GGCTTCTGCA

```

151	CGCCCAAAAG	CCGAAGCCTA	TGCGGTTCCT	TATTTCGATT	TCCAACGTAT
201	GACCGCATTG	GCGGTTCGCA	ACCCTTGGCG	TACCGCGTCC	GACGCGCAAA
251	AACAAGCGTT	GCGCAAAGAA	TTTCAAACCC	TGCTGATCCG	CACCTATTCC
301	GGCAGCATGC	TGAAATTCAA	AAAGCGCAGC	GTCAACGTCA	AAGACAATCC
351	CATCGTCAAT	AAGGCGCGCA	AGGAATTCGT	CGTCCGTGCC	GAAGCATCGCA
401	TCCC CGGTCA	GAGGCCGTC	AATATGGACT	TTACCACCTA	CCAAAGCGGC
451	GGCAAATACC	GTACCTACAA	CGTCGCCATC	GAAGGCACGA	GCTTGGTTAC
501	CGTGATCCGC	AACCAATTTC	GCGAAATCAT	CAAAGCCAAA	GGCATCGACG
551	GGTGTATTGC	CGAGTTGAAA	GCGAAAAACG	CGGGCAATAA	A

This corresponds to the amino acid sequence <SEQ ID 2760; ORF 912.ng>:

q912.pep

```

1  VKKSSFISAL GIGILSIGMA FASPADAVGQ IRQATQVLT ILKSGDAASA
51  RPKAEAYAVP YFDFQRM TAL AVGNPWR TAS DAQQAALAKE FQTLRLRTYS
101 GTMLKFKNAT VNVKDNPIVN KGGKEIVVRA EVGIPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGTSLVTVYR NQFGEIHKAK GIDGLIAELK AKNGGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2761>:

m912.seq

1	ATGAAAAAAT	CCTCCCTCAT	CAGCGCATTG	GGCATCGGTA	TTTGTAGCAT
51	CGGCATGGCA	TTTGCCGCCC	CTGCCGACGC	GGTAAGCCAA	ATCCGTCAAA
101	ACGCCACTCA	AGTATTGAGC	ATCTTAAAAA	ACGGCGATGC	CAACACCGCT
151	CGCCAAAAAG	CCGAAGCCGA	TGCCATTCCC	TATTTGGAAT	TCCAACGTAT
201	GACCGCATTG	CGCGTCGGCA	ACCTTTGGCG	CACCGCGTCC	GACGCGCAAA
251	AACAAAGCGT	GGCCAAAGAA	TTTCAAACCC	TGCTGATCCG	CACCTATTCC
301	GGCACGATGC	TGAAATTAAA	AAACGCCAAC	GTCAACGTGA	AAGACATCC
351	CATCGTCAAT	AAAGGCGGCA	AAGAAATCAT	CGTCCGCGCC	GAAGTCGGCG
401	TACCCGGGCA	AAAACCCGTC	AACATGGACT	TCACCACCTA	CCAAGCGGC
451	GGTAAATACC	GTACCTACAA	CGTCGCCATT	GAAGGCGCGA	GGCTGGTTAC
501	CGGTGTACCG	AACCAATTCC	GCGAAACCAT	CAAAAGCGAA	GCCTGGGACG
551	GACTGATTGC	CGAGTTGAAA	GCGAAAAACG	CGGGCAATAA	A

This corresponds to the amino acid sequence <SEQ ID 2762; ORF 912>:

m912.ppt

1 MKKSSLSIAL GIGILSIGMA FAAPADAVSQ IRQATQVLS ILKNGDANTA
51 RQKAEAYAIP YFDFQRMAL AVGNPWRAS DAQKQALAKE FQTLIRTY
101 GTMLKLKLAN VNVKDNPIVN KGGKEIIVRA EVGVPQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLVTVYR NQFGEIHKAK GVDGLIAELK AKNGGK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 912 shows 91.8% identity over a 196 aa overlap with a predicted ORF (ORF 912.ng) from *N. gonorrhoeae*:

q912/m912

	10	20	30	40	50	60
g912.pep	VKKSSFISALGIGILSIGMAFASPADAVGOIRONATQVLTILKSGDAASARPKAEAYAVP					
m912	MKKSSLISALGIGILSIGMAFAAPADAVSQIRONATQVLSILKNGDANTARQKAEYAIIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
g912.pep	YFDIFORMTALAVGNPWRTASDAQQALAKEFQTLLIRTYSGTMLKPKNATVNVKDNPINV					
m912	YFDIFORMTALAVGNPWRTASDAQQALAKEFQTLLIRTYSGTMLKLKNANVNVKDNPINV					
	70	80	90	100	110	120
	130	140	150	160	170	180
g912.pep	KGGKEIIVRAEVGIPGQKPVNMDFTTYQSGGKYRTYNVAIEGTSLVTYVRNQFGEIIKAK					
m912	KGGKEIIVRAEVGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYVRNQFGEIIKAK					
	130	140	150	160	170	180
	190					
g912.pep	GIDGLIAELKAKNGGKX					

1306

```

      |||||
m912  GVDGLIAELKAKNGGKX
      190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2763>:

```

a912.seq
1   ATGAAAAAAT CCTCCTTCAT CAGCGCATTG GGCATCGGTA TTTTGAGCAT
51  CGGCATGGCA TTTGCCGCCC CTGCCGACGC GGTAAACCAA ATCCGTCAAA
101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA GCGGTGATGC CAACACCGCC
151 CGCCAAAAAG CCGAAGCCTA TCGGATTCCC TATTTCGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG CACCGCGTCC GACGCGCAA
251 AACAAGCGTT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAATTTAAA AAACGCCAAC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAAGGCGGCA AAGAAATCAT CGTCCCGGCC GAAGTCGGCG
401 TACCGGGGCA AAAACCCGTC AACATGGACT TCACCACCTA CCAAAGCGGC
451 GGTAATAACC GTACCTACAA CSTCGCCATC GAAGGCGCGA GCCTGGTTAC
501 CGTGATACGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GGCGTGGACG
551 GACTGATTGC CGAGTTGAAG GCTAAAAACG GCAGCAAGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2764; ORF 912.a>:

```

a912.pep
1   MKKSSFISAL GIGILSIGMA FAAPADAVNQ IRQNATQVLS ILKSGDANTA
51  RQKAEAYAIP YFDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRITYS
101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVPQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLVTYR NQFGEIIRAK GVDGLIAELK AKNGSK*

```

m912/a912 98.0% identity in 196 aa overlap

```

      10      20      30      40      50      60
m912.pep  MKKSSLISALGIGILSIGMAFAAPADAVSQIRQNATQVLSILKNGDANTARQKAEAYAIP
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a912      MKKSSFISALGIGILSIGMAFAAPADAVNQIRQNATQVLSILKSGDANTARQKAEAYAIP
      10      20      30      40      50      60

      70      80      90      100     110     120
m912.pep  YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRITYSGTMLKLKNANVNVKDNPIVN
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a912      YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRITYSGTMLKLKNANVNVKDNPIVN
      70      80      90      100     110     120

      130     140     150     160     170     180
m912.pep  KGGKEIIVRAEVGVPQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNVQFGEIIRAK
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a912      KGGKEIIVRAEVGVPQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNVQFGEIIRAK
      130     140     150     160     170     180

      190
m912.pep  GVDGLIAELKAKNGGKX
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a912      GVDGLIAELKAKNGSKX
      190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2765>:

```

g913.seq
1   atGAAAAAAA CCGCCTACGC CATCCTCCTG CTGATCGGGT TCGCTTCCGC
51  CCCTGCATTT GCAGAAACCC GCCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCGGTTTC CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCTT
151 GCGCGCGCGG GCTACCGCAA AGTTACGCCG AAACCCGTCC GCGCCGGCGT
201 GTCCAATTTT TTTAACAACC TCGCGCAGCT GGTCAGTTCG GGCAGCAATA
251 TCTTGCGTTT GGACatCAAA cgcgcAAGcg aAGACctcgT CCGcgtcggc
301 atCAATACCA CCTTCGTTT GGcgcGGCTC ATTGATATTG CCGGcgcGGg
351 cggcgttccc gacaataaaa AcacTttgGg cgacacgttt gcctcgtGGG
401 GctgGAAAAa cagcaATTAT TTCGTgttgc CCGtcttagg cccgtccacc

```

1307

```

451 gtccgcgacg cgctcggcac gggcattacc tCTGTTTATC CGCccaagaa
501 tategttttc catacccttg ccggacgctg GGgcacgact gCCGCTGCCG
551 CCGTcagtac gcgcgaaggc ctctcgatt tgaccgacag Tctggacgaa
601 gccgccatCG ACAAATACAG CTACACGCGc gacctctata tgAAAGTCCG
651 CGcacgGCag AccgGTGCAA CACCTGCCGA AGgtacggaa gataacatcg
701 acatcgacat cgACGAATTG GTCGAAAGTG CCGAAACCGG CGCGGCAGAG
751 CCCGCCGTTC ACGAAGATTG CGTATCCGAA ACACAGGCAG AAGCAGCAGG
801 GGAAGCCGAA ACGCAACCTG GAACACAACC CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2766; ORF 913.ng>:

```

g913.pep
  1 MKKTAYAILL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
 51 AARGYRKVTP KPVRAVSNF FNNLRDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGVP DNKNTLGDTF ASWGWNKSNY FVLPVLGPST
151 VRDALGTGIT SVYPPKNIVF HTPAGRWTGTT AAAAVSTREG LLDLTDSLDE
201 AAIDKYSYTR DLYMKVRRARQ TGATPAEGTE DNIDIDIDEL VESAETGAAB
251 PAVHEDSVSE TQAEAAEGAE TQPGTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2767>:

```

m913.seq
  1 ATGAAAAAAA CCGCCTATGC CTTCCTCCTG CTGATCGGGT TCGCTTCCGC
 51 CCCTGCATTT GCCGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTT CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCTT
151 GCCGCGCGCG GCTACCGCAA AGTTGCGCGG AAACCCGTCC GCGCCGCGCT
201 GTCCAATTTT TTTAACAACC TGTGCGACGT GGTCACTTC GGCAGCAATA
251 TCTTGCCTT GGACATCAAA CGCGCAAGCG AAGACCTGT CCGCGTCGGC
301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCGACATCG CCGGCGCGGG
351 CGGCATTCCC GACAATAAAA ACACCTTGGG CGACACGTT GCCTCGTGGG
401 GATGGAAAAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC
451 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCCTG TCGGACGCTG GGGCACGACT GCGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTgCTCGATT TGACCGACAG TCTGGACGAA
601 GCCGCCATCG ACAAATACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
651 TGCGCGGCAG ACCGGTGCAA CACCTGCCGA AGgTACGAA GATAACATCG
701 ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGGCGCGGC GGAAACTGCC
751 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2768; ORF 913>:

```

m913.pep
  1 MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
 51 AARGYRKVAP KPVRAVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASWGWNKSNY FVLPVLGPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWTGTT AVSAVSTREG LLDLTDSLDE
201 AAIDKYSYTR DLYMKVRRARQ TGATPAEGTE DNIDIDELVE SAETGAAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 913 shows 94.9% identity over a 277 aa overlap with a predicted ORF (ORF 913.ng) from *N. gonorrhoeae*:

```

g913/m913
      10      20      30      40      50      60
g913.pep  MKKTAYAILLLIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAPAARGYRKVTP
          |||||:|||||
m913      MKKTAYAFLLLIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAPAARGYRKVAP
          |||||:|||||
      10      20      30      40      50      60

      70      80      90     100     110     120
g913.pep  KPVRAVSNFFNNLRDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGVP
          |||||:|||||
m913      KPVRAVSNFFNNLCDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP
          |||||:|||||
      70      80      90     100     110     120

```

1308

	130	140	150	160	170	180
g913 . pep	DNKNTLGDTFASWGWKNSNYFVL	PVLGPSTVRDALGTGITSVYPPKNIVFHTPAGRWGTT				
m913	DNKNTLGDTFASWGWKNSNYFVL	PVLGPSTVRDALGTGITSVYSPKNIVFRTVPVGRWGTT				
	130	140	150	160	170	180
	190	200	210	220	230	240
g913 . pep	AAAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDIDEL					
m913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDI--DEL					
	190	200	210	220	230	
	250	260	270			
g913 . pep	VESAETGAAEPAVHEDSVSETQAEAAAGEAETQPGTQPX					
m913	VESAETGAAETAVQEDSVSETQAEAAAGEAETQPGTQPX					
	240	250	260	270		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2769>:

```

a913 . seq
1  ATGAAAAAAA CCGCCTATGC CTTCTCCTG CTGATCGGGT TCGCTTCCGC
51  CCCTGCATTT GCCGAAACCC GCGCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTT CAAATCAAC GACCAAGCCG ACCGCTACAT TTTGCCCCCT
151 GCGCGCGCGG GCTACCGCAA AGTTGCGCCG AAACCCGTCC GCGCCGCGGT
201 GTCCAATTTT TTTAACAACC TGTGCGACGT GGTGAGCTTC GGCAGCAATA
251 TCTTGCGCTT AGACATCAAA CGCGCAAGCG AAGACCTTGT CCGCGTCGGT
301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCGACATCG CCGGCGCGGG
351 CGGCATTCCC GACAATAAAA ACACCTTGGG CGACACGTTT GCTTCGTGGG
401 GATGGAAAAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC
451 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCCTG TCGGACGCTG GGGCAGCACT GCCGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTGCTCGATT TGACCGACAG TCTGGACGAA
601 GCCGCCATCG ACAATAACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
651 TGC GCGGCAG ACCGCTGCAA CACCTGCCGA AGGTACGGAA GATAACATCG
701 ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGGCGCGGC GGAACTGCC
751 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTGGAAC ACAACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2770; ORF 913.a>:

```

a913 . pep
1  MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAP
51  AARGYRKVAP KPVRAVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASWGWKNSNY FVLPLVGPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWGTT AVSAVSTREG LLDLTDSLDE
201 AAIDKYSYTR DLYMKVRRARQ TGATPAEGTE DNIDIDELVE SAETGAAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQPGTQP*

```

m913/a913 100.0% identity in 275 aa overlap

	10	20	30	40	50	60
m913 . pep	MKKTAYAFLL	LIGFASAPAF	AETRPADPYE	GYNRAVFKFN	DQADRYIFAP	AARGYRKVAP
a913	MKKTAYAFLL	LIGFASAPAF	AETRPADPYE	GYNRAVFKFN	DQADRYIFAP	AARGYRKVAP
	10	20	30	40	50	60
	70	80	90	100	110	120
m913 . pep	KPVRAVSNF	FNNLCDVVSF	GSNILRLDIK	RASEDLVRVG	INTTFGLGGL	IDIAGAGGIP
a913	KPVRAVSNF	FNNLCDVVSF	GSNILRLDIK	RASEDLVRVG	INTTFGLGGL	IDIAGAGGIP
	70	80	90	100	110	120
	130	140	150	160	170	180
m913 . pep	DNKNTLGDTFASWGWKNSNYFVL	PVLGPSTVRDALGTGITSVYSPKNIVFRTVPVGRWGTT				
a913	DNKNTLGDTFASWGWKNSNYFVL	PVLGPSTVRDALGTGITSVYSPKNIVFRTVPVGRWGTT				

1309

	130	140	150	160	170	180
	190	200	210	220	230	240
m913.pep	AVSAVSTREGLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDELVE					
a913	AVSAVSTREGLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDELVE					
	190	200	210	220	230	240
	250	260	270			
m913.pep	SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
a913	SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2771>:

g914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCAGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCCG CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GacgtttGag gCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGG AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTTGGACGG ATAAAGAAAC
351 GGATACGGAG CTGGGCTTCC GTCTCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAGTGTC AGTCGTGTTC TGCCGATTCT
451 taggctTCGA CGATTTTGTG CACCAGAGGA TGCCGGACAA CGTCTTCGCC
501 GGTGAAGGTA TGGAAATACA GTCTTGCCAC GCCGTGCAGT TTCTCACGTG
551 CGTCTTTCAA TCCCGATTG ATGTTTTTGG GCAGGTcgaT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCgccgaag ccGATGCGGG TCAGGAACAT
651 TTTCATTTGT TCGGGCGTGg tgTtttGcgC TTCGTCGAGG ATGATGTATG
701 CGCCGTTGAg cgTCCTGCCG CGCATATAG

```

This corresponds to the amino acid sequence <SEQ ID 2772; ORF 914.ng>:

g914.pep

```

1  MKKCILGILT ACAAMPAPAD RISDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCGDEA
101 IRCRKFD*CI GWTDKETDTE LGFRLCFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTRG CRTTSSPVKV WKYSPATPCS PSRASFPNDL MFLGRSIWL
201 SPVMTAFAPK PMRVRNIFIC SGVVFCASSR MMYAPLSVLP RI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2773>:

m914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCCG CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGAG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGA AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTTGGACGG ATAAAGAAAC
351 GGATACGGAT ACGGAGCTTG GCTTCOGTAT CTGTTTTTCT CTGCCTGATT
401 TTCCATGCAT CGGGTTTCAG ACGGCATTGG AATGTCAGTC GTGTTCTGCC
451 GATTCTTAGG CTTCGACGAT TTTTGCACCC AAAGGATGCC GGACAACGTC
501 TTCGCCGGTA AAGGTGTGGA AATACAGCCC TTCCACGTTG TGCAGTTTCT
551 CACGCGCATC TTTTAATCCC GATTGTATGT TTTTGGGCAG GTCGATTTGG
601 CTGGTGTCG CCGTAATGAC GGCTTTCGCG CCGAAGCCGA TCGCGGTCAG
651 GAACATTTTC ATTTGTTCCG GCGTGGTGTT TTGCGCTTCC TCGAGGATGA
701 TGTATGCGCC GTTGAGCGTC CTGCCGCGCA TATAG

```

This corresponds to the amino acid sequence <SEQ ID 2774; ORF 914>:

m914.pep

```

1  MKKCILGILT ACAAMPAPAD RIGDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEA
101 IRCRKFDXCI GWTDKETD TD TELGFRICFS LPDFPCIGFQ TALECQSCSA

```

1310

151 DSXASTIFCT KGCRTTSSPV KVKYSPSTL CSFSRASFPN DLMFLGRSIW
 201 LVSPVMTAFA PKPMVRNIF ICSGVVFCAS SRMMYAPLSV LPRI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 914 shows 96.7% identity over a 244 aa overlap with a predicted ORF (ORF 914.ng) from *N. gonorrhoeae*:

g914/m914

	10	20	30	40	50	60
g914.pep	MKKCILGILTACAAMPADFADRIDLEAQLAQLHRVAVLESGGNTVKIDLFGSNSTMYVC					
m914	MKKCILGILTACAAMPADFADRIDLEAQLAQLHRVAVLESGGNTVKIDLFGSNSTMYVC					
	10	20	30	40	50	60
	70	80	90	100	110	119
g914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCDEAIRCKFDXCIGWTDKETDT-					
m914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCDEAIRCKFDXCIGWTDKETDTD					
	70	80	90	100	110	120
	120	130	140	150	160	170
g914.pep	-ELGFRLCFSLPDPFCIGFQTALEQCSCSADSXASTIFCTRGCRRTSSPVKVKYSPATP					
m914	TELGFRICFSLPDPFCIGFQTALEQCSCSADSXASTIFCTKGCRRTSSPVKVKYSPSTL					
	130	140	150	160	170	180
	180	190	200	210	220	230
g914.pep	CSFSRASFPNPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
m914	CSFSRASFPNPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
	190	200	210	220	230	240
	240					
g914.pep	LPRIX					
m914	LPRIX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2775>:

a914.seq

```

1  ATGAAAAAAT GTATTTTG3G CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCAGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGAG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTCGCA AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAG CTTGGCTTCC GTATCTGTTT TTCTCTGCCG GATTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAATGTC AGTCGTGTTC TGCCGATTCTG
451 TAGGCTTCGA CGATTTTTTG CACCAAAGGA TGCCGACAA CGTCTTCGCC
501 GGTAAAGGTG TGGAAATACA GCCCTTCCAC GCCGTGCAST TTCTACGCG
551 CATCTTTTAA TCCCGATTG ATGTTTTTGG GCAGGTCGAT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCGCCGAAG CCGATGCGGG TCAGGAACAT
651 TTTCAATTGT TCGGGCGTGG TGTCTGCGC TTCGTCGAGG ATGATGTATG
701 CGCCGTTGAG CGTCTGCCG CGCATATAG
  
```

This corresponds to the amino acid sequence <SEQ ID 2776; ORF 914.a>:

a914.pep

```

1  MKKCILGILT ACAAMPADFAD RIGDLEARLA QLEHRVAVLE SGSNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEEA
101 IRCRKFD*CI GWTDKETDTE LGFRICFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTKG CRTTSSPVKV WKYSPSTPCS FSRASFPNL MFLGRSIWLV
201 SPVMTAFAPK PMVRNIFIC SGVVFCASSR MMYAPLSVLP RI*
  
```

1311

m914/a914 98.4% identity in 244 aa overlap

	10	20	30	40	50	60
m914 .pep	MKKCILGILTACAAMPADFADRIDGLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC					
a914	MKKCILGILTACAAMPADFADRIDGLEARLAQLEHRVAVLESGSNTVKIDLFGSNSTMYVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m914 .pep	SVTPPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD					
a914	SVTPPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD--					
	70	80	90	100	110	
	130	140	150	160	170	180
m914 .pep	TELGFRICFSLPDFPCIGFQTALEQCSCSADXSASTIFCTKGCRTTSSPVKVKYSPSTL					
a914	TELGFRICFSLPDFPCIGFQTALEQCSCSADXSASTIFCTKGCRTTSSPVKVKYSPSTP					
	120	130	140	150	160	170
	190	200	210	220	230	240
m914 .pep	CSFSRASFPDLMLFLGRSIWLVSVMATAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
a914	CSFSRASFPDLMLFLGRSIWLVSVMATAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
	180	190	200	210	220	230
m914 .pep	LPRIX					
a914	LPRIX					
	240					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2777>:

g915 .seq

```

1  ATGAAGAAAA CCCTGTTGGC AATTGTTGCC gtTTTCGCCT TAAGTGCCTG
51  CCGGCaggcg gaAGaggcac cgccgCCTTT ACCCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTattgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2778; ORF 915.ng>:

g915 .pep

```

1  MKKTLAIVA VFALSACRQA EEAPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2779>:

m915 .seq

```

1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTTCGCCT TAAGTGC.tg
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCcCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGCG AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGCGGTAAG

```


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451 GTTGTCTGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2780; ORF 915>:

m915.pep

1 MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
 101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
 151 VVGFDMPDT YIFK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 915 shows 97.0% identity over a 164 aa overlap with a predicted ORF (ORF 915.ng) from *N. gonorrhoeae*:

m915/g915

	10	20	30	40	50	60
m915.pep	MKKTLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
g915	MKKTLAIVAVFALSACRQAEEAPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m915.pep	DQPVWFSTIKQMFYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWMDAKKAFYVIDS					
	:					
g915	DQPVWFSTVQMFYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDTYIFKX					
g915	GFIGGMAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDAYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2781>:

a915.seq

1 ATGAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
 51 CCGGCAGGCG GAAGAGGGAC CGCCGCTTT ACCCGGCAG ATTAGCGACC
 101 GTTCGGTCGG AACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
 151 AAAGCCAGA TTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTCTC
 201 CACCATCAAG CAGATGTTTC GCTATACCAA GCTGCCCGAA GAGCCTAAG
 251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
 301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
 351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
 401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGCGCGTAAG
 451 GTTGTCTGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2782; ORF 915.a>:

a915.pep

1 MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
 101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
 151 VVGFDMPDT YIFK*

m915/a915 99.4% identity in 164 aa overlap

	10	20	30	40	50	60
m915.pep	MKKTLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
a915	MKKTLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m915.pep	DQPVWFSTIKQMFYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWMDAKKAFYVIDS					
a915	DQPVWFSTIKQMFYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWMDAKKAFYVIDS					

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	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
a915	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2783>:

g917.seq

```

1  ATGGTCAAac atctgccacT cgcCGTCctg actgctTtgc tgcttgCagc
51  gtgcGGCGGT Tcggacaaac cgcctgccga Aaaaccggca ccggcgGaAA
101 accaaAacgt atTgaAAATT TataACTGGT CGGAATACGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGT GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAATCCG
251 GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAAT CGATAAGTCG ATGATTCCCA ATTATAAACA
351 TCTCAACCCT GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGACCAG
401 AATACGCCGT GCCGTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAGTG
501 GGATTTGGTG TTCAACCCCG AATACACGTT CAAACTCAAA CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATTT ATCCCATGGT GTTGAACAT
601 TTGGGCAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTGCTC AAGAAAAACC GCCCAATAT CAAACGCTT ACTTCGTCG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
751 GGCGGAGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAaaaaATC CGCGTGATGA TGCCGAAAGA GGGCGTGGG ATTGGGTGG
851 ATTCCTTCGT GATCCGAAA GATGCGAAAA ACGTCGCCAA CGGCGACAAA
901 TACATCAACG ACTTCCTCGA TCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 cgttacCTAC GCGCCTTCGA GCAAGCCGGC GCGCGATTG ATGGAGGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCGA CGGGGGAAGA TTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCGGCCGGCG GCATTGAAGT TTATGGTGCG
1101 CCAGTGGCAG GATGTGAAGG CGGGGAAAT A

```

This corresponds to the amino acid sequence <SEQ ID 2784; ORF 917.ng>:

g917.pep

```

1  MVKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51  TVADFEKKNG IKVTDVYDS DETLESKVL T GSKGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS MIPNYKHLNP ENMRLMDGVD PDHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDNQWDLV FNPEYTFKLK QCGISYLSA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDNLIAKRR AEBAGGKEKI RVMPKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPARDL MEDEFKNDNT IFPSGEDLKN
351 SFIMVPIRPA ALKFMVRQWQ DVKAGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2785>:

m917.seq

```

1  ATGACCAAAC ATCTGCCCTT GGCCGTCTTG ACTGCTTTGC TGCTTGCAAGC
51  GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCA CCGGCGGAAA
101 ACCAAAACGT ATTGAAAATT TACAACGGT CGGAATATGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACA GGCAAGTCCG
251 GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGCCACG
401 AATACGCCGT GCCGTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAGTG
501 GGATTTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT
601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTT ACTTCGTCG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC

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751 GCGGCGGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 G3AAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACCTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGGC
1101 CCACTGGCAG GATGTGAAGG CGGGGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2786; ORF 917>:

```

m917.pep
  1 MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
 51 TVADFEKKNG IKVTYDVYDS DETLESKVLT GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDNQWDLV FDPEYTSKLG QCGISYLSA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDNLIAKRR AEEAGGKEKI RVMPKEGVI IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 917 shows 97.6% identity over a 376 aa overlap with a predicted ORF (ORF 917.ng) from *N. gonorrhoeae*:

m917/g917

m917.pep	10	20	30	40	50	60
	MTKHLPLAVLTALLLAACGGSDKPPAEKPAENQNVLKIYNWSEYVDPETVADFEKKNG					
g917	MVKHLPLAVLTALLLAACGGSDKPPAEKPAENQNVLKIYNWSEYVDPETVADFEKKNG					
m917.pep	70	80	90	100	110	120
	IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
g917	IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNFVGRQIKAGAYQKIDKSMIPNYKHLNP					
m917.pep	130	140	150	160	170	180
	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLG					
g917	EMMRLMDGVDPDHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFNPEYTFKLK					
m917.pep	190	200	210	220	230	240
	QCGISYLSAAEIYPMVLNLYLGKNPNSSNTEDIREATALLKKNRPNIKRFSSGFIDDLA					
g917	QCGISYLSAAEIYPMVLNLYLGKNPNSSNTEDIREATALLKKNRPNIKRFSSGFIDDLA					
m917.pep	250	260	270	280	290	300
	RGDTCVTIGFPGDNLIAKRRAEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK					
g917	RGDTCVTIGFPGDNLIAKRRAEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK					
m917.pep	310	320	330	340	350	360
	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNFSFIMVPIQPA					
g917	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNFSFIMVPIQPA					
	310	320	330	340	350	360
	370					

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m917.pep ALKFMVRQWQDVKAGKX
 |||||
 g917 ALKFMVRQWQDVKAGKX
 370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2787>:

a917.seq
 1 ATGACCAAAC ATCTGCCCTT GCGCGTCTTG ACTGCTTTGC TGCTTGACG
 51 GTGCGGCGGT TCGGACAAAC CGCTGCCGA AAAACCGGCG CCGGCGGAAA
 101 ACCGAAACGT ATTTGAAATT TACAACGTGT CGGAATACGT CGATCCGGAA
 151 ACCGTTGCCG ATTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
 201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAAATCTG
 251 GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
 301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
 351 CCTCAACCCC GAAATGATGA GGCTGATGGA CCGGGTCGAT CCCGGCCACG
 401 AATACGCCGT GCCGTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
 451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAGTG
 501 GGATTTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
 551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAATAT
 601 TTGGGTAAAA ACCGAAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
 651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
 701 GCTTTATCGA TGATTTGGCG CGCGGCATA CCTGCGTAAC AATCGGTTTC
 751 GCGGCGGATT TGAACATCGC CAAACGCGT GCCGAAGAAG CCGGCGGCAA
 801 GGAAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
 851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
 901 TACATCAACG ACTTCCTCGA CCGGAAGTG TCGGCGAAAA ACGGCAATTT
 951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
 1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
 1051 AGCTTTATCA TGGTGCCTAT CCAGCCGCGC GCATTGAAGT TTATGGTGCG
 1101 CCAGTGGCAG GATGTGAAGG CGGGGAATA A

This corresponds to the amino acid sequence <SEQ ID 2788; ORF 917.a>:

a917.pep
 1 MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENRNVLKI YNWSEYVDPE
 51 TVADFEKKNG IKVTYDVYDS DETLESKVLV GKSGYDIVAP SNAFVGRQIK
 101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
 151 ERVKKALGTD KLPDQWDLV FDPEYTSKLG QCGISYLSA AEIYPMVLNY
 201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
 251 GGDNLIAKRR AEEAGGKEKI RVMPKEGVG IWVDSFVIPK DAKNVANAHK
 301 YINDFLDPEV SAKNGNEVTY APSSKPAREL MEDEFKNDNT IFPTEDLKN
 351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

m917/a917 99.7% identity in 376 aa overlap

	10	20	30	40	50	60
m917.pep	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKKNG					
a917	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENRNVLKIYNWSEYVDPETVADFEKKNG					
	10	20	30	40	50	60
m917.pep	IKVTYDVYDSDETLESKVLTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
a917	IKVTYDVYDSDETLESKVLTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
	70	80	90	100	110	120
m917.pep	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDQWDLVFDPEYTSKLG					
a917	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDQWDLVFDPEYTSKLG					
	130	140	150	160	170	180
m917.pep	QCGISYLSAAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
a917	QCGISYLSAAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
	190	200	210	220	230	240
m917.pep						
a917						

1316

```

a917      QCGISYLDAAEIFYMVLNLYGKNPNSSNTEDIREATALLKKNRPNIKRTSSGFIDDLA
           190      200      210      220      230      240

           250      260      270      280      290      300
m917.pep  RGDTTCVTIGFGGDLNIAKRRAEEAGGKEKIRVMMPEKGVGINVDSFVIPKDAKNVANAHK
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a917      RGDTTCVTIGFGGDLNIAKRRAEEAGGKEKIRVMMPEKGVGINVDSFVIPKDAKNVANAHK
           250      260      270      280      290      300

           310      320      330      340      350      360
m917.pep  YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a917      YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           310      320      330      340      350      360

           370
m917.pep  ALKFMVRQWQDVKAGKX
           ||||||||||||||||
a917      ALKFMVRQWQDVKAGKX
           370

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2789>:

```

g919.seq
1  ATGAAAAAAC ACCTGCTCCG CTCCGCCCTG TACGGcatCG CCGCCgccAT
51  CctcgCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCCG GACCGGCCGG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGGCCG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATT TGCCTTTCAGT CTGCAATCCT
251 TCCGCTCCG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTCAAAC CCCCGTGCAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTCACGC cgtGGCagg tgcaggcaAC GGAAGcCTTG
401 CaggtaaggT TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAC GGGCCCGCTT CCCGATTTC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCG CTGCCTGCCG GTTTCGGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGAc ggGAAAAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 TACACGCGCG ACCTCTCCCG ATTCCCCATC ACCGCGCGCA CAACGGcaat
651 caaaGGCAGG TTTGAaggAA GCCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCGgcgCT GACGGCAAag cccCCATCCT CggttaagcC
751 GAagaccCcg tcgaacttTT TTTTCATGCAC AtccaaggCT CGGGCCCGCT
801 GAAAAACCcg tccggcaaat acatCCGCAt cggaTaccgc gacAAAAACG
851 AACAtccgTa tgtttccatc ggACGctaTA TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcac aaagcCTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCGGTCGG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCGGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GCGGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCACAG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2790; ORF 919.ng>:

```

g919.pep
1  MKKHLRLSAL YGIAAAILAA CQSRSIQTFP QPDTSVINGP DRPAGIPDPA
51  GTTVAGGGAV YTVVPHLSMP HWAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKRFFER YFTPNQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTEARFPIY GIPDDFISVP LPAGLRGGKN LVRIQTGKN SGTIDNAGGT
201 HTADLSRFPI TARTTAIKGR FEGSRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAYS GNEGVPVAGL
351 TPLMGEYAGA IDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2791>:

```
m919.seq
1  ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TACGGCATCG CCGCCGCCAT
51  CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC CGACCCGCC
151 GGAACGACGG TCGCGGCCGG CGGGGCCGTC TATACCGTTG TACCGCACCT
201 GTCCCTGCCC CACTGGGCGG CGCAGGATT TCGCCAAAAGC CTGCAATCCT
251 TCCGCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TCGCGCCAAG CCTTCAAAC CCCCGTCCAT TCCTTTCAGG CAAAACAGTT
351 TTTTGAACGC TATTTACGC CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCCGCTT CCCGATTTC GGTATTCCCG ACGATTTTAT
501 CTCCTGCCCC CTGCTGCGG GITTGCGGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACCGCCG ACCTCTCCG ATTCCCCATC ACCGCGCGCA CAACAGCAAT
651 CAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCGATACT CGGTACGCC
751 GAAGACCTG TCGAATCTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCyTA CGTTTCCATC GGACGCTATA TGGCGGATAA GGGCTACCTC
901 AAACCTCGAC AAACCTCCAT GCAGGGCATT AAGTCTTATA TCGGCGAAAA
951 TCCGCAACGC CTCGCCAAG TTTTGGGTCA AAACCCAGC TATATCTTT
1001 TCCGCGAGCT TGCCGGAAGC AGCAATGACG GCCCTGTCGG CGCACTGGGC
1051 ACGCCGCTGA TGGGGGAATA TGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGTGCG CCCTTATTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCTCAACCG CCGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GGCACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTC CTACCCAACG
GTATGAAGCC CGAATACCG CCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2792; ORF 919>:

m919.pep

```
1  MKKYLFRAL YGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
51  GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SPQAKQFFER YTFWQVAGN GSLAGTVTGY YEPVLKGDDE
151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIQTGKN SGTIDNTGGT
201 HTADLSRFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFEMH IQSGSRLKTP SGKIIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KSYMQRNPQR LAEVLGQNPS YIFFRELAGS SNDGPVGAIG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF 919.ng) from *N. gonorrhoeae*:

m919/g919

```

      10      20      30      40      50      60
m919.pep  MKKYLFRALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
          ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
g919      MKKHLRSALYGIAAAILAACQSRSIQTFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
          10      20      30      40      50      60

      70      80      90     100     110     120
m919.pep  YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSPQAKQFFER
          ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
g919      YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSPQAKRFFER
          70      80      90     100     110     120
```

1318

	130	140	150	160	170	180
m919.pep	YFTPWQVAGNGSLAGTVTGYEYVPLKGDGDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA					
	: :					
g919	YFTPWQVAGNGSLAGTVTGYEYVPLKGDGRTERARFPIYGIPDDFISVPLPAGLRGGKN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m919.pep	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
	: :					
g919	LVRIRQTGKNSGTIDNAGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m919.pep	DGKAPILGYAEDPVLEFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMAADKGYL					
	: :					
g919	DGKAPILGYAEDPVLEFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMAADKGYL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m919.pep	KLGQTSMQGIKSYMRQNPQRLAEVLGQNPYSIIFRELAGSSNDGPVGALGTPLMGEYAGA					
	: :					
g919	KLGQTSMQGIKAYMRQNPQRLAEVLGQNPYSIIFRELAGSGNEGVPVGALGTPLMGEYAGA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m919.pep	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFYFWGYGDEAGELAGK					
	: : :					
g919	IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFYFWGYGDEAGELAGK					
	370	380	390	400	410	420
	430	440				
m919.pep	QKTTGYVWQLLPNGMKPEYRPX					
g919	QKTTGYVWQLLPNGMKPEYRPX					
	430	440				

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2793>:

```

a919.seq
1  ATGAAAAAAT ACCTATTCCG CGCGGCCCTG TCGGGCATCG CGCGCGCCAT
51  CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCCG TCGGCATCCC CGACCCCGCC
151 GGAACGACGG TCGGCGGCGG CGGGCCGTT TATACCGTTG TGCCGCACCT
201 GTCCCTGCCC CACTGGGCGG CGCAGGATT CGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAACC GCCAAGGCTG GCAGGATGTG
301 TCGGCCCAAG CCTTTCAAAC CCCCCTCCAT TCCGTTCAAG CAAAACAGTT
351 TTTTGAACGC TATTTACGC CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCCGCTT CCGGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCCTGCCG GTTTGCGGAG CGGAAAAGCC CTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAT AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACCGCGG ACCTCTCCCA ATTCCCCATC ACTGCGCGCA CAACGGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AATCAACGG CGGCGCGCTT GACGGCAAAG CCCCATACT CGGTTACGCC
751 GAAGACCCCG TCGAATTTT TTTTATGCAC ATCCAAGGCT CGGGCCGCTC
801 GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCCTA CGTTTCCATC GGACGCTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAACGC CTCGCCGAG TTTTGGGGCA AAACCCAGC TATATCTTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTCCG CGCACTGGGC
1051 ACGCCGCTGA TGGGCGAGTA CGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTGGGGCGCG CCCTTATTG TCGCCACCGC CCATCCGTT ACCCGCAAAG

```

1319

1151 CCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GGCGACGAAG CCGCGCAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCCAACG
1301 GTATGAAGCC CGAATACCGC CCGTAA

This corresponds to the amino acid sequence <SEQ ID 2794; ORF 919.a>:

a919.pep

```

      1 MKKYLFRAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
    51 GTTVGGGAV YTVVPHLSLP HWAAQDFAKS LOSFRLGCAN LKNRQGWQDV
   101 CAQAFQTPVH SVQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDR
   151 RTAQAFFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
   201 HTADLSQFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
   251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
   301 KLGQTSMQGI KAYMQQNQR LAEVLGQNPS YIFFRELTGS SNDGPVGALG
   351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
   401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

m919/a919 98.6% identity in 441 aa overlap
      10      20      30      40      50      60
m919.pep MKKYLFRALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
      10      20      30      40      50      60

      70      80      90     100     110     120
m919.pep YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER
      70      80      90     100     110     120

      130     140     150     160     170     180
m919.pep YFTPWQVAGNGSLAGTVTGYEPVLKGDDRRRTAQAFFPIYGIPDDFISVPLPAGLRSGKA
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      YFTPWQVAGNGSLAGTVTGYEPVLKGDDRRRTAQAFFPIYGIPDDFISVPLPAGLRSGKA
      130     140     150     160     170     180

      190     200     210     220     230     240
m919.pep LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGRFLPYHTRNQINGGAL
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGRFLPYHTRNQINGGAL
      190     200     210     220     230     240

      250     260     270     280     290     300
m919.pep DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
      250     260     270     280     290     300

      310     320     330     340     350     360
m919.pep KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      KLGQTSMQGIKAYMQQNQRQRLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA
      310     320     330     340     350     360

      370     380     390     400     410     420
m919.pep VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
      370     380     390     400     410     420

      430     440
m919.pep QKTTGYVWQLLPNGMKPEYRFX
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      QKTTGYVWQLLPNGMKPEYRFX
      430     440
```


Expression of ORF 919

The primer described in Example 1 for ORF 919 was used to locate and clone ORF 919. This sequence was purified and expressed in *E. coli* as provided in Figure 1 #. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 919 is provided in Figure 5 #. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 is provided in Exhibit C #.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2795>:

```
g920.seq (partial)
1  ..ccgatgcagc tggttaccga aaaAGGTAAG GAAAACATGA TTCAACGCGG
51  CACATACAAC TACCAATACC GCAGCAACCG TCCCGTCAAA GACGGCAGCT
101 ACCTCGTTAC CGCCGAATAT CAGCCTACTT TCCGGTCAAA AAACAAAGCA
151 GGCTGGAAAC AGGCTGGCAT CAAAGAAATG CCTGACGCAA GCTATTGCGA
201 ACAAAACCGT ATGTTTCGTA AAAACATTGT CAACGTGGGA CACGAAAGCG
251 CGGACACCGC CATCATCACC AAACCGGTCG GACAAAACCT GGAAATCGTC
301 CCGCTGGACA ATCccgcccga caTTCACgtg ggctaacgCt tcaaaGTccg
351 cgttCtgttc cgtGGCgaac cgCTGcccaa tgccACCgtt accgCtaccAT
401 TTGacggctt cGAcaccagc gaccgcagca aaacgcacaa Aaccgaagcc
451 caagcctTCT ccgacaccac cgacggcgaa ggcgaaagtgg acatcatCCC
501 CTGCGcccaa GGCTTtttga aAgcGAGTGT CGAATAcaaa gccgAttccc
551 CCGATcaaAG CCTGTGccga AAACAggcga ACTACaCaac TTtaaccttc
601 caaatcgccc attctCacca tTAa
```

This corresponds to the amino acid sequence <SEQ ID 2796; ORF 920.ng>:

```
g920.pep (partial)
1  ..PMQLVTEK GK ENMIQRGTYN YOYRSNRPVK DGSYLVTA EY QPTFRSKNKA
51  GWKQAGIKEM PDASYCEQTR MFGKNIVNVG HESADTAIIT KPVGQNLEIV
101 PLDNPADIHV GXRFKVRVLF RGEPLPNATV TATFDGFDTS DRSKTHKTEA
151 QAFSDTTDGE GEVDIIPLRQ GFWKASVEYK ADFPDQSLCR KQANYTTLT F
201 QIAHSHH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2797>:

```
m920.seq
1  ATGAAGAAAA CATTGACACT GCTCTCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCACGCC CACCGmGTCT GGGTCGAAAC CGCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCTCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAwACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCTG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAArCCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTACG GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAwmCCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CmCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCAAATCG GTCATTGCGA
801 CCATTAA
```

This corresponds to the amino acid sequence <SEQ ID 2798; ORF 920>:

```
m920.pep
1  MKKTLTLLSV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYOYRSNRPV KDGSYLVIAE
101 YQPTFWSKKK ACWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD T
```

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 920 shows 91.3% identity over a 207 aa overlap with a predicted ORF (ORF 920.ng) from *N. gonorrhoeae*:

q920/m920

[illegible]

a920.seq

1	TGAAAGAAAA	CATGTGACACT	GCTCGCCGTT	TCCGCCCTAT	TTGCCGCATC
51	CGCCCCAGCC	CACCGCGTGT	GGGTGCAAA	CGCCCCACAG	CACGGCGCGC
101	AATACCTTAA	AGCGCACTTG	GGCTACGGGC	AATTTCCCGA	ACTCGAAGAT
151	ATCGCCAAAG	ACCGCTGCA	CATCTTCAGC	AAACCGATGC	AGCTGGTTAC
201	CGAAAAAGGC	AAGGAAAACA	TGATTCAACG	CGGCACATAC	AACTACCACT
251	ACCGAAGCAA	CCGTCCCGTT	AAGGACGGCA	GTTACCTCGT	CATCGCGGAA
301	TATCAGCCTA	CTTTCTGGTT	AAAAACAATA	CGAGGCTGGA	CAAGGCGGG
351	CATCAACAAC	ATGCTGTAGC	CAAGTATTGT	GCACAAACC	ACGATGTTCT
401	GCAAAAAACAT	CGTCAACGTC	GGACACGAAA	CGCGGGACAC	CGGCATCATC
451	ACCAAACCGG	TGCGACAAAA	CTTGGAATC	GTCCCGCTGG	ACAATCCCGC
501	CAACATTCAC	GTAGGCGAAC	GCTTCAAAGT	CCGCGTTCTG	TTCCGTTGGC
551	AACCGCTGCC	CAATGCCACC	GTTACCGCCA	CTTTGACGG	CTTCGACACC
601	AGCGACCGCA	GCAAAACGCA	CAAAACGAA	GCACAGGCTT	TCTCCGACAG
651	CACAGACGAC	AAAGGCGAAG	TGGACATCAT	CCCTTGCGC	CAAGGCTTCT
701	GGAAAGCCAA	TGTCGAACAC	AAAGCCGACT	TCCCGGATCA	AAGCGTGTGC
751	CAAAAACAGG	CGAACTACTC	GACTTTAACC	TTCAAATCG	GCCATTGCGA
801	CCATTAA				

a920.pep

1	*KKTLLTLLAV	SALFAASAHA	HRVWVETAHT	HGGEYLKADL	CYGEFPELEP
51	IAKDRLHIFS	KPMQLVTEKG	KENMIQCEQT	NYQYRSNRFP	KDGSYLVAIE
101	YQPTFESSKNK	AGWKQAGIKG	MPDASRYCEQ	RMFGKNINVP	HGESADTAIE
151	TKPVGQNLLEI	VPLDNPAIH	VGERFKVRVL	FRGEPLPNAT	VTATFDGFD
201	SDRSKTHKTE	AQAFSDSTDD	KGEVDIIPLR	QGFWKANVEH	KADFPDQSVC
251	OKOANYSTILT	FOIGHSHH*			

m920/a920 97.0% identity in 267 aa overlap

	10	20	30	40	50	60
m920.pep	MKKTLLTLLSVSALFATSAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
a920	XKKTLTLLVSAFSAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
	10	20	30	40	50	60
m920.pep	70	80	90	100	110	120
	KPMQLVTEKGKKNMIQRTYNYQYRSNRPVKDGSYLVIAEYQPTFWSKKKAGWKQAGIKE					
a920	KPMQLVTEKGKKNMIQRTYNYQYRSNRPVKDGSYLVIAEYQPTFWSKKNAGWKQAGIKQ					
	70	80	90	100	110	120
m920.pep	130	140	150	160	170	180
	MPDASYCEQTRMFGKNIVNVGHESADTAITKPVGQNLEIVPLDNPANIHVGERFKVRVL					
a920	MPDASYCEQTRMFGKNIVNVGHESADTAITKPVGQNLEIVPLDNPANIHVGERFKVRVL					
	130	140	150	160	170	180
m920.pep	190	200	210	220	230	240
	FRGEPLPNATVTATFDGFDTSDRSKTHXKEAQAFSDSTDGKGEVDIIXLRQGFWKANVEH					
a920	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDGKGEVDIIPLRQGFWKANVEH					
	190	200	210	220	230	240
m920.pep	250	260	269			
	KTDFPDQSVQCQKQANYSTLTFOIGHSHHX					
a920	KADFPDQSVQCQKQANYSTLTFOIGHSHHX					
	250	260				

g920-1.seq

g920-1.pep

m920-1.seq

1	ATGAAGAAAA	CATTGACACT	GCTCGCCGTT	TCCGCCCTAT	TTGCCACATC
51	CGCCGACGCC	CACCGCGTCT	GGGTGCGRAAC	CGGCCACACG	CACGGCGGGC
101	AATACCTTAA	AGCCGACTTG	GGCTACGCGC	AACTTCCCGA	ACTCGAAGCC
151	ATCGCCAAAG	ACCGCCTGCA	CATCTTCAGC	AAACCGATGC	AGCTGGTTAC
201	CGAAAAGAGC	AGGAAAAACA	TGATTCAACG	CGGCACATAC	AATCTACGAT
251	ACCGAAGCAA	CCGTCCGCTT	AAGGACGGCA	GTTACTCTGT	CATCGCCGAA

1323

```

301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCTG
401 GCAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAGCCAA TGTCGAACAC AAAACCGACT TCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GTCATTTCGA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2804; ORF 920-1>:

m920-1.pep

```

1 MKKTLTLLAV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51 IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLIVIAE
101 YQPTFWSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TRPVQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KTDFFDQSV
251 KQANYSTLT FQIGHSHH*

```

m920-1/g920-1 96.3% identity in 268 aa overlap

	10	20	30	40	50	60
m920-1.pep	MKKTLTLLAVSAI	FATSAHAHRVWVETAHT	HGGEYLKADL	GYGEFPELEPIAKDRLHIFS		
g920-1	MKKTLTLLAVSALFATSAH	PHRVWVETAHTHGGEYLKADL	GYGEFPELEPIAKDRLHIFS			
	10	20	30	40	50	60
m920-1.pep	KPMQLVTEKGKENMIQRGT	YNYQYRSNRPVKDGSYL	IVIAEYQPTFWSKNKAGWKQAGIKE			
g920-1	KPMQLVTEKGKENMIQRGT	YNYQYRSNRPVKDGSYL	IVIAEYQPTFRSKNKAGWKQAGIKE			
	70	80	90	100	110	120
m920-1.pep	KPMQLVTEKGKENMIQRGT	YNYQYRSNRPVKDGSYL	IVIAEYQPTFWSKNKAGWKQAGIKE			
g920-1	KPMQLVTEKGKENMIQRGT	YNYQYRSNRPVKDGSYL	IVIAEYQPTFRSKNKAGWKQAGIKE			
	70	80	90	100	110	120
m920-1.pep	MPDASYCEQTRMFGKNIVNVGHESADTAII	TKPVQNLEIVPLDNPANIHVGERFKVRVL				
g920-1	MPDASYCEQTRMFGKNIVNVGHESADTAII	TKPVQNLEIVPLDNPANIHVGERFKVRVL				
	130	140	150	160	170	180
m920-1.pep	MPDASYCEQTRMFGKNIVNVGHESADTAII	TKPVQNLEIVPLDNPANIHVGERFKVRVL				
g920-1	MPDASYCEQTRMFGKNIVNVGHESADTAII	TKPVQNLEIVPLDNPANIHVGERFKVRVL				
	130	140	150	160	170	180
m920-1.pep	FRGEPLPNATVTATFDGFDTS	DRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH				
g920-1	FRGEPLPNATVTATFDGFDTS	DRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKASVEY				
	190	200	210	220	230	240
m920-1.pep	FRGEPLPNATVTATFDGFDTS	DRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH				
g920-1	FRGEPLPNATVTATFDGFDTS	DRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKASVEY				
	190	200	210	220	230	240
m920-1.pep	KTDFFDQSVCKQANYSTLT	FQIGHSHHX				
g920-1	KADFFDQSLCQKANYTTLT	FQIGHSHHX				
	250	260	269			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2805>:

a920.seq

```

1 TGAAGAAAA CATTGACACT GCTCGCGTTC TCCGCCCTAT TTGCCGCATC
51 CGCCACGCC CACCGCTCTT GGTGCGAAAC CGCCACACAG CACGGCGGGC
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTCCCGGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCACT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAGCAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCTG
401 GCAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAGCCAA TGTCGAACAC AAAGCCGACT TCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GCCATTTCGA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2806; ORF 920-1.a>:

```
a920.pep
1  *KKLTLLAV SALFAASAH HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVAIE
101 YQPTFWSKNK AGWKQAGIKQ MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNL EI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDSTDD KGEVDIPLR QGFWKANVEH KADFPDQSVC
251 QKQANYSTLT FQIGHSHH*
```

m920-1/a920 98.9% identity in 267 aa overlap

	10	20	30	40	50	60
m920-1.pep	MKKTLTLLAVSALFATS	SAHAHRVWVETAHTHG	GEYLKADLGYGEFPE	LEPIAKDRLHIFS		
a920	XXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXX
	10	20	30	40	50	60
	70	80	90	100	110	120
m920-1.pep	KPMQLVTEKGKENMIQR	GTYNQYRSNRPVKDGS	YLVIAEYOPTFWSKNK	AGWKQAGIKE		
a920	XXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXX
	70	80	90	100	110	120
	130	140	150	160	170	180
m920-1.pep	MPDASYCEQTRMFGKN	IVNVGHESADTAIITK	PVGQNL EIVPLDNP	ANIHVGERFKVRVL		
a920	XXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXX
	130	140	150	160	170	180
	190	200	210	220	230	240
m920-1.pep	FRGEPLPNATVTATFD	GFDTSDRSKTHKTEAQ	AFSDSTDDKGEVDI	IPLROGEFWKANVEH		
a920	XXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXX
	190	200	210	220	230	240
	250	260	269			
m920-1.pep	KTDFPDQSVCKQKQAN	YSTLTFQIGHSHHX				
a920	XXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXX				
	250	260				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2807>:

```
g921.seq
1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTCC TTTCCGggtG
51  Ccagctctatt tatGtgccca cattgacggA aatccccgTg aatcccatca
101 ataCCGtcaa aacggaagCA CCTGCAAAAG GTTTTCGCCT CGCCCTTCG
151 CATTGGCGCG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGcgGCG CAATATCTGA
251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCTGA TGACAGTATG
301 TATGAAATCT ACCTGCGTTC GCGGTAGAC AGCCAGCGCG GCGAAATCAA
351 TACGGAACAG TCCAAGCTGT ATATCGAGAA TGCCTTGCGC GGCTGGCAGC
401 AGCGTtggAA AAATATGGAT GCCAAACCCG ATAATCCCGC ATTTACCAAC
451 TTTTGTATGG AAGTGATGAA GATGAGCCC TTGAAATGA
```

This corresponds to the amino acid sequence <SEQ ID 2808; ORF 921.ng>:

```
g921.pep
1  MKKYLPLSI AAVLSGCOSI YVPTLTEIPV NPINTVKTEA PAKGFRLAPS
51  HWADVAKISD EATRLGYQVG IGKMTKVQAA QYLNNFRKRL VGRNAVDDSM
101 YEIYLRSAVD SQRGEINTEQ SKLYIENALR GWQQRWKNMD AKPDNPAFTN
151 FLMEVMMQMP LK*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2809>:

```
m921.seq
1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTTC TTTCCGGCTG
51  CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTC AATCCTATCA
101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTTCCGCCT TGCTCTTCG
151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA
```

251 ACAACTTCAG AAAACGCGCTG GTCGGACGCA ATGCCGTGCGA TGACAGTATG
301 TATGAAATCT ACCTGCGTCT GGCATAGAC AGCCAGCGGG GCGCAATCAA
351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
401 AGCGTTGGAA AAATATGGAT GTCAAAACCA ACAACCCGCG ATTTACCAAC
451 TTTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

```

1  MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLESS
51  HWTDVAKISD EATRLGYQVG IGMKTKVQAA QYLNFRKRL VGRNAVDDSM
101 YBIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
151 FLMEVMKMQP LK*

```

m921/g921

1	ATGAAAAAA	ACCTTATCCC	TCTTTCATT	GTGCGAGTTC	TTTCCGGCTG
51	CCAGTCTATT	TATGTGCCCA	CATTGACGGA	AATCCCCGTG	AATCCTATCA
101	ATACCGTCAA	AACGGAAGCA	CCTGCAAAG	GTTTCCGCT	TGCTCTTCG
151	CATTGGACGG	ATGTTGCCAA	AATGACGCAT	GAAGCGACGC	GCTTGGGCTA
201	TCAGGTGGGT	ATCGGTAAAA	TGACCAAGT	TCAGGCGCGG	CAATATCTGA
251	ACAACCTTCAG	AAAACGCCTG	GTCGGACGCA	ATGCCGTCGA	TGACAGTATG
301	TATGAAATCT	ACCTGCGTTC	GGCGATAGAC	AGCCAGCGGG	GCGCAATCAA
351	TACGGAACAG	TCCAAGCTGT	ATATCCAGAA	TGCTTTCGCG	GGCTGGGAGC
401	AGCGTTGGAA	AAATATGGAT	GTCAAACCCA	ACAACCCCGC	ATTTACCAAC
451	TTTTTGATGG	AAGTGATGAA	GATCAGCCCC	TTGAAATGA	

```

1  MKKYLIPLSI VAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRCLASS
51 HWTDVAKISD EATRLGYQVG IGMKTKVQAA QYLNNFRKRL VGRNAVDDSM
101 YEIYLRSAID SORGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
151 FLMEVMKMQP LK*

```

10 20 30 40 50 60
 m921.pep MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFR LASSHWTDVAKISD
 |||||:||||||||||||||||||||||||||||||||||||||
 a921 MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFR LASSHWTDVAKISD
 10 20 30 40 50 60

1326

	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
a921	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
a921	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2813>:

g922.seq

```

1  ATGGAAGA GAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CCCGCACACC CCGGGCAAAT GAAGCCCAAG
101  CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151  GCAGCCGTAC CGGTATCCGA CAGCGGGTTT GCCGCCAATG CAAATGTCCG
201  CCGTTTTGTG GACGATGAAG TCGGGAAAGG GGATTTTTC CAGGCGGAAT
251  GGCAGGATTT TTTTGACAAA GCGGCTTACA AGGCGGACAT CGTCAAGATT
301  ATGCACCGAC CCTCCACATC GCGtCCGTGG TATGtgttcc gCacggGAAa
351  ttcGGgcagg gcgaaAtttc ACggcgCGCG Caggttttat GcggaaAacc
401  gcgcggttat cgatgatgtg gcgCAAAaT acggcgGCC TGCCGAGCTT
451  ATCGTGGCGA TTATCGGGAT TGAACGAAT TACGGCAAAA ATACGGGCAG
501  TTTCGTGTG GCGGACGCAT TGGCGACTTT AGGCTTTGAT TATCCCCGCC
551  GC3CCGGGTT TTTCCAAAAA GAATTGGTCG AGCTTTTAAA GCTGGCAAAA
601  GAAGAAGGCG GTGATGTTTT GCCTTTAAG GGCagcTATG CGGGTGCAAT
651  GGGTATGCCG CAATTTATGC CTTCGAGCTA CCGGAAATGG GCGGTGGATT
701  ATGAcgggga cggacatCGG GATATAtggg GCAACGtcgg tgatgtcgcg
751  gcatcggtTG CCAATTatcT gaagCAGCAC GGTGGCGCA CgggcggTAA
801  AATGTTGGTG TCGGCGAcgt tggcgccggg tgccgATGTT CAggcAATCA
851  TTGGCGAAAA AACCGCCCTG ACGCGGACGG TGGCGGATTT GAaggCGTAc
901  ggcacatccc ccggggaaac GCTCGCAGAT GATGAAAAGg cgGTTTGTt
951  CAACTGGAA ACCGCACCCG GCGTGTTTGA ATATTATTtG GGCTTGAACA
1001  ATTTTATATC GGTATGCGAG TACAACCACA GCCGGATGTA TGTAACGgcg
1051  gtcaggGACA TTGCCAATTC GCTCGCGCGC CCGGATTGT Aa

```

This corresponds to the amino acid sequence <SEQ ID 2814; ORF 922.ng>:

g922.pep

```

1  MEKRKILPLA ICLAALSACT AMEARTPRAN EAQAPRADEM KKERPAFPA
51  AAVPVSDSGF AANANVRRFV DDEVGKGDFS QAEWQDFFDK AAYKADIVKI
101  MHRPSTSRPW YVFRtGNSGR AKFHGARRFY AENRAVIDDV AQKYGVPAEL
151  IVAIIGIETN YGKNTGSFRV ADALATLGFD YPRRAGFFQK ELVELLKLAK
201  EEGDVFAFK GSYAGAMGMP QFMPSSYRKW AVDYDGDGHR DIWGNVGDVA
251  ASVANYMKQH GWRTGGKMLV SATLAPGADV QAIIGEKAL TRTVADLKAY
301  GIIPGETLAD DEKAVLFKLE TAPGVFEYLL GLNNFYTVWQ YNHSRMVYTA
351  VRDIANSLGG PGL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2815>:

m922.seq

```

1  ATGAAAAAGA GAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCACACC CCGGGCAAAT GAAGCCCAAG
101  CCCCCCGCGC GGTGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151  GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201  CGCCAATGCA AATGTCCGCC GTTTGTGTGA CGATGAAGTC GGGAAAGGGG
251  ATTTTTCCTG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301  GCGGACATCG TCAAGATTAT GCACCGCCCC TCACATCGC GTCCGTGGTA
351  TGTGTTCCGC ACGGGAATTT CCGGCAAGGC GAAATTCGC GCGCGCGGCC
401  GGTTTTATGC GGAAAACCGC GCGCTTATCG ATGATGTGCG GCAAAAATAC
451  GGCGTGCCTG CCGAACTTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501  CCGCAAAAAT ACGGCGAGTT TCCGTGTGCG GGACGCATTG GCGACCTTAG
551  GCTTTGATTA CCCCCCGCGC GCCGGGTTTT TCCAAAAAGA ATTGGTCGAG

```

m922.ppt

ORF 922 shows 95.9% identity over a 369 aa overlap with a predicted ORF (ORF 922.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m922 . pep	MKKRKILPLAICLAALSACTAMEARPPRANEAQAPRAVEMKKESRPAFDAAAVFDAAAP					
	:					
g922	MEKRKI LPLAI CLAALSACTAMEARTPRANEQAQAPRADEMCKESRPAFDA-----AVP					
	10	20	30	40	50	
	70	80	90	100	110	120
m922 . pep	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR					
	:					
g922	VSDSGFAANANVRRFVDDEVGKGDFSQA EWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR					
	60	70	80	90	100	110
	130	140	150	160	170	180
m922 . pep	TGNSGKAKFRGARIFYAENRALIDDVAQKYGVPAELIVAVIGIETNYGKN TGSFRVADAL					
	: : : : : : : : : : :					
g922	TGN SGR AKFH GAR IFYA EN R AVIDDV AQ KY GVP AE LI V AI I GI ET NY GK NT GS FR VA DAL					
	120	130	140	150	160	170
	190	200	210	220	230	240
m922 . pep	ATLGFDYP RRAG FF Q K E LV EL L KL AKEE GG DV F AF KG SY AG AM GP QF MP SS Y RK W AV DY					
g922	ATL GF D Y P R RA G FF Q K E LV EL L KL AKEE GG DV F AF KG SY AG AM GP QF MP SS Y RK W AV DY					
	180	190	200	210	220	230
	250	260	270	280	290	300
m922 . pep	DGDGH RD I WG NV GD VA AS VAN YM KQH GW RTGG KM LVS AT LAP GA D V QA I I GEKT AL TR TV					
g922	DGDGH RD I WG NV GD VA AS VAN YM KQH GW RTGG KM LVS AT LAP GA D V QA I I GEKT AL TR TV					
	240	250	260	270	280	290
	310	320	330	340	350	360
m922 . pep	ADLKAYGI IPGEELADEDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRM YVT AVR DI					
g922	ADLKAYGI IPGETLADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNH SRMY VT AVR DI					

300 310 320 330 340 350

m922.pwp

g922

a922.seq

5

a922.pap

5

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m922.pwp

a922

m922.pwp

a922

m922.per

a922

1329

```

m922.pep  ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          190      200      210      220      230      240

          250      260      270      280      290      300
m922.pep  DGDGHRDIWGNVGDVAASVANYMKQHGWRGTGGKMLVSATLAPGADVQAIIGEKALTTRTV
          |||||||||||||||||:|||||||||||||||:|||||||||||||||||
a922      DGDGHRDIWGNVGDVAASVANYMKQHGWRGTGGKILVSATLAPGADVQAIIGEKALTTRTV
          250      260      270      280      290      300

          310      320      330      340      350      360
m922.pep  ADLKAYGIIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922      ADLKAYGIIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          310      320      330      340      350      360

          370
m922.pep  ANSLGGPGLX
          |||||||||
a922      ANSLGGPGLX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2819>:

```

g923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACCGATG GCGTGTGCGG CATTTCTGTC
51  CGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAACGCGCG TGCCGTGCGG
151 GGAAAACGCC GCATTCCCGA ACACCGCCTG CTCCTGCCTG CCTTGTTCCG
201 CGGTTGGACG GCGGCATACT TGGGTAGTAG GATGTTTCAGG CATAAAACGG
251 CGAAAAGCG TTTTGTGTG CTGTTCCGTC TGACTGTTTC GGGCAATGTC
301 CTGGCGACCT GCATCCTGAT TGATTATTTT GTTCCGCCCG AACTTTTGTG
351 AAAACTCGGG CAACATCTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2820; ORF 923.ng>:

```

g923.pep
1  MKRQAFFKPM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRRRAVR
51  GKRRIPRHRL LLPALPGGWT GAYLGSRMFR HKTAKKRFV LFRITVSGNV
101 LATCILIDYF VPPELFVKLG QHL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2821>:

```

m923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTTCTGTC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAACGGTG CGCCATACGG
151 GGGCAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CATTGCTCGG
201 CGGCTGGGTG GCGCGGTATT TCGGCAGCAT GACATTCAAA CATAAGACAG
251 CGAAAAGCG TTTTGTGTG CTGTTCCGTC TGACTGTTTC AGGTAATGTC
301 TTGGCGACCC TCATCCTGAT TTATAGTGA TTAAATTTAA ACCAGTACGG
351 CGTTGCCTCG CCTTGCCGTA CTATTGTAC TGTCTGCGGC TTCGTGCGCT
401 TGTCTGATT TTTGTTAATC CACTATAT.T ATTTTGTCCC GCCTGAATT
451 TTCGTAAAAC TCGGCAGAA TACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2822; ORF 923>:

```

m923.pep
1  MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRAIR
51  GQRRIPRHRL LLPALLGGWV GAYFGSMTFK HKTAKKRFV LFRITVSGNV
101 LATLILYSG LNLNOYGVAS PCRTICTVCG FVALS*FLLI HXYFVPPPEF
151 FVKLGQNT*

```

Computer analysis of this amino acid sequence gave the following results:

1330

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 923 shows 68.8% identity over a 157 aa overlap with a predicted ORF (ORF 923.ng) from *N. gonorrhoeae*:

g923/m923

```

      10      20      30      40      50      60
g923.pep  MKRQAFFKPMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRRIPEHRL
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
m923      MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCAIRGQRRRIPEHRL
          10      20      30      40      50      60

      70      80      90      100
g923.pep  LLPALFGGWTGAYLGSRMFRHKHTAKKRFVVLFRLLTVSGNVLATCILID-----
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
m923      LLPALLGGWVGAYFGSMTFKHKHTAKKRFVVLFRLLTVSGNVLATLILYISGLNQLNQYGVAS
          70      80      90      100      110      120

                                110      120
g923.pep  -----YFVPPPELFVKLGQHLX
          |||||  |||||  |||||  |||||
m923      PCRTICTVCGFVALSXFLLIHYIYFVPPPEFFVKLGQNTX
          130      140      150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2823>:

```

a923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTCTGTGC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTAC GCAATATTGT
101 CCCTCTATGC GTTTCACCTT TACGGCATCG ACAAACGCGG TGCCGTGCGG
151 GGAAAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CCTTGTTTCG
201 CGGTTGGGCG GGCGCATACT TGGGCAGCAG GATATTCAGG CATAAACCGG
251 CGAAAAAGCG TTTTGTGTG CTGTTCCGTC TGAAGTTTC GGGCAATGTC
301 CTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTTAA ACCAGTACGG
351 CGTTGCCTCG CCTTA.GCTC AAAGAGAACG ATTCTCTAAG GTGCTGAAGC
401 ACCAAGTGAA TCGGTTCCGT ACTATTGTA CTGTCTGCGG CTTCTGCGCC
451 TTGTCCTGAT TTTTGTTAAT CCACTAT.AT TATTTTGTCC CGCCTGAATT
501 TTTCGTAAAA CTCGGGCAGA ATACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2824; ORF 923.a>:

```

a923.pep
1  MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLEYAFAL YGIDKRRRAVR
51  GKRRRIPEHRL LLPALFGGWA GAYLGSRIFR HKHTAKKRFV LFRLLTVSGNV
101 LATLILYISG LNLNQYGVAS PXAQRERFSK VLKHQVNRFR TICTVCGFVA
151 LS*FLLIHYX YFVPPPEFFVK LQNT*

```

m923/a923 84.6% identity in 175 aa overlap

```

      10      20      30      40      50      60
m923.pep  MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCAIRGQRRRIPEHRL
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a923      MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRRIPEHRL
          10      20      30      40      50      60

      70      80      90      100      110      120
m923.pep  LLPALLGGWVGAYFGSMTFKHKHTAKKRFVVLFRLLTVSGNVLATLILYISGLNQLNQYGVAS
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a923      LLPALFGGWAGAYLGSRIFRHKHTAKKRFVVLFRLLTVSGNVLATLILYISGLNQLNQYGVAS
          70      80      90      100      110      120

                                130      140      150      159
m923.pep  PC-----RTICTVCGFVALSXFLLIHYXYFVPPPEFFVKLGQNTX
          |  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a923      PXAQRERFSKVLKHQVNRFTICTVCGFVALSXFLLIHYXYFVPPPEFFVKLGQNTX
          130      140      150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2825>:

```
g925.seq
  1 ATGAAACAAA TGCTTTTGGC cgtcggcgtg ggcgcggtgt TGGCGGGCTG
 51 CGGCAaggat gcCGGCGGtt acgaggggTA TTGGCGCGAA AAGTCGGACA
101 AAAAagaggG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTTCCTTAAT
151 AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGCGG
351 ACAACCGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGA AAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG
```

This corresponds to the amino acid sequence <SEQ ID 2826; ORF 925.ng>:

```
g925.pep
  1 MKQMLLAVGV GAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLN
 51 KINVFTGKEE SLLLSEKDGA LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKKCGQT QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNKPTLL F*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2827>:

```
m925.seq (partial)
  1 ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
 51 CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG TATGATTGCC GTCAAAAAG AAAAAGGCAA TTACTTCCTT
.....
```

This corresponds to the amino acid sequence <SEQ ID 2828; ORF 925>:

```
m925.pep (partial)
  1 MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL..
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 925 shows 94.0% identity over a 50 aa overlap with a predicted ORF (ORF 925.ng) from *N. gonorrhoeae*:

m925/g925

	10	20	30	40	50
m925.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKKEKGNVFL				
g925	MKQMLLAVGVGAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKNINVFTGKE				
	10	20	30	40	50
g925	ESLLLSEKDGA LSINTGIGE IPIKLSDDGKELYVERRRYVK TDAAMKDKII AHQKKCGQT				
	60	70	80	90	100
	110				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2829>:

```
g925-1.seq
  1 ATGAAACAAA TGCTTTTGGC CGTCGGCGTG CCGGCGGTGT TGGCGGGCTG
 51 CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTTCCTTAAT
151 AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGCGG
351 ACAACCGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGA AAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG
```

This corresponds to the amino acid sequence <SEQ ID 2830; ORF 925-1.ng>:

g925-1.pep

1332

```

1  MKOMLLAVGV AAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNYFLN
51 KINVFTGKEE SLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
101 TDAAMKDKI IAHQKCGQT AQAYLDARNA LPSNQTYYQOQ AAIEQLKRR
151 EAEFDELEKE IKCNGKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2831>:

```

m925-1.seq
1  ATGAAACAAA TGCTTTTACG CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTACTTCCTT
151 AATAAAATCC ACGTGGTTAC AGGCAAGGAA GAGTCCTTGC TTTTGTCTGA
201 AAAAGACGGC GCGCTTTCGA TAAACACAGG GATAGGGGAA ATCCCGATCA
251 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGTAG GCAGTATGTC
301 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
351 CGGACAAACA GCACAGGCAT ACCGCGACGC GCGAAATGCG TTGCCGTCAA
401 ACCAGACGTA TCAGCAGCAT CTGGCGGCGA TCGAGCAATT GAAACGGCGG
451 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAT GCAACGGCAG
501 AAGCCCGCGA TTGTTGCTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 2832; ORF 925-1>:

```

m925-1.pep..
1  MKOMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGYFL
51 NKIHVVTGKE ESLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
101 KTDAMKDKI IAHQKCGQT AQAYRDARNA LPSNQTYYQOQ LAAIEQLKRR
151 FEAEFDELEK EIKCNGRSPA LLL*

```

m925/g925 92.5% identity in 173 aa overlap

	10	20	30	40	50	60
m925-1.pep	MKOMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGYFLNKIHVVTGKE					
g925-1	MKOMLLAVGVAAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNYFLNKINVFTGKE					
	10	20	30	40	50	
	70	80	90	100	110	120
m925-1.pep	ESLLSEKDGALSINTGIGEIPKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKCGQT					
g925-1	ESLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAAMKDKIIAHQKCGQT					
	60	70	80	90	100	110
	130	140	150	160	170	
m925-1.pep	AQAYRDARNALPSNQTYYQOHLAAIEQLKRRFEAEFDELEKEIKCNGRSPALLLX					
g925-1	AQAYLDARNALPSNQTYYQOQAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2833>:

```

a925-1.seq
1  AATAAAATCA ACGTGTTTAC AGGTAAGGAA GAATCTATGC TTTTGTCTGA
51 AAAAGACGGC GCGCTTTCGA TAAACACGGG GATAGGGGAA ATCCCGATCA
101 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGCAG GCAGTATGTC
151 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
201 CGGACAAACG GCACAGGCAT ATCTCGACGC GCGAAATGCG TTGCCGTCAA
251 ACCAGACGTA TCAGCAGCAT CAGGCGGCGA TCGAGCAGTT GAAACGGCGG
301 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAT GCAACGGCAA
351 ACCGACATTG TTGTTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2834; ORF 925-1.a>:

```

a925-1.pep
1  NKINVFTGKE ESMLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
51 KTDAMKDKI IAHQKCGQT AQAYLDARNA LPSNQTYYQOQ QAAIEQLKRR
101 FEAEFDELEK EIKCNGKPTL LF*

```

a925-1/m925-1 92.7% identity in 123 aa overlap

		10	20	30
a925-1.pep		NKINVFTGKEESMLLSEKDGALSINTGIGE		
m925-1	AGGYEGYWREKSDKKEGMIAVKKEKGYFLNKIHVVTGKEESLLSEKDGALSINTGIGE			
	30	40	50	60
	40	50	60	70
				80
				90

1333

```

a925-1.pep  IPIKLSDDGKELYVERRQYVKTDAAAMKDKIIAHQKKCGQTAQAYLDARNALPSNQTYYQH
|||||
m925-1      IPIKLSDDGKELYVERRQYVKTDAAAMKDKIIAHQKKCGQTAQAYRDARNALPSNQTYYQH
          90      100      110      120      130      140

          100      110      120
a925-1.pep  QAAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX
|||||
m925-1      LAATIEQLKRRFEAEFDELEKEIKCNGRSPALLLX
          150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2835>:

```

g926.seq (partial)
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCGGAAGGG CGGTTGGCAG TCAAAGCGGA AGGGAAGGT
151 TCGTATGCAA ATTTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG ACAGTTGTGT CAAGacAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAGGCT
301 ACGgaagact tGAGCAGGCA GCTGGTCGGT TTCAAACGTC CAATCCAATA
351 TCTGCATATC TGGGCGGAAG GCAGGCGTGT GCGGGGCGCG CCTtaccGCA
401 TCCGTTTACA CGGCATATTG GAACAATAcg GttggACAAT cgggCagaac
451 tgcCGACAGT GGGGGGCaag tccgaacgtt gcaactGAa...

```

This corresponds to the amino acid sequence <SEQ ID 2836; ORF 926.ng>:

```

g926.pep (partial)
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEKGK
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 TEDLSRQLVG FKLPIQYLHI WAEGRRVAGA PYRIRSDGIL EQYGTWIGQN
151 CROWGASPNV ATE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2837>:

```

m926.seq
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCAGAAGGG CGGTTGGCAG TGAAGCGGA AGGGAAGGT
151 TCGTATGCAA ATTTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAATACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GCGGAAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACGTC CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCGTGT GCGGGGCGCG CCTTACCGCA
401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CGGCAGAACC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGGTTTTC ACGAAATCGG TATGCCGTCT GAAACCGAAA
551 CCCCAGAACG CTGTGCGGCG CGCACGAGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2838; ORF 926>:

```

m926.pep
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEKGK
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 AEELSRQLVG FKLPIQYLHI WADGRRVAGA PYRILPDGIL EQYGTWVGR
151 ADGGGQVRTL QLNNGNLNIR LVFTEIGMPS ETETPERCAA RTR*

```

g926/m926 91.6% identity in 155 aa overlap

```

          10      20      30      40      50      60
g926.pep  MKHTVSASVILLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEKGKSYANFDWTYQ
|||||
m926      MKHTVSASVILLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAECKGKSYANFDWTYQ
          10      20      30      40      50      60

          70      80      90      100     110     120
g926.pep  PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAEQTEDLSRQLVGFKLPIQYLHI
|||||
m926      PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAELSRQLVGFKLPIQYLHI
          70      80      90      100     110     120

          130     140     150     160
g926.pep  WAEGRRVAGAPYRIRSDGILEQYGTWIGQNCROWGASPNVATE

```

1334

|||||
m926 WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS
130 140 150 160 170 180

a926.seq

1 ATGAAACACA CTGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51 GCAATTACCT CAAATAACG AAAACCTGTG GCAGCCGTCC GAACACACCC
101 GCAGTTTCAC GCGGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTCGATTG GACATACCAA CCGCCCGTGG AAACATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GSCGGAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACTGC CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCCTGT GCGGGGCGCG CTTACCGCA
401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CAGCAGAACCC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAATTT
501 GAACATCAGG CTGGTTTTC CCGAGATTGG TATGCCGTCT GAAACCGAAA
551 CCCAAGAACA ATGCGCGGCA CGCATACAGT AA

a926.pep

1 MKHTVSASVI LLLTACAQLP QNNENLWQPS EHTRSFTEAG RLAVKAEGKG
51 SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVQAES
101 AEELSRQLVG FKLPIQYLHI WADGRPVAGA PYRILPDGIL EQYGWTVGRT
151 ADSSGQVRTL QLNNGNLIR LVFTEIGMPS ETETQECCAA RIQ*

m926/a926 96.9% identity in 191 aa overlap

	10	20	30	40	50	60
m926.pep	MKHTVSASVILLTACAQLPQNNENLWQPSSEHISFAAEGRLAVKAEGKGSYANFDWTYQ					
a926	MKHTVSASVILLTACAQLPQNNENLWQPSSEHTRSFTEAGRLAVKAEGKGSYANFDWTYQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m926.pep	PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVQAESAEEELSRQLVGFKLPIQYLHI					
a926	PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVQAESAEEELSRQLVGFKLPIQYLHI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m926.pep	WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
a926	WADGRPVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
	130	140	150	160	170	180
	190					
m926.pep	ETETPERCAARTRX					
a926	ETETQECCAAARIQX					
	190					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2839>:

g927.seq

1 atgaaaacct acGCacAggC ACTCTATacc GCAGCCCTGC TCACCGCCTG
51 CAGCCCGcga GCcgatTcaa accaTCCGTC CGGAcAaAAT GCCCCGGCCA
101 ATACCGAATC cgacGgaaAA AACATtacc TGctcaatgc cTcgtacgat
151 gtGACACGGT ATTTttacaa agaatacgac cacTtggttg tcggaaCATA
201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAA TCCACGCGC
251 GCTTCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
301 GTAACCATGA ACCAATCTTC CGACATCGAC CTGCTCGAAA AAAA.GGACT
351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGATCACGCC GCACCCTACA

1335

401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCaa ACAGAtccgC
 451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAAGAC
 501 CTCGGGCAAC GGACGCTACG CCTTCCTCGG CGCATACGGT TACGGTCTGA
 551 AAGCCAACAA CGGcaaCGAG CA3GAAGCCC AAAAActCGT CGCATCCATC
 601 CTCAAAAACA CACCCGTTTT TGAAAACGGC GGACGGC.C CGCCGCCACC
 651 ACCTTCACAC AACGCAACAT CGGCGACGTA CTCATCACTT TTGAAAACga
 701 agCcaactac gtCAGCAAAA AACTGA

This corresponds to the amino acid sequence <SEQ ID 2840; ORF 927.ng>:

g927.pep

1 MKTYAQALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
 51 VTRYFYKEYD HLFVGTYSQSE HPGTSVSIQQ SHGGFSKQAL SVANGLQADV
 101 VTMNQSSDID LLEKXGLVEK GWQALPDHA APYTSTMVFL VRKNNPKQIR
 151 DWNDLAKDGV NIVIAKTSN GRYAFLGAYG YGLKANNGNE QEAQKLVASI
 201 LKNTPVFENG GRXPPPPSH NATSATYSSL LKTKPTTSAK N*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2841>:

m927.seq

1 ATGAAAACCT ACGCACCGGC ACTCTATACC GCAGCCCTGC TCACCGCCTG
 51 CAGCCCCGCA GCCGATTCAA ACCATCGTTC CGGACAAAT GCCCCGCCA
 101 ATACCGAATC CGACGGAAAA AACATTACCC TGCTCAACGC CTCATACGAT
 151 GTGGCAGGG ATTTTACAA AGAATACAAC CCCTATTATA TCAAAACATA
 201 CCAATCGAA CACCCCGGCA CATCCGTCAG CATCCAACAG TCCACGGCG
 251 GCTCCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
 301 GTAACCATGA ACCAATCCTC CGACATCGAC CTGCTCGAAA AAAAAGGACT
 351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGACCACGCC GCGCCCTACA
 401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCAA ACAGATCCGC
 451 GATTGGAACG ACCTTGCCAA AGACGGC3TT AACATCGTCA TCGCCAATCC
 501 CAAACCTCG GGCAACGGAC GCTACGCCTT CCTCGGCGCA TACGGTTACG
 551 GTCTGAAAAA CACCAACGGC AACGAACAGG AAGCCCAAAA ACTCGTCGCA
 601 TCCATCTCA AAAACACCCC CGTTTTGAA AACGGCGGAC GCKCgCCACC
 651 ACCACCTTCA CACAACGCAA CATCGGCGAC GTACTCATCA CTTTGA
 701 CGAAGCCAAC TACGTAGC AAAAACTGA

This corresponds to the amino acid sequence <SEQ ID 2842; ORF 927>:

m927.pep

1 MKTYAPALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
 51 VARDFYKEYN PLFIKTYQSE HPGTSVSIQQ SHGGSSKQAL SVANGLQADV
 101 VTMNQSSDID LLEKKGLVEK GWQALPDHA APYTSTMVFL VRKNNPKQIR
 151 DWNDLAKDGV NIVIANPKTS GNGRYAFLGA YGYGLKTTNG NEQEAQKLVA
 201 SILKNTPVFE NGRXPPPPS HNATSATYSS LLKTKPTTSA KN*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 927 shows 94.2% identity over a 243 aa overlap with a predicted ORF (ORF 927.ng) from *N. gonorrhoeae*:

g927/m927

	10	20	30	40	50	60
g927.pep	MKTYAQALYTAALLTACSPAADSNDHPSGQNAPANTESDGKNITLLNASYDVTRYFYKEYD					
m927	MKTYAPALYTAALLTACSPAADSNDHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN					
	10	20	30	40	50	60
g927.pep	HLFVGTYSQSEHPGTSVSIQQSHGGFSKQALSVANGLQADVVTMNQSSDIDLLEKXGLVEK					
m927	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK					
	70	80	90	100	110	120
g927.pep	GWQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIA--KTSNGRYAFLGA					
m927	GWQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSNGRYAFLGA					
	130	140	150	160	170	180

1336

	180	190	200	210	220	230
g927.pep	YGYGLKANNGNEQEAQKLVASILKNTPVFENGGRXPPPPPSHNATSATYSSLLKTKPTTS					
	:					
m927	YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRXPPPP-SHNATSATYSSLLKTKPTTS					
	190	200	210	220	230	
	240					
g927.pep	AKNX					
m927	AKNX					
	240					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2843>:

```

a927.seq
1  ATGAAACCT  ACGCACCGGC  AACTATACC  GCAGCCCTGC  TCAGCGCCTG
51  CAGCCCCGCA  GCCGATTCAA  ACCATCCGTC  CGGACAAAAT  GCCCCGGCCA
101 ATACCGAATC  CGACGGAAAA  AACATTACCC  TGCTCAACGC  CTCATACGAT
151 GTGGCACGGG  ATTTTACAA  AGAATACAAC  CCCTATTFTA  TCAAAACATA
201 CCAATCCGAA  CACCCCGGCA  CATCCGTCAG  CATCCAACAG  TCCCACGGCG
251 GCTCCAGCAA  ACAGGCATTA  TCCGTAGCCA  ACGGCCTTCA  AGCCGATGTC
301 GTAACCATGA  ACCAATCCTC  CGACATCGAC  CTGCTCGAAA  AAAAAGGACT
351 GGTAGAAAAA  GGCTGGCAAC  AAGCCTCCC  CGACCACGCC  GCGCCCTACA
401 CCAGCACTAT  GGTTCCTT  GTCCGAAAA  ACAACCCCAA  ACAGATCCGC
451 GATTGGAACG  ACCTTGCCAA  AGACGGCGTT  AACATCGTCA  TCGCCAATCC
501 CAAACCTCG  GGCAACGGAC  GTACGCCTT  CCTCGGCGCA  TACGGTTACG
551 GTCTGAAAC  CACCAACGGC  AACGAACAGG  AAGCCCAAAA  ACTCGTCGCA
601 TCCATCCTCA  AAAACACCCC  CGTTTTGAA  AACGGCGGAC  GCGCGCCACC
651 ACCACCTTCA  CACAACGCAA  CATCGCGGAC  GTACTCATCA  CTTTGAAAA
701 CGAAGCCAAC  TACGTCAGCA  AAAAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2844; ORF 927.a>:

```

a927.pep
1  MKTYAPALYT  AALLSACSPA  ADSNHPGQON  APANTESDGK  NITLLNASYD
51  VARDFYKEYN  PLFIKTYQSE  HPGTSVSIQQ  SHGGSSKQAL  SVANGLQADV
101 VTMNQSSDID  LLEKKGLVEK  GWQALPDHA  APYTSTMVFL  VRKNNPKQIR
151 DWNDLAKDGV  NIVIANPKTS  GNGRYAFLGA  YGYGLKTTNG  NEQEAQKLVA
201 SILKNTPVFE  NNGRAPPPPS  HNATSATYSS  LLKTKPTTSA  KN*

```

m927/a927 99.2% identity in 242 aa overlap

	10	20	30	40	50	60
m927.pep	MKTYAPALYTAALLTACSPAADSNHPGQONAPANTESDGKNITLLNASYDVARDFYKEYN					
a927	MKTYAPALYTAALLSACSPAADSNHPGQONAPANTESDGKNITLLNASYDVARDFYKEYN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m927.pep	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK					
a927	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m927.pep	GWQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA					
a927	GWQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m927.pep	YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRXPPPPSHNATSATYSSLLKTKPTTSA					
a927	YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRAPPPPSHNATSATYSSLLKTKPTTSA					
	190	200	210	220	230	240

m927.pep KNX
 |||
 a927 KNX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2845>:

g929.seq
 1 ATGAAATGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
 51 CGCCCTGGTT TTGGCACTGC CCGTACcga CGGGGTCAAG CCTCAGGCTT
 101 GGACGCTGCT GGCTATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
 151 GTTATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
 201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
 251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
 301 TCGCGCGGTT TGCTCAAAAC AGGCTGCGG ATGCGTATCG GATATTGTT
 351 TATCGCCGTT TTTGGAAGAA AAacgctggg CATCGGTTAC AGTCTCGCTC
 401 TTCCGAACT GCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
 451 GGCGGCATTA TACATCgaT TATGCagtcg attgCcgCA GttacggctC
 501 caatCCCGCA AAAGGCACag aaggcaagat gggtAAATAT TtggcTTtgg
 551 tcaattaTCA TTCcaatCCC atttcgctcg ctAtggctat taCTGcaact
 601 gCCCCcaacc CTTTAATcgt caacttgatt gccGaaaaTt taggcagtag
 651 tttccgtCTT Tcttgggggg cgTGGGcgtg ggcaaTGGCT Gttcccggeg
 701 ttatcgctt TTcgtTATG CCTTTGATTT TATATTTTT GTATCCGCCT
 751 GAAATTAAG AAACGCCCAA TGCTGttcAA TTTGCCAAAG ACCGCTGAG
 801 CGAGATGGGT AAAATGtcgg CAGACGAAAT CATTATGGCG GTCATTTTCG
 851 GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
 901 CACGCTTTTA GTATCAacgc caccGCCACC GCATTATCG GATTAAGCCT
 951 GCTTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTT AAAGAAAAA
 1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGCGCGCA
 1051 TTTTtaATA Aactcggact gattaaatGG TTCTCCGAG TGTGCGCGA
 1101 Aagtgtcggc GGTTTGGCG TTAGCGGCAC GGCTGCGGC GTAATCCTCG
 1151 TGCTTGCTta TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
 1201 ATTACCGCTA GTTTCGGCGC ATTTCTGCT GCTGCGTTT CACTGAATGC
 1251 CCCGGCGATG CCGACTGCGC TGATGATGGC GGCCGCATCC AACATTATGA
 1301 TGACCTTCAC TCATTATGCG ACCGGTACTT CACCTGTGAT TTTCCGCTCG
 1351 GGCTACACCA CAATGGGAGA ATGGTGAAG GCGGTTTTA TCATGAGCGT
 1401 AGTCAATTTT CTGATTTTTT CCGTTATCGG CAGCATTTGG TGGAAAGTTC
 1451 TGGGATATTG GTAA

This corresponds to the amino acid sequence <SEQ ID 2846; ORF 929.ng>:

g929.pep
 1 MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
 51 VMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
 101 SRGLLKTLGL MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG
 151 GGIHHPIMQS IAGSYGSNPA KGTGKMGKY LALVNYHNSP ISSAMAITAT
 201 APNPLIVNLI AENLGSSFRL SWGANAWAMA VPGVIAFFVM PLILYFLYPP
 251 EIKETPNAVQ FAKDRLSEMG KMSADEIIMA VIFGILLLLW ADVPALITGN
 301 HAFSINATAT AFIGLSLLLL SGVLTWDJVL KEKSAWDII WFGALIMMAA
 351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTAH
 401 ITAMFGAFLA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
 451 GYTTMGEWWK AGFIMSVVNF LIFSVIGSIW WKVLGYW*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2847>:

m929.seq
 1 ATGAAATGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
 51 CGCCCTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
 101 GGACGCTGCT GGCCATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
 151 GCCATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
 201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
 251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
 301 TCGCGCGGTT TGCTCAAAAC AGGCTGCGG ATGCGTATCG GATATTGTT
 351 TATCGCGGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
 401 TTTCCGAACT GCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC

```

451 GCGGGCATTACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501 CAATCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAATATCA TTCCAATCCC ATTTCTGTCG CTATGTTTAT TACTGCAACT
601 GCCCCAACCC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651 TTTCCGCTCT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
701 TTATCGCCTT TTTCTGTTATG CCTTTGATT TATATTTwyT GIATCCGCCT
751 GAAATTAAAG AAACGCCCAA TGCCGTTCAA TTTGCCAAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGAATTGGGA CGATGTTTTG AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGTTTTCGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGGAG TGTGGCGGA
1101 AAGTGTCCGC GGTTTGGGCG TTAGCGGCAQ GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACGCTTA GTTTCGGCGC ATTTTTCGCT GCTGCGGTTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GgCCGCATCC AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCCGTTCC
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTTGG TGGAAAGTTC
1451 TGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2848; ORF 929>:

m929.pep

```

1  MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLA PVTPTSNTARG
151 GGIIHPIMQS IAGSYGSNPA KGTGKMGKY LALVNYHSNP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYXLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAHYMA HYMFASSTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 929 shows 98.8% identity over a 487 aa overlap with a predicted ORF (ORF 929.ng) from *N. gonorrhoeae*:

g929/m929

	10	20	30	40	50	60
g929 .pep	MKLGFKPIPLAIAAVLCALVLALPVPDGVKPKQAWTLLAMFVGVIAAIIGKVMPLGALSII					
m929	MKLGFKPIPLAIAAVLCALVLALPVPDGVKPKQAWTLLAMFVGVIAAIIGKAMPLGALSII					
	10	20	30	40	50	60
g929 .pep	AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
m929	AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
	70	80	90	100	110	120
g929 .pep	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTGKMGKY					
m929	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTGKMGKY					
	130	140	150	160	170	180
g929 .pep	LALVNYHSNP ISSAMAITATAPNPLIVNIAENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
m929	LALVNYHSNP ISSAMFITATAPNPLIVNLIENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
	190	200	210	220	230	240

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	190	200	210	220	230	240
	250	260	270	280	290	300
g929.pep	PLILYFLYPPEIKETPNVQFAKDRLEMGKMSADEIIMAVIFGILLLLWADVLPALITGN					
m929	PLILYXLYPPEIKETPNVQFAKDRLEMGKMSADEIIMAVIFGILLLLWADVLPALITGN					
	250	260	270	280	290	300
	310	320	330	340	350	360
g929.pep	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
m929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
	310	320	330	340	350	360
	370	380	390	400	410	420
g929.pep	FSGVLAESVGGGLGVSGTAAGVILVLAIFYAHYMFASSTTAHITAMFGAFLAAVSLNAPAM					
m929	FSGVLAESVGGGLGVSGTAAGVILVLAIFYAHYMFASSTTAHITAMFGAFAAAVSLNAPAM					
	370	380	390	400	410	420
	430	440	450	460	470	480
g929.pep	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFSVIGSIW					
m929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
g929.pep	WKVLGYWX					
m929	WKVLGYWX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2849>:

a929.seq

```

1  ATGAAATTGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCTTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
101 GACGCTGCTT GGCCATGTTT ATCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GCCATGCCGT TGGGTGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
201 AACGGGCGTA ACCGCCGACA AACGGGGTGC GCGGATGAGC GATGCGTTGA
251 GTGCGTTTCG CAATCCGTTC ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
451 GCGGCGATTA TACATCCGAT TATGCAGTCG ATTGCCGCGC GTTACGCTC
501 CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTTCGTCGG CTATGTTTAT TACTGCAACT
601 GCCCCAACCC CTTAATCGT CAACTTGATT GCCGAAATTT TAGGCAGTAG
651 TTTCCGTCCT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGCG
701 TTATCGCCTT TTTCGTTATG CCTTTGATTT TATATTTTAT GTATCCGCTT
751 GAAATTAAAG AAACGCCCAA TGCCGTTCAA TTGCCAAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGTT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGTTGAT TGACTTGGGA CGATGTTTTC AAAGAAAAAA
1001 GCGCGTGGGA TACSATTATT TGGTTTGGCG CATTGATTAT GATGGCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGAG TGTGGCGGA
1101 AAGTGTGCGC GGTGTGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCGCGC ATTTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCG TGATGATGGC GGCCGCATCT AACATTATGA
1301 TGACCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCCGTTCC
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTC TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTC TCGTTATCGG CAGCATTTGG TGGAAAGTTC
1451 TGGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2850; ORF 929.a>:

```

a929.pep
  1  MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF IGVIAAIIGK
 51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101  SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLA PVTPSNTARG
151  GGIIHPIMQS IAGSYGSNPA KGTEGKMCKY LALVNYHNSP ISSAMFITAT
201  APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
251  EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301  HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351  FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMEFASTTAH
401  ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451  GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

m929/a929 99.6% identity in 487 aa overlap

m929.pep	10	20	30	40	50	60
	MKLGFKPIPLAIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAII GKAMPLGALSII					
a929	10	20	30	40	50	60
	MKLGFKPIPLAIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAII GKAMPLGALSII					
m929.pep	70	80	90	100	110	120
	AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMI SRGLLKTGLG MRIGYLFIAV					
a929	70	80	90	100	110	120
	AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMI SRGLLKTGLG MRIGYLFIAV					
m929.pep	130	140	150	160	170	180
	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMCKY					
a929	130	140	150	160	170	180
	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMCKY					
m929.pep	190	200	210	220	230	240
	LALVNYHSNPISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
a929	190	200	210	220	230	240
	LALVNYHSNPISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
m929.pep	250	260	270	280	290	300
	PLILYXLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN					
a929	250	260	270	280	290	300
	PLILYFLYPPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN					
m929.pep	310	320	330	340	350	360
	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
a929	310	320	330	340	350	360
	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
m929.pep	370	380	390	400	410	420
	FSGVLAESVGGLGVSGTAAGVILVLAYMYAHYMEFASTTAHITAMFGAFFAAAVSLNAPAM					
a929	370	380	390	400	410	420
	FSGVLAESVGGLGVSGTAAGVILVLAYMYAHYMEFASTTAHITAMFGAFFAAAVSLNAPAM					
m929.pep	430	440	450	460	470	480
	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNLIFFVIGSIW					
a929	430	440	450	460	470	480
	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNLIFFVIGSIW					
m929.pep	WKVLGYWX					

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a929 WKVLGYWX

g930.seq not found yet

g930.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2851>:

m930.seq

```

1  ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTCGCTTTT TGTCTTGGTG
51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTC TGCCATTAAAC GAATGGGTGT TGGAAGGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAAGTG CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAgTGG aAGCTTCAAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2852; ORF 930>:

m930.pep

```

1  MKLPLSYLPN IRFLSWCCLL AGIIPATLL ASPNPAEIRM QODIQORORE
51  EQLRQTMQPE SDVRLHOKNT GETVNQIMGD DSSQPCFAIN EWVLEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGSFN *

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2853>:

g930-1.seq (partial)

```

1  GGCAAGTGTC TGCATGCCGG CGACATTAAT CAAATCATGT CCTTAGCACA
51  AAATSCTTTG ATCGGCAGGG GATATACCAC GACCCGTATC TTGGCTGCGC
101 CACAGGATTG GAATAGTGGC AAGCTTCAAT TAACCTGAT GCCGGGCTAT
151 CTGCGCTCCA TACGAATCGA TCGGTCCAAC GATGATCAAA CCCATGCAGG
201 ACGTATTGCA GCATTCCAAA ACAAAATTCC CACCCGCTCG AACGATCTGT
251 TGAATCTGCG TGATTTGGAA CAAGGACTGG AAAATCTCAA ATGTCTCCCG
301 ACTGCGGAAG CCGATCTCCA AATCGTTCCC GTAGAGAGAG AACCAAACCA
351 AAGTGATGTC GTGGTGCAAT GCCGGTAACG TCTGCTGCCC TACTGTGTGA
401 GTGTGGGGAT GGATAATTCG GGTAGTGAGG CGACAGGAAA ATACCAAGGA
451 AATATCACTT TCTCTGCCGA CAATCCTTTT GGAAGTGTG ATATGTTCTA
501 TGTAAATTAT GGACGTTCAA TTGGCGGTAC GCCCGATGAG GAAAATTTTG
551 ACGGCCATCG CAAAGAAGGC GGATCAACAC ATTACGCCGT ACATTATTCA
601 GCCCCTTTTC GTAAATGGAC ATGGGCATTC AATCACAATG GCTACCGTTA
651 CCATCAGGCG GTTTCGGGAT TATCGGAAGT CTATGACTAT AATGGAAAAA
701 GTTACAACAC TGATTTGGGC TTCAACCGCC TGTGTATATC TGATGCCAAA
751 CGCAAAACCT ATCTCAGTGT AAAACGTGTG ACAGGGGAAA CAAAAAGTTA
801 CATTGATGAT GCCGAAGTGA CTGTACAACG GCGTAAACCC ACAGGTTGGT
851 TGGCAGAACT TTCCCACAAA GGATATATCG GTGCGAGTAC GGCAGATTTT
901 AAGTTGAAAT ATAAACACCG CACCGGCATG AAAGATGCTC TCGCGCGGCC
951 TGAAGAAGCC TTTGGCGAAG GCACGTCACG TATGAAAATT TGGACGGCAT
1001 CGGCTGATGT AAATACTCCT TTTCAAATCG GTAAACAGCT ATTTGCCTAT
1051 GACACATCCG TTCATGCACA ATGGAACAAA ACCCCGCTAA CATCGCAAGA
1101 CAAACTGGCT ATCGGCGGAC ACCACACCGT ACGTGGCTTC GACGGTGAAA
1151 TGAGTTTGCC TGCCGAGCGG GGATGGTATT GCGGCAACGA TTTGAGCTGG
1201 CAATTTAAAC CAGGCCATCA GCTTTATCTT GGGGCTGATG TAGGACATGT
1251 TTCAGGACAA TCCGCCAAAT GGTATTCGGG CCAAACCTTA GCCGGCACAG
1301 CAATTGGGAT ACGCGGGCAG ATAAAGCTTG GCGGCAACCT GCATTACGAT
1351 ATATTTACCG GCCGTGCATT GAAAAAGCCC GAATATTTTC AGACGAAGAA
1401 ATGGGTAACG GGGTTTCAGG TGGGTATTTC GTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2854; ORF 930-1.ng>:

g930-1.pep (partial)

```

1  GKCLHAGDIN QIMSLAQNAL IGRGYTTTRI LAAPQDLNSG KLQLTLMPGY
51  LRSIRIDRSN DDQTHAGRIA AFQNKFPTRS NDLLNLRDLE QGLENLKCLP
101 TAEADLQIVP VEREPNQSDV VVQWR*RLLP YCVSVGMDNS GSEATGKYQG
151 NITFSADNPF GLSDMFYVNY GRSIGGTPDE ENFDGHRKEG GSNNYAVHYS
201 APFGKWTWAF NHNGYRYHOA VSGLSEVYDY NGKSYNTDFG FNRLLYRDAK
251 RKTYSVSKLW TRETKSYIDD AELTVQRRKT TGWLAELSHK GYIGRSTADF
301 KLKYKHGTGM KDALRAPEEA FEGGTSRMKI WTASADVNTF FOIGKOLFAY
351 DTSVHAQWNK TPLTSQDKLA IGGHHTVRGF DGEMSLPAER GWYWRNDLSK
401 QFKPGHQLYL GADVGHVSGO SAKWLSGQTL AGTAIGIRGQ IKLGGNLHYD

```

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451 IFTGRALKKP EYFQTKKVVTF GFQVGYSF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2855>:

m930-1.seq

```
1 ATGAACTTC CTTATCCTA TTTGCCTAAT ATTGCTTTT TGTCTGGTG
51 CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTGTGTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTF TGCCATTAAAC GAAGTGGTGT TGGAGGCGGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA GCACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAGTGG CAAGCTTCAA TTAACCTGA TACCAGCTA
501 TCTGCCCTCC ATACGAATCG ATCGGTCTAA CGATGATCAA ACCCATGCAG
551 GACGTATTGC AGCATTCCAG AACAAATTTT CCACCCGCTC GAACGATCTG
601 TTGAATCTGC GTGATTGGA ACAAGGACTG GAAAATCTCA AACGTCTCCC
651 GACTGCGGAA GCCGATCTCC AAATCGTTCC CGTAGAGGGA GAACCAAACC
701 AAAGTGATGT CGTGGTGCAA TGCGGCAAC GTCTGCTGCC CTACCGTGTG
751 AGTGTGGGGA TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG
801 AAATATCACT TTCTCTGCCG ACAATCCTTT GGGACTGAGT GATATGTTCT
851 ATGTAATTA TGGACGTTTC ATTGGCGGTA CGCCCGATGA GGAAAGTTT
901 GACGGCCATC GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC
951 AGCCCTTTTC GGTAAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT
1001 ACCATCAGCG AGTTTCCGGA TTATCGGAAAG TCTATGACTA TAATGGAAAA
1051 AGTTACAATA CTGATTTCGG CTCAACCGC CTGTTGTATC GTGATGCCAA
1101 ACGCAAAACC TATCTCGGTG TAAACTGTG GATGAGGGAA ACAAAAGTT
1151 ACATTGATGA TGCCGAACAT ACTGTACAAC GCGCTAAAC TGCGGGTTGG
1201 TTGCCAGAAC TTTCCACAA AGAATATATC GGTCGCAGTA CGGCAGATTT
1251 TAAGTTGAAA TATAACGCG GCACCGGCAT GAAAGATGCT CTGCGCGCGC
1301 CTGAAGAAAC CTTTGGCGAA GGCACGTCAC GTATGAAAT TTGGACGGCA
1351 TCGGCTGATG TAAATACTCC TTTTCAATC GGTAAACAGC TATTGCTTA
1401 TGACACATCC GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG
1451 ACAACTGGC TATCGGCGGA CACCACCCG TACGTGGCTT CGACGGTGAA
1501 ATGAGTTTGT CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG
1551 GCAATTTAAA CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG
1601 TTTGAGGACA ATCCGCCAAA TGGTTATCGG GCCAACTCT AGTCGGCACA
1651 GCAATTGGGA TACGCGGGCA GATAAAGCTT GGCGGCAACC TGCATTACGA
1701 TATATTTTAC GGCCGCGCAT TGAAAAAGCC CGAATTTTTC CAATCAAGGA
1751 AATGGCAAG CGGTTTTCAG GTAGCTATA CGTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2856; ORF 930-1>:

m930-1.pep

```
1 MKLFLSYLPN IRFLSWCCLL AGIIAPATLL ASPNPAEIRM QQDIQQRQRE
51 EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EVVLEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGKLQ LTLIPSYLRS IRIDRSNDDQ THAGRIAAFQ NKFPTRSNDL
201 LNLRLDLEQL ENLKRLLPTAE ADLQIVPVEG EPNQSDVVVQ WRQRLLPYRV
251 SVGMNDSGSE ATGKYQGNIT FSADNPLGLS DMFYVNYGRS IGGTPDEESF
301 DGHRKEGGSY NYAVHYSAPF GKWTWAFNHN GYRYHQAVSG LSEVYDYNK
351 SYNTDFGFNR LLYRDAKRKT YLGVKLWMRE TKSIIIDAEI TVQRRKTAGW
401 LAELSHKEYI GRSTADFKLK YKRGTMKDA LRAPEEAFGE GTSRMKIWTA
451 SADVNTPFQI GKQLFAYDTS VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE
501 MSLSAERGWY WRNDLSWQFK PGHQLYLGA D VGHVSGQSAK WLSGQTLVGT
551 AIGIRGQIKL GGNLHYDIFT GRALKKPEFF QSRKWASGFQ VGYTF*
```

m930-1/g930-1 95.4% identity in 478 aa overlap

	90	100	110	120	130	140
m930-1.pep	AINEVVLEGEHHRFQFALKRALRETGFQAGKCLHAGNINQIMSLAQNALIGR	GYTTTRI				
g930-1.pep						
				10	20	30
	150	160	170	180	190	200
m930-1.pep	LAAPQDLNSGKLQTLTIPSYLRSIRIDRSNDDQTHAGRIAAFQNKFPTRSNDDL	NLRDLE				
g930-1.pep	LAAPQDLNSGKLQTLTIPSYLRSIRIDRSNDDQTHAGRIAAFQNKFPTRSNDDL	NLRDLE				
	40	50	60	70	80	90
	210	220	230	240	250	260
m930-1.pep	QGLNLRKLFPTAEADLQIVPVEGEPNOSDVVQWRQRLLPYRVSVGMNDSGSE	ATGKYQG				

a930-1.pep not yet found

g931.seq

```
1 ATGAAACCCA AATTCAAAC CGTTTAACC GCGTGTCTT TGGCGGTTTC
51 CCTGCCGTCT ATGGCGGCAA CCGCGTCTT GATGAAACC GATATGGGCA
101 ATATCCGTGT GGTTTTGGAC GAATCCAAAG CCTCCAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACCAACAGA TTTTCCACCG
201 CGTcatCGGC GGCTTCGTCA TCCAAGGCGA CGGATTGACC GAGGACTTGG
251 TGCAAAAGGC AACCATAAG GCCGTTGCCA ACGAATCCGG caacgGCTTG
301 AAAAACACCG TCGGCACCAT CGCAATGGCG CGGACGGCAG CCCCCGATTC
351 CGCCGCCCGC CAATCTTTTA TCAATCTGGC GGACACGGT TCGCTCGACT
401 ACAAAACCGG ACAATACGGC TACACCGTTT TCGGCAGGGT AGAAAGCGGA
451 ATGGACACCG TTTCAAAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501 TTGATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTGCG GTTGTGTGCG
551 GGCAGTAACA CGCAGACAGA CGTTCAGACG GCGTCGCCCC TTTCCAAAAA
601 AACGCCGTTT AA
```

g931.pep

1	MKPKFKTVLT	ALLLAVSLPS	MAATRVLMET	DMGNIRLVLD	ESXASKTVAN
1	FVRYARKGFY	DNTAIFHRVIG	GFVIQGDGLT	EDLVQKATDK	AVANESGNGL
101	KNTVGTIAMA	RTAAPDSAAA	QFFINLADNG	SLDYGKNQYG	YTVFGRVESG
151	MDTVSKIARV	KTATRGFFYQN	VPVQPVKIRR	VLVYG*	

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2859>:

m931.seq

```

1  ATGAAACCCA AATTCAAAC CGTTTAAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCCCCAAAAC CGTTGCTAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACGACACCG TTTTTCACCG
201 CGTTATCGAC GGTTTTGTTA TCCAGGCGCG TGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AAAAACACCG CCGGCACCAT CGCCATGGCG CGGACGACAG CCCCCGATTG
351 CGCCACCAGC CAATTCTTTA TCAATCTGGC GGACCA.kCT TCGCTCGACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
451 ATGAACACCG TTTCCAAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAACG GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGTC
551 GGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2860; ORF 931>:

m931.pep..

```

1  MKPKFKTVLT ALLLAVSLPS MAATHVIMET DMGNIRLVLD ESKAPKTVAN
51  FVRYARKGFY DDTVFHRVID GFVIQGGGLT EDLAQKASDK AVANESGNGL
101 KNTAGTIAMA RTTAPDSATS QFFINLADXX SLDYKNGQYG YTVFGRVESG
151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 931 shows 91.9% identity over a 185 aa overlap with a predicted ORF (ORF 931.ng) from *N. gonorrhoeae*:

g931/m931

	10	20	30	40	50	60
g931.pep	MKPKFKTVLTALLLAVSLPSMAATRVLMDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
m931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
	70	80	90	100	110	120
g931.pep	DNTIFHRVIGGFVIQGGGLTEDLVQKATDKAVANESGNGLKNTVGTIAMARTAAPDSAAA					
m931	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
g931.pep	QFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKTATRGFYQNPVQPVKIRR					
m931	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNPVQPVKIRR					
	130	140	150	160	170	180
g931.pep	VVVGQX					
m931	VVVGQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2861>:

a931.seq

```

1  ATGAAACCCA AATTCAAAC CGTTTAAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CACCCAAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACAATACGA TTTTTCACCG
201 CGTCATCGGC GGCTTCGTTA TCCAAGGCGG CGGATTGACC GASGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AAAAACACTG TCGGCACCAT CGCCATGGCG CGGACGGCCG ATCCGGATTG
351 CGCCACCAGC CAATTCTTTA TCAATCTGGT GGACAATGAT TCGCTCAACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC

```

1345

451 ATGAACACCG TTTCCAAAT CGCCCGCTC AAAACCGCCA CGCGCGGCTT
 501 TTATCAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTCTCG
 551 GGCAGTAA

This corresponds to the amino acid sequence <SEQ ID 2862; ORF 931.a>:

a931.pep
 1 MKPKFKTVLT ALLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
 51 FVRYARKGFY DNTIFHRVIG GFVIQGGGLT EDLAQKASDK AVANESGNGL
 101 KNTVGTIAMA RTADPDSATS QFFINLVDND SLNYKNGQYG YTVFGRVESG
 151 MNTVSKIARV KTATRGFYQN VEVQPVKIRR VVVGQ*

m931/a931 94.6% identity in 185 aa overlap

	10	20	30	40	50	60
m931.pep	MKPKFKTVLTALLAVSLPSMAATHVLMETDMGNIRLVLD	ESKAPKTVANFVRYARKGFY				
a931	MKPKFKTVLTALLAVSLPSMAATHVLMETDMGNIRLVLD	ESKAPKTVANFVRYARKGFY				
	70	80	90	100	110	120
m931.pep	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
a931	DNTIFHRVIGGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTVGTIAMARTADPDSATS					
	130	140	150	160	170	180
m931.pep	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPQPVKIRR					
a931	QFFINLVDNDSLNYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPQPVKIRR					
	130	140	150	160	170	180
m931.pep	VVVGQX					
a931	VVVGQX					

g932.seq not found yet

g932.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2863>:

m932.seq
 1 ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
 51 GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCTCA TTTTGGGAAT
 101 TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
 151 CAATATCCAT CGAAAGCAA ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
 201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
 251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAAACAA
 301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAATGA

This corresponds to the amino acid sequence <SEQ ID 2864; ORF 932>:

m932.pep
 1 MKYIVSISLA MGLAACSFEGG FKPNPWAAS FWELKNYANP YPGSASAALD
 51 QYPSKARRRQ LKDMQECGYD PIDGKSBAD ACLRKKGWCR KGFDYPYENK
 101 KYEWPREEGK TK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 932 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 932.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2865>:

g934.seq
 1 ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCG CACTCACC GC

g934.pep

1	<u>MKKI IASALI</u>	ATFALTACQD	DTQARLERQQ	KQIEALQQQL	AQQADDTVYQ
51	LTPEAVKDTI	PAQAQANGNN	GQPVTKRRA	AVYLRPIDRK	LAAAKPDWRG
101	GRRVYQRAG	KOIHPTGQOPR	QRPSPRACC	LPSTVTPQCA	HQQGFEHAQP
151	PCKYTGGLGA	ALPPDNPAPR	QLPPSYRACF	RQKAVNPARQ	CRLKGFQTAF
201	LYLLGALLCC	RLIFRRHFVS	KRLMSGWOF*		

m934.seq (partial)

1	CGGCTCGAAC	AGCAGCAGAA	ACAGATTGAA	GCCCTGCAAC	AGCAGCTCGC
51	ACACGACGGCA	GACGATACGG	TTTACCAACT	GACTCCCGAA	GCAGTCAAAG
101	ACACCATTCC	TGCCGAAGCA	CAGGCAAACG	GCAACCAACg	GCAACCCGTT
151	ACCGGTAA .A	CAGGGCAGC	AGTATATTTA	CGACCAATCG	ACAGGAAGCT
201	3GCTGCTGCA	AAGCCTGGTC	GCGCGCGCGG	CAGGCGCGTT	TATCGCGAAC
251	3GCTTG6CAA	ACAAATTCC	ACGGGCAGGC	AACCAAGACA	GTCCCGTCGC
301	CGGGCGCGCG	CGTGACGCTC	ACCATCAGTC	CGCAGCCTCC	AATGCGCGCA
351	yCAGCAGGGA	TTTGAACACG	CGCAGCTTCC	GTGCAAAAAC	ACAGGCGGCG
401	CAKCGCGAGC	GTTACCGCCC	GACAAACGCG	CCGsCCGsCA	ATTACCGCCG
451	CCCCGCTATG	CGCGGTTTCG	GCAGGAGGCG	GTAACCCCGG	CGCGCCAATG
501	CGTGTGAAG	AGTTTTCACA	CGGCATTnT	GCATTGTGTA	GGGACATTGT
551	TATGTTGCGG	TGTTGATTTT	AGACGGCATT	TTGTTTCCAA	GCCTTTGATC
601	TGGGATGGC	AATTCTGA			

m934.pep (partial)

```

1  ..RLEQQQKQIE ALQQLAQQA DDTVYQLTPE AVKDTIPAEA QANGNGGPV
51  TGXRRRAVYL RPIDRKLAA KPGRRGRRV YRQRAGKQIH TGRQPRQSR
101 PARACSLPSV RTPQCAHQG FEHAQPCKT TGGAXAALP DNAPXROLPP
151 PRYARFLQEA VNPARQRLK SFQTAFXHLL GTLCCRLIF RRHFVSKRLM
201 SGWQF*

```

Homology with a predicted ORF from *N.gonorrhoeae*

m934/g934

[illegible]

1347

```

m934.pep  QSRRPARACSLPSVRTPQCAHQQGFHAQPPCKTTGGAXAALPPDNAPXRQLPPPRYARF
          | |||:|||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g934      QPRRPSRACCLPSVRTPQCAHQQGFHAQPPCKTTGGAGAALPPDNAPARQLPPSRYARF
          130      140      150      160      170      180

          160      170      180      190      200
m934.pep  RQEAVNPARQCRLKSFQTAFXHLLGTLCCRLIFRRHFVSKRLMSGWQFX
          ||:||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||
g934      RQKAVNPARQCRLKGFQTAFLYLLGALLCCRLIFRRHFVSKRLMSGWQFX
          190      200      210      220      230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2869>:

```

a934.seq
1  ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTGC CACTCGCCGC
51  CTGCCAAGAC GACGCGCAGG CGCGGCTCGA ACAGCAGCAG AACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CAGACGATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCGAAG CACAGGCAAA
201 CGGCAACAAC GGGCAACCCG TTACCGG. TA AAGACGGGCA GCAGTATATT
251 TACGACCAAT CGACAGGAAG CTGGCTGTGT CAAAGCCTGG TCGGCGCGGC
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGCG AAACAAATTC ACACGGGCAG
351 GCAACCAAGA CAGTCCCGTC GCCCGGCGCG CGCGTGCCGC CTACCATCAG
401 TCCGCACATC CCAATGCGCG CACCAGCAGG GATTTGAACA CCGCAGCCT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCACA GCGTTACCGC CCGACAACGC
501 CCCCGCCCGC CAATTACCGC CGCCCCGCCA TGCCCGGTTT CSGCAGAAGG
551 CGGTAAATCC GCGTGCCAA TCGCGTCTGA AGGGCTTTCA GACGGCATT
601 TTGTATTTGT TAGGGACATT GTTATGTTGC CGTTTGATT TTAGACGGCA
651 TTTTGTTC AAGAGTTTGA TGTGGGATG GCAATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2870; ORF 934.a>:

```

a934.pep
1  MKKIIASALI ATFALAACQD DAQARLEQQQ KQIEALQQQL AQQADDTVYQ
51  LTPEAVKDTI PAEAQANGNN GQVPTX*RRR AVYLRPIDRK LAAAKPGRRG
101 GRRVYRQRAG KQIHTGRQPR QSRRPARACR LPSVRTSQCA HQQGFHAQAP
151 PCKTTGGAGA ALPPDNAPAR QLPPRHARF RQKAVNPACQ CRLKGFQTAF
201 LYLLGTLCC RLIFRRHFVS KSLMSGWQF*

```

m934/a934 94.1% identity in 205 aa overlap

```

          10      20      30
m934.pep  RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a934      MKKIIASALIATFALAACQDDAQARLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
          10      20      30      40      50      60

          40      50      60      70      80      90
m934.pep  PAEAQANGNNGQPVTCXRRRAVYLRPIDRKLAAPKPGRRGRRVYRQRAGKQIHTGRQPR
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a934      PAEAQANGNNGQPVTCXRRRAVYLRPIDRKLAAPKPGRRGRRVYRQRAGKQIHTGRQPR
          70      80      90      100     110     120

          100     110     120     130     140     150
m934.pep  QSRRPARACSLPSVRTPQCAHQQGFHAQPPCKTTGGAXAALPPDNAPXRQLPPPRYARF
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a934      QSRRPARACRLPSVRTSQCAHQQGFHAQPPCKTTGGAGAALPPDNAPARQLPPPRHARF
          130     140     150     160     170     180

          160     170     180     190     200
m934.pep  RQEAVNPARQCRLKSFQTAFXHLLGTLCCRLIFRRHFVSKRLMSGWQFX
          ||:||||| |||||:|||||:|||||:|||||:|||||:|||||
a934      RQKAVNPACQCRKLGFTAFYLLGTLCCRLIFRRHFVSKSLMSGWQFX
          190     200     210     220     230

```

g935.seq not found yet

1349

```

601 AATAGAAATG CCAATAATGC CGCGCCGCAG TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCGGGCGGCA GGCTTGAATT
701 ATGAAATCGA GCGGAAAAA CTGACGGCGT TGGCAGATAA TCATTATTTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTCA GTAAAAAATC
801 AGCTTATGAC GACGGGTTCG GCAGAGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCG
901 GGCAGCGACG GCTTTGATGC GAAAACAAA CGGGTAAACA ACCGCCGCCT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCACTTG TCCCATACTT
1001 ACCGCCCAAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG STCGGCAGGA
1101 CCGGTTTTAT GTTTCGTCGG CAAAACGTTT GGGCGAATCG SCAACTGTGT
1151 TCGGCGGCTG GCAGTTTGTG CGGTTTGTGC CGAAACGCGA AACCGTGGGC
1201 GGCAGCGTCA ATAATGCCGC CTACCGGCGC AACCGTGTTC ATGCCGGCTG
1251 GCGCGCAGAG TGGCGGCGAGT TGGCGGCTTT GAACAGTCGG STTTCCGCGT
1301 CTTATGCCCG CCGCAACTAT AAGGGCGTTG CGGCTTCTC SACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CCGCGTTGAA TTATCGTTTC GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT STTTGTGTGC
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2874; ORF 935.a>:

```

a935.pep
1 MLYFRYGFIV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51 KVDNDAPRVV DGDFLLAHPK MLEHSLRDVL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLPAAEFD
151 DFRKLSAERH FAEAEKLDLP APVLENVGRF RKAEGLTGW RESGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTALADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDATK RVNNRRLPPY MLAGVGVQQL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGGWQFV REVVPKRETVG
401 GAVNNAAYRR NGVYAGWAE WRQLGLNSR VSASYARNY KGVAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPPA KRRNSEVFVS
501 ADWRF*

```

m935/a935 98.8% identity in 505 aa overlap

	10	20	30	40	50	60
m935.pep	MLYFRYGFIVVWCAAGVSAAYGADAPAILDDKALLQVQRSVSDKWAESDWKVDNDAPRVV					
a935	MLYFRYGFIVVWCAAGVSAAYGADAPAILDDKALLQVQRSVSDKWAESDWKVDNDAPRVV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m935.pep	DGDFLLAHPKMLEHSLRDALNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
a935	DGDFLLAHPKMLEHSLRDVLNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m935.pep	AEAVARYRELHGENAADERILLDLAAAEFDDFRKLSAERHFAEAAKLDLPAPVLENVGRF					
a935	AEAVARYRELHGENAADERILLDLAAAEFDDFRKLSAERHFAEAEKLDLPAPVLENVGRF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m935.pep	RKKTEGLTGWRFSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNIEIEAEK					
a935	RKAEGLTGWRFSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNIEIEAEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m935.pep	LTPLADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
a935	LTALADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
	250	260	270	280	290	300

g935.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2871>:

m935.seq

```

1  ATGTTGTATT TCAGATACGG CTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTCAGGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCAGATTGG
151 AAAGTTGAAA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTGTTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGGC CGACGCGCTC AACGGCAATC
251 AGGCGGATTT AATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGGAAAGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAAC TG CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCGGAGG CGGCAAAATT
501 GGATTTGCCG GCACCGGTTT TGGAAAATGT GGGGCGTTT CGGAAAAAAT
551 CCGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC
601 AATAGAAATG CCAATAATGC CGCGCCGCAA TATGCCC GC AAAACGGAGG
651 CCGGCAGATA TGCACTGTCA GCCGGGCGGA GCGGGCGCA GGTTTGAATT
701 ATGAAATCGA GCGGAAAAAG CTGACGCCGT TGGCAGATAA TCATTATTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTC GTAAAAAATC
801 AGCTTATGAT GACGGGTTCC GCAGGGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTGCCGT TTTATCAGGT GCAGTTGTGC
901 GGCAGCGACG GCTTTGATGC GAAAAAATAA CCGGTAAACA ACCGCCGCTT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGACGCTG TCCCATACTT
1001 ACCGCCAAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GCAGGCAGGA
1101 CCGGTTTTAT GTTTCGTCGG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTTGTG CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GGCGCGGTCA ATAATGCCGC CTACCGGCGC AACGGTGTT ATGCCGTTG
1251 GGCGCAGGAG TGGCGGCAGT TGGCGGTTT GAACAGTCGG GTTTCGCGT
1301 CTTATGCCCG CCGCAACTAT AAGGGCATG CGGCTTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CGGCGTTGAA TTATCGTTT GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTCTG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2872; ORF 935>:

m935.pep

```

1  MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVORS VSDKWAESDW
51  KVENDAPRVV DGDFLLAHPK MLEHSLRDAL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEFD
151 DFRKLSAERH FAEAAKLDP APVLENVGRF RKKTEGLTGW RFSGGISPAV
201 NNRNANNAPO YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTPLADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDAKTK RVNRRRLPPY MLAGVGVQL SHYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFQGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVIAGWAE WRQLGGLNSR VSASYARRNY KGIAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPIA KRNSEVFVS
501 ADWRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2873>:

a935.seq

```

1  ATGTTGTATT TCAGATACGG TTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTCAGGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCGGATTGG
151 AAAGTTGACA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTGTTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGGC CGACGTGCTC AACGGCAATC
251 AGGCGGATTT GATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGGAAAGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAAC TG CACGGGGAAA
401 ATGCGGCAGA CGACCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCCGAGG CGGAAAAAAT
501 GGATTTGCCG GCGCGGTTT TGGAAAATGT GGGGCGTTT CGGAAAAAAG
551 CCGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC

```

1350

	310	320	330	340	350	360
m935.pep	GSDGFDATKRVNNRRLPPYNLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
a935	GSDGFDATKRVNNRRLPPYNLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
	310	320	330	340	350	360
	370	380	390	400	410	420
m935.pep	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAQE					
a935	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAQE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m935.pep	WRQLGGLNSRVSSASYARRNYKGIAAFSTEAQRNREWNVSLALSHDKLSYKGIVPALNYRF					
a935	WRQLGGLNSRVSSASYARRNYKGIAAFSTEAQRNREWNVSLALSHDKLSYKGIVPALNYRF					
	430	440	450	460	470	480
	490	500				
m935.pep	GRTESNVPIAKRRNSEVFVSADWRF					
a935	GRTESNVPIAKRRNSEVFVSADWRF					
	490	500				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2875>:

g936.seq

```

1  ATGAAACCCA  AACCACACAC  CGTCCGCACC  CTGATTGCCG  CCGTCCTCAG
51  CCTTGCCCTC  GCGGGCTGCT  TCAGCGCAGT  CGTCGGCGGG  GCCGCCGTCG
101 GCGCAAAATC  CGTCATCGAC  CGcggAACCA  CCGgcgcgca  AACCGATGac
151 aACGTTATGG  CGTTGCGTAT  CGAAACCACC  GCCCGTTCCT  ACCTGCGCCA
201 AAACAACCAA  ACCAAAGGCT  ACACGCCCCA  AATCTCCGTC  GTCGGCTACA
251 ACCGCCACCT  GCTGCTGCTC  GGACAAGTCG  CCACCGAAGG  CGAAAAACAG
301 TTCGTCGGTC  AGATTGCACG  TTCCGAACAG  GCCGCCGAAG  GCGTATACAA
351 CTACATTACC  GTCGCCTCCC  TGCCGCGCAC  TGCGGGCGAC  ATCGCCGGCG
401 ACACCTGGAA  CACGTCCAAA  GTCCGCGCca  cgCTGCTGGG  CATCAGCCCC
451 GCTACACAGG  CGCGCGTCAA  AATCATTACC  TACGGCAATG  TAACCTACGT
501 TATGGGCATC  CTCACCCCGG  AAGAACAGGC  GCAGATTACC  CAAAAAGTCA
551 GCACCACcgT  CGGCGTACAA  AAAGTCATTA  CCCTTACCA  AACTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2876; ORF 936.ng>:

g936.pep

```

1  MKPKPHTVRT  LIAAVLSLAL  GGCFSAVVGG  AAVGAKSVID  RRTTGAQTDD
51  NVMALRIETT  ARSYLRQNNQ  TKGYTPQISV  VGYNRHLLLL  GOVATEGEKQ
101 FVGQIARSEQ  AAEGVYNYIT  VASLPRTAGD  IAGDTWNTSK  VRATLLGISP
151 ATQARVKIIT  YGNVTYVMI  LTPEEQAQIT  QKVSTTVGVQ  KVITLYQNYV
201  QR*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2877>:

m936.seq (partial)

```

1  ATGAAACCCA  AACCGCACAC  CGTCCGCACC  CTGATTGCCG  CCATTTCAG
51  CCTTGCCCTT  AGCGGCTGCG  TCAGCGCAGT  AATCGGAAGC  GCCGCCGTCG
101 GCGCGAAATC  CGCCGTCGAC  CGCCGAACCA  CCGCGCGCA  AACCGACGAC
151 AACGTTATGG  CGTTGCGTAT  CGAAACCACC  GCCCGTTCCT  ATCTGCGCCA
201 AAACAACCAA  ACCAAAGGCT  ACACGCCCCA  AATCTCCGTC  GTCGGCTACA
251 ACCGCCACCT  GCTGCTGCTC  GGACAAGTCG  CCACCGAAGG  CGAAAAACAG
301 TTCGTCGGTC  AGATTGCACG  TTCCGAACAG  GCCGCCGAAG  GCGTGTACAA
351 CTATATTACC  GTCGCCTCCC  TGCCGCGCAC  TGCC...

```

This corresponds to the amino acid sequence <SEQ ID 2878; ORF 936>:

m936.pep (partial)

```

1  MKPKPHTVRT  LIAAIFSLAL  SGCVSIVIGS  AAVGAKSAVD  RRTTGAQTDD
51  NVMALRIETT  ARSYLRQNNQ  TKGYTPQISV  VGYNRHLLLL  GOVATEGEKQ
101 FVGQIARSEQ  AAEGVYNYIT  VASLPRTA...

```

ORF 936 shows 93.8% identity over a 128 aa overlap with a predicted ORF (ORF 936.ng) from *N. gonorrhoeae*:

m936/q936

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAksAVDRRTTGAQTDDNVMA ^{LRIETT}					
	: : : :					
g936	MKPKPHTVRTLIAAVLSLALGGCFS ^{AVVGGA} AVGAKSVIDRRTTGAQTDDNVMA ^{LRIETT}					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYLRONNOTKGYPQISVVGYNRHLLILGQVATEGEKQFVGQIARSEQAAEGVNYIT					
g936	ARSYLRONNOTKGYPQISVVGYNRHLLILGQVATEGEKQFVGQIARSEQAAEGVNYIT					
	70	80	90	100	110	120
	130					
m936.pep	VASLPRTAXXX					
g936	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAOIT					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2879>:

a936.seq

1	ATGAAACCCA	AACCGCACAC	CGTCCGCACC	CTGACTGCCG	CGGTCTCTAG
51	CCTTGCCCTC	GGCGGCTGCG	TCAGCGCAGT	CGTCGGCGGC	GCGGCGGCTCG
101	CGCGCAAAATC	CGCCGCTCGAC	CGAGCGCAACCA	CGCGCGCGCA	AACCGACGAC
151	AACGTAATGG	CGCTGCGTAT	CGAAACCACC	GCCCCTCTCT	ATCTGCGCCA
201	AAACAACCAA	ACCAAAGGCT	ACACGCGCCA	AATCTCCGTT	GTCGGCTACA
251	ACCGCGACCT	GCTGCTGCTC	GGACAAGTCG	CAACCGAAGG	CGAGAACACG
301	TTCGTCGGTC	AGATTGCACG	TTCGGAACAG	GCCGCGGAAG	CGGTGTACAA
351	CTACATTACC	GTCGCCTCC	TGCCGCGCAC	TGCGCGGAC	ATCGCCGGCG
401	ACACTTGGAA	CACATCCAA	GTCGCGGCCA	CGCTGTTGGG	CATCAGCCCC
451	CGCACACAGG	CGCGCGTCAA	ATTCGTTACC	TACGGCAAC	TAACTACGTC
501	TATGGGCATC	CTCACCCCG	AAGAACAGGC	GCAGATTACC	CAAAAAGTCA
551	GCAACACCGT	CGGCGTACAA	AAAGTCATCA	CCCTCTAGCA	AAACTACGTC
601	CAACGCTGA				

This corresponds to the amino acid sequence <SEQ ID 2880; ORF 936.a>:

a936.pep

1	MKPKPHTVRT	LTAAVLSLAL	GGCVSAVVGG	AAVGAKSVD	RRTTGAQTD
51	NVMALRIETT	ARSYLRQNNQ	TKGYTPQISV	VGYNRHLLLL	GQVATEGEKQ
101	FVGQIARSEQ	AAEGVYNYIT	VASLPRTAGD	IAGDTWNTSK	VRATLLGISP
151	ATQARVKIVT	YGNVTYVMGI	LTPEEQAQIT	QKVSTTVGVQ	KVITLYQNYV
201	OR*				

m936/a936 95.3% identity in 128 aa overlap

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAVGA	SAVDRRTTGAQTDDNV	MALRIETT			
a936	MKPKPHTVRTLTAAVLSLALGGCVSAVVGGA	AVGA	SAVDRRTTGAQTDDNV	MALRIETT		
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYLQN	QNTKGYT	POISVVGYNRH	LLLLQVATEGEKQ	FVGGIARSEQAAEGV	NYN
a936	ARSYLQN	QNTKGYT	POISVVGYNRH	LLLLQVATEGEKQ	FVGGIARSEQAAEGV	NYN
	70	80	90	100	110	120
m936.pep	VASL	PRTA				

1352

```

          |||||
a936      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
          130      140      150      160      170      180

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2881>:

g936-1.seq

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51 CCTTSCCCTC GGCGGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGccgAACCA CCGgcgcgca AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCCTCC TGCCGCGCAC TCGGGCGGAC ATCGCCGGCG
401 AACTTGGAA CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACcgT CGGCGTACAA AAAGTCATTA CCCTCTACCA AAACCTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2882; ORF 936-1.ng>:

g936-1.pep

```

1  MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVTILYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2883>:

m936-1.seq

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51 CCTTGCCTTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGGAAATC CGCGCTCGAC CGCCGAACCA CCGCGCGCA AACCGACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGGTACAA
351 CTATATTACC GTCGCCCTCC TGCCGCGCAC TCGGGCGGAC ATCGCCGGCG
401 AACTTGGAA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACCGT CGGCGTACAA AAAGTCATCA CCCTCTACCA AAACCTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2884; ORF 936-1>:

m936-1.pep

```

1  MKPKPHTVRT LIAAIFSLAL SGCVSAVIGS AAVGAKSAVD RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIV YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVTILYQNYV
201 QR*

```

m936-1/g936-1 95.5% identity in 202 aa overlap

```

          10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAASVDRRTTGAQTDDNVMAIRIETT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g936-1      MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGAASVDRRTTGAQTDDNVMAIRIETT
          10      20      30      40      50      60

          70      80      90      100     110     120
m936-1.pep  ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g936-1      ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT
          70      80      90      100     110     120

          130     140     150     160     170     180
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

1353

```

g936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAOIT
              130      140      150      160      170      180

              190      200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
g936-1      QKVSTTVGVQKVITLYQNYVQRX
              190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2885>:

```

a936-1.seq
1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGACTGCCG CCGTCCTCAG
51 CCTTGCCCTC GCGGCTGCG TCAGCGCAGT CGTCGGCGGC GCGGCGGTCTG
101 GCGCGAAATC CGCGCTCGAC CGCGGAACCA CCGGCGCGCA AACCGACGAC
151 AACCTAATGG CGCTGCGTAT CGAAACCACC GCCCGCTCCT ATCTGCGCCA
201 AAACAACCAA ACCAARAGCT ACACGCCCCA AATCTCCGTT GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAGAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCAAG GCGTGTACAA
351 CTACATTACC GTCGCCCTCC TGCCGCGCAC TGCCGCGCAC ATCGCCGGCG
401 ACACCTTGGA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACCGT CGGCGTACAA AAAGTCATCA CCTCTACCA AACTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2886; ORF 936-1.a>:

```

a936-1.pep
1  MKPKPHTVRT LTAAVLSLAL GGCVS AVVGG AAVGAKSAVD RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIVT YGNVTYVMGI LTPPEEQAOIT QKVSTTVGVQ KVTITLYQNYV
201 QR*

```

a936-1/m936-1 97.0% identity in 202 aa overlap

```

              10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAASAVDRRTTGAQTDDNVMLRIETT
              |||||
a936-1      MKPKPHTVRTLTAAVLSLALGGCVSAVVGGAASAVDRRTTGAQTDDNVMLRIETT
              10      20      30      40      50      60

              70      80      90      100     110     120
m936-1.pep  ARSYLRQNNQTKGYTPQISVVGYNRHLLLGGQVATEGEKQFVGQIARSEQAAEGVYNYIT
              |||||
a936-1      ARSYLRQNNQTKGYTPQISVVGYNRHLLLGGQVATEGEKQFVGQIARSEQAAEGVYNYIT
              70      80      90      100     110     120

              130     140     150     160     170     180
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAOIT
              |||||
a936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAOIT
              130     140     150     160     170     180

              190     200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
a936-1      QKVSTTVGVQKVITLYQNYVQRX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2887>:

```

g937.seq
1  atGAAAAATA TTCTCTTAgT ATTTGTTAGC TTTGTGCCAT TATGTGTCCG
51 CACTGATCTG CCGCTGAaTa tCGAAGACAT AATGaccgAC AAGGGAAAAT
101 GGAAaactGGA AACTTccctt acctacctgA acaGCGAAAA cagCCGCGCC
151 GCACTTGCCT CACCGGTTTA CATTcAGACC GGCTCCGCTT CCTTTATCCC
201 CGTCCCGACC GAAATTCAGG AAAACGGCAG CAATACCGAT ATGCTCGCCG
251 GCACGCTCGG TTTGCGCTAC GGACTGAcCg GCAataccgA CATTTACGGC
301 AGCGGCAGCT ATCTGTGGCA CGAAGAACGC AAACTCGacg GCAACGGCAA

```

g937.pep

1	MKNILLVFFVS	FVPLCVRTL	PLNIEDIMTD	KGKWKLETSL	TYLNSNSRA
51	<u>ALAS</u> PVYIQT	GSASIPVPT	EIQENGSTDI	MLAGTLGLRY	GLTGNTDIYG
101	SGSYLWHEER	KLDGNGKTRN	KRMSDISAGI	SHTFLKDGKN	PALIAFLEST
151	VYEKSRNKAS	SGKSWLIGAT	TYKADIPVL	SLTAAAYRNG	SKTLSDDVKY
201	KAGNYWMLNP	NISFAANDRI	SLTGDIQWLG	KQPRIDGKK	ESARNTSTYA
251	HFGAGFGFTK	TAALNASARF	NVSGQSSSEL	KLGVQHTF*	

m937.seq

1	ATGAAGCGCA	TCTTTTGGCC	CGCTTGCCC	GCCATCTGCG	CTTTATCCAC
51	TTATGCCGAC	CTGCCCTTGA	CGATTGAAGA	CATAATGACC	GACAAGGGAA
101	AATGGAAACT	GGAAACTTCC	CTTACCTTAC	TGAACAGCGA	AAACAACCGC
151	GCGCAACTTG	CGGACCCTGG	TTACATTCAA	ACCGCGCGAA	CCTCGTTTAT
201	CCCCATTCCG	ACCGAAATCC	AaGAAAaCGG	CAGCAATACC	GATATGCTCG
251	TCGGCAGCCT	CGGTTTGCCT	TACGGACTGA	CCGGGAATAC	CGACATTTAC
301	GGCAGCCGCA	GCTATCTGTG	GCACAGAGTA	CGCAAATCTG	ACGGCAACAG
351	CAAAACCGGC	ACAAACCGGA	TGTCCGAGCT	ATCCCTCGGC	ATCAGCCACA
401	CTTTCCTTAA	AGACGACAAA	AACCCGCGCC	TATACAGCTT	CTTTGAAGC
451	ACGGTTTACG	AAAAATCGCG	CAACAAAGCC	TCGTGCGGAA	AATCCTGGCT
501	CATCGGC3CC	CCGACTTACA	AAGCCATAGA	TCCGATTGTC	CTTTCCCTCA
551	CGCCCGCCTA	CCGACTCAAC	GGCAGCAAAA	CCCTTTTCAG	CGGCATCCGC
601	TACAAATCGG	GCAACTACCT	GCTGCTCAAC	CCCAACTCT	CATTTGCTCG
651	CAACGACAGA	ATCAGCCTGA	CCGGAGGCAT	CCAATGGCTG	GCGAGGCAGC
701	CCGACCGGAC	GGACGGCAAA	CGGAATCCTT	CCAGAAACAC	ATCCACCTAC
751	GCCCATTTTC	GCGCAGGTTT	CGGTTTCACC	AAACCACCGG	CTTTAAACGC
801	ATCGGCACGT	TTCAAGCTTT	CAGGGCAAAG	CAGTTCGGAA	CTGAAATTGG
851	GCGTACAGCA	TACATTTTAA			

m937.pcp..

1	<u>MKRIFLPALP</u>	<u>AILPLSTYAD</u>	<u>LPLTIEDIMT</u>	<u>DKGKWKLETS</u>	<u>LTLYLSENNR</u>
51	<u>AELAAPVYIQ</u>	TGATSFIP	TEIQENG	DMLVGTGLR	YGLTGNTDIY
101	GSYSYLWHEE	RKLDGNSKTR	NKRMSDVSLG	ISHTFLKDDK	NPALISFLES
151	TVYEKSRNKA	SSGKSWLIGA	TTYKAIDPIV	LSLTAAYRIN	GSKTLSDGIR
201	YKSGNYLLLN	PNISFAANDR	ILSTGGIQWL	GRQPDRTDGK	RESSRNTSTY
251	AHFGAGGFGT	KTTALNASAR	FNVSGQSSSE	LKFGVOHTF*	

Homology with a predicted ORF from *N.gonorrhoeae*

q937/m937

	10	20	30	40	50	59
g937.pep	MKNILL-VFVSFVPLCVRTLPLNIEDIMTDKGKWKLETSLTYLNSENSRAALASPVYIQ					
	: :: :: :	:	:			: :
m937	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
	10	20	30	40	50	60
	60	70	80	90	100	119
g937.pep	TGSASFIPVPTEIQENGSNNTDMLAGLTGLRYGLTGNTDIYGSGSYLWHEERKLDGNGKKT					

[illegible]

```

a937.seq
1  ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51  TTATGCCGCA CTGCCCTTGA CGATTGAAGA CATATATACC GACAAGGGCA
101 AATGGAAACT GGAAACTTCC CTTACTTACC TGAACAGCGA AAACAACGCA
151 GCCGAACCTG CCGCACCGGT TTACATCCAA ACCGCGCGAA CCTCGTTTAT
201 CCCCATTTCC ACCGAAATCC AAGAAACCGG CAGCAATACC GATATGCTCG
251 TTGGCACGCT CGGTTTGGCC TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCACGGCGA GCTATCTGTG GCACGAAGAA CGGAAACTCG ACGGCAACGG
351 CAAAACCCGA AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCAGA
401 CCTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAGGCC TCGTCGGGAA ARTCCTGGCT
501 CATCGCGGCC ACCACTTACA AAGCATCGA CCCCCTCTCT CTCTATTGA
551 CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCTTTTCAAG CAACACCAAA
601 TACAAGCAG CCAATTTACTG GATGCTGAAT CCCAATATAT CCTTCGCGCG
651 CAACGACAGA ATCAGCTTCA CGGGCGGCAT CCAATGGCTG GGCAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTCC GCGCAGGTTT CGGTTTCACC AAAACCACSG CTTTAAACGC
801 ATCCGCGACG TTCACGTTT CAGGGCAAAG CAGTTCGGAA CTGAAATTTG
851 CGGTACAGCA TACGTTTAA

```

```
a937.ppep
1 MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSNNR
51 AELAAPVYIQ TGATSFIPIP TEIQENGST DMLVGLTGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDVSLG ISHTFLKDDK NALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKADDPVV LSLTAAYRIN GSKTSSNTK
201 YKAGNYWMLN PNISFAANDR ISLTGGIQWL GKQPDRLDGK KESARNSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSE LKFGVOHTF*
```

	10	20	30	40	50	60
m937.pep	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNAELAAPVYIQ					
a937	:	:	:	:	:	:
	10	20	30	40	50	60
	MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNAELAAPVYIQ					
	70	80	90	100	110	120
m937.pep	TGATSFIPITPEIQENGSNTDMLVGTLGLRYGLTGNTDIYGSGSYLWHEERKLDSNGSKTR					
a937	:	:	:	:	:	:
	TGATSFIPITPEIQENGSNTDMLVGTLGLRYGLTGNTDIYGSGSYLWHEERKLDSNGSKTR					
	70	80	90	100	110	120

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	130	140	150	160	170	190
m937.pep	NKRMSDVS LGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a937	NKRMSDVS LGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m937.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a937	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m937.pep	RESSRNTSTYAHFGAGFGFTKTTALNASARFNVSGSSSELKFGVQHTFX					
a937	KESARNTSTYAHFGAGFGFTKTTALNASARFNVSGSSSELKFGVQHTFX					
	250	260	270	280	290	

g939.seq not found yet

g939.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2893>:

m939.seq (partial)

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCATCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAATATCGG
201 CATCCGCGAC GTAAACGCAC CC...
```

This corresponds to the amino acid sequence <SEQ ID 2894; ORF 939>:

m939.pep (partial)

```

1  MKRLTLLAFV LAAGAVSASP KADVEKGQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD VNAP...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2895>:

a939.seq

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCATCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAATATCGG
201 CATCCGCGAC GGTAAACGCA CCCACGGTTC GGCAGCTGTG ATGAAACCGG
251 TGGTAATGAA TTTGAGCGAT CAGGATATTT TGAACGTATC CGCATTCTAT
301 GCCAAACAGC AGCCCAAATC CGGTGAAGCC AATCCTAAGG AAAATCCCGA
351 ATTGGGTGCG AAAATCTATC GCGGCGGTTT GAGCGATAAA AAAGTGCCGG
401 CGTGATATGC CTGCCACGGT CCGAGCGGTG CCGGTATGCC GGGGGCGGGA
451 AGCGAAATTC AGGCTTATCC GCGTTTGGGC GGTGAGCATC AGGCATATAT
501 TGTGTAACAG ATGAATGCCT ACAAGTCCGG TCAGCGTAAA AATACCATCA
551 TGGGAAGATAT TGCAAACCGT ATGTCTGAAG AAGATTTGAA AGCGGTCGCC
601 AACTTTATCC AAGTTTGGC TTAA
```

This corresponds to the amino acid sequence <SEQ ID 2896; ORF 939.a>:

a939.pep

```

1  MKRLTLLAFV LAAGAVSASP KADVEKGQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD GKRTHGSAV MKPVVMNLSQ QDILNVSAFY
101 AKQPKSGEA NPKENPELGA KIYRGGLSDK KVPACMSCHG PSAGMPGGG
151 SEIQAYPRLG GQHQAIVIEQ MNAYKSGQRK NTIMEDIANR MSEDCLKAVA
201 NFIQGLR*
```

m939/a939 100.0% identity in 70 aa overlap

	10	20	30	40	50	60
m939.pep	MKRLTLLAFVLAAGAVSASP KADVEKGQVAATVCAACHAADGNSGIAMYPRLAAQHTAY					
a939	MKRLTLLAFVLAAGAVSASP KADVEKGQVAATVCAACHAADGNSGIAMYPRLAAQHTAY					

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		10	20	30	40	50	60
	70						
m939.pep	IYHQTIGIRDVNAP						
a939	IYHQTIGIRDGKRTHGSAAVMKPVVMNLSDDQDILNVSAFYAKQPKSGEANPKENPELGA						
		70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2897>:

```
g950.seq
1  ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
51  GGCCGCCGCG GCCGTTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
101 TTTAAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
201 TAAAGCAGGC GAAAGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
251 AAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
301 GAAAGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2898; ORF 950.ng>:

```
g950.pep
1  MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVOKSAQG SCGASKSAEG
51  SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA
101 EGKCGEGKCG SK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2899>:

```
m950.seq
1  ATGAACAAAA ACATTGCTGC CSCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51  GGCCGCCGCG GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTTAAAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGCTTC TAAAGCAGGC GAAAGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2900; ORF 950>:

```
m950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 950 shows 86.6% identity over a 112 aa overlap with a predicted ORF (ORF 950) from *N. gonorrhoeae*

m950/g950 86.6% identity in 112 aa overlap

	10	20	30	40	50
m950.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----				
g950	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVOKSAQSGASKSAEGSCGASKSAEG				
	10	20	30	40	50
					60
	60	70	80	90	100
m950.pep	-----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK				
g950	SCGAAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX				
	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2901>:

```
a950.seq
1  ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51  GGCCGCCGCG GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTTAAAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGCTTC TAAAGCAGGC GAAAGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA
```



```

51 EIKNERARLA AVGERVNRVF TLLGGETALQ KGQAGTALAT YNMLMLERTKS
101 PEVAERALEM AVSLNAFEQA EMYQKWRQI EPIPGEAQKR AGWLRNVLRE
151 GGNCHLDGLE EVLAQSDDVQ KRRI FLLLVQ AAVQGGVAVQ KASKAVRRRA
201 LKYEHLPEAA VADAVFGVQG REKEKAIEAL QRLAKLDTEI LPPTLMTLRL
251 TARKYPEILD GFFEQDTQON LSAVWQEMEI MNLVSLRKP DAYARLNVLI
301 EHNPNANLYI QAAILAANRK EGASVIDGYA EKAYGRGTGF QRGRAAMTAA
351 MIYADRRDYA KVRQWLKVS APEYLFDKGV LAAAAAELD GGRAALROIG
401 RVRKLPEQQG RYFTADNLSK IOMLALSCLP DKREALIGLN NIIAKLSAAG
451 STEPLAEALA QRSIIYEQFG KRGKMIADLE TALKLTPDNA QIMNNLGYSL
501 LSDSKRLDEG FALLQYAYQI NPDDTAVNDS IGWAYYLGKD AESALPYLRY
551 SFENDPEPEV AAHLGEVLWA LGERDQAVDV WTQAAHLRGD KKIWRETLKR
601 YGIALPEPSR KPRK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2905>:

```

m951.seq
1 ATGATTATGT TACCTAACCG TTTCAAAATG ITAACTGTGT TGACGGCAAC
51 CTTGATTGCC GGACAGGTAT CTGCCGCGG AGCGGGTGGC GGGGATATGA
101 AACAGCCGAA GGAAGTCGGA AAGGTTTCA GAAAGCAGCA GCGTTACAGC
151 GAGGAAGAAA TCAAAAACGA ACGCGCACGG CTTCGCGCAG TGGCGCAGCG
201 GGTTAATCAG ATATTACGT TGCTGGGAGG GGAACCGGCC TTGCAAAAGG
251 GGCAGGCGGG AACGGCTCTG GCAACCTATA TGCTGATGTT GGAACGCACA
301 AAATCCCCCG AAGTCGCGGA ACGCGCCTTG GAAATGGCGG TGTGCTGAA
351 CGCGTTTAAA CAGGCGGAAA TGATTATCA GAAATGGCGG CAGATTGAGC
401 CTATACCGGG TAAGGCGCAA AAACGGGCGG GGTGGCTGCG GAACGTGCTG
451 AGGGAAGACG GAAATCAGCA TCTGGACGGA CTGGAAGAAG TGCTGCTCA
501 GCGGACGAAA GGACAGAAC GCAGGCTGTT TTTATTGTTG GCACAAGCCG
551 CCGTGCAACA GGACGGGTTG GCGCAAAAG CATCGAAAGC GGTTCGCCGC
601 GCGCGCTTGA AATATGAACA TCTGCCGAAA GCGCGGTTG CCGATGTGGT
651 GTTCAGCGTA CAGGACGCG AAAAGGAAAA GGAATCGGA GCTTTGCAGC
701 CTTTGGCGAA GCTCGATACG GAAATATTGC CCCCCACTTT AATGACGTTG
751 CGTCTGACTG CACGCAATA TCCGAAATA CTGACGGCT TTTTCGAGCA
801 GACAGACACC CAAACCTTT CGGCCGCTG GCAGGAAATG GAAATTATGA
851 ATCTGGTTTC CCGCACAGG CTGGATGATG CCTATGCGCG TTTGAACGTG
901 CTGTGGAAAC GCAATCCGAA TGACAGCTG TATATTGAG CAGCGATATT
951 GCGGCAAAAC CGAAAAGAG GTGCTTCCGT TATCGACGGC TAGCCGAAA
1001 AGGCATACGG CAGGGGACG GAGGAACAGC GGAGCAGGGC GGCCTAACG
1051 GCGCGATGA TGTATGCCGA CCGCAGGAT TACGCCAAG TCAGGCAGTG
1101 GCTGAAAAAA GTATCCGCGC CGGAATACCT GTTCGACAAA GGTGTGCTGG
1151 CCGTGGCGGC GGCTGTCGAG TTGGACGGCG GCAGGGCGCG TTTGGCGCAG
1201 ATCGGCAGGG TGCGAAACT TCCGAACAG CAGGGCGGT ATTTACGGC
1251 AGACAATTTG TCCAAAATAC AGATGCTCGC CCTGTCGAG CTGCCGATA
1301 AATCGGAGGC TTTGAGGGG TTGGACAAGA TTATCGAAAA ACCGCTGCC
1351 GGCAGTAATA CAGAGTTACA GGCAGAGGCA TTGGTACAGC GGTGAGTTGT
1401 TTACGATCGG CTTCGCAAGC GGAATAAAT GATTTCAGAT CTGAAAGGG
1451 CGTTCAGGCT TGCACCGGAT AACGCTCAGA TTATGAATAA TCTGGGCTAC
1501 AGCCTGCTGA CCGATTCCAA ACGTTTGGAC GAAGTTTTCG CCCTGCTTCA
1551 GACGGCATAC CAATCAACC CGGACGATAC CGCTGTCAAC GACAGCATAG
1601 GCTGGGCGTA TTACCTGAAA GCGGACGCGG AAAGCGGCT CCGTATCTG
1651 CCGTATTCTG TTGAAAACGA CCGGAGCCG GAAGTTGCCG CCCATTGCGG
1701 CGAAGTGTG TGGGCATTGG GCGAACGCGA TCAGGCGGTT GACGTATGGA
1751 GCGAGGCGGC ACACCTTACG GGAGACAAGA AATATGGCG GGAACGCTC
1801 AAACGTCACG GCATCGCATT GCCCAACCT TCCGAAAC CTGGAATA
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 2906; ORF 791>:

```

m951.pep
1 MIMLPNRFKM LTVLTATLIA GOVSAAGGGA GDMKQKEVG KVERKQORYS
51 EEEIKNERAR LAAVGERVNO IFTLLGGETA LQKQAGTAL ATYMLMLERT
101 KSEVAERAL EMAVSLNAFE OAEMIYOKWR QIEPIPKAQ KRAGWLRNVL
151 RERNQHLDG LEEVLAQADE GQNRVFLLL AQAAVQDGL AQKASKAVRR
201 AALKYELPE AAVADVFSV QGREKEKAI ALQRLAKLDT EILPPTLMTL
251 RLARKYPEI LDGFFEQTD QNLSAVWQEM EIMNLVSLHR LDDAYARLNV
301 LLERNPNADL YIQAAAILAN RKEGASVIDG YAEKAYGRGT EEQSRRAALT
351 AAMMYADRRD YAKVRQWLKK VSAPEYLFDK GVLAATAAVE LDGGRALRQ
401 IGRVRKLPEQ QGRYFTADNL SKIQMLALS LKPKREALRG LDKIIEKPPA
451 GSNTLQAEA LVQSRVVYDR LGKRKKMISD LERAFRLAPD NAQIMNNLGY
501 SLLTCSKRLD EGFALLQYAY QINPDDTAVN DSIWAYYLLK GDAESALPYL
551 RYSFENDPEP EVAHLGEVL WALGEREQAV DVWTQAAHLT GDKKIWRETL
601 KRHGIALPQP SRKPRK*

```

Computer analysis of this amino acid sequence gave the following results:

ORF 951 shows 88.6% identity over a 616 aa overlap with a predicted ORF (ORF 951) from *N. gonorrhoeae*

m951/g951 88.6% identity in 616 aa overlap

	10	20	30	40	50	60
m951.pep	MIMLPNRFKMLTLVLTATLTIAGQVSAAGGGAGDMKQPKFVGKVFRRKQQRYSSEEEIKNERAR					
g951	MIIMLPARFTILSVLAAALLAGQAYAA--GAADVLPKEVGKVLRRKHRRYSSEEEIKNERAR					
	10	20	30	40	50	
m951.pep	70	80	90	100	110	120
g951	LAAGVERVNOIETLLGGETALQKGQAGTALATYMLMLERTKSPVEAERALEMAVSLNAFE					
	60	70	80	90	100	110
m951.pep	130	140	150	160	170	180
g951	QAEMIQYKWRQIEPIPGKAQKRAGWLNRNVLREGRNQHLDGLEEVLAQADEGQNNRVFLL					
	120	130	140	150	160	170
m951.pep	190	200	210	220	230	240
g951	AOAAVQDGLAOKASKAVRRAALKYEHLPAAAVADVVSQVGREKEKAIGALQRLAKLDT					
	180	190	200	210	220	230
m951.pep	250	260	270	280	290	300
g951	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV					
	240	250	260	270	280	290
m951.pep	310	320	330	340	350	360
g951	LLERNPNADLYIQAAAILAANRKEGASVIDGYAEKAYGRGTQEQRRAALTAAAMYADRRD					
	300	310	320	330	340	350
m951.pep	370	380	390	400	410	420
g951	YAKVRQWLKKVSAPLEYLFDKGVLA AAAA AVELDGGRAALRQIGRVRKLP EQQGRYFTADNL					
	360	370	380	390	400	410
m951.pep	430	440	450	460	470	480
g951	SKIQMLALSKLPDKREALRGLDKIIEKPPAGSNTLEQAEALVQRSVVDRLGKRKKMISD					
	420	430	440	450	460	470
m951.pep	490	500	510	520	530	540
g951	LERAFRLAPDNAQIMNNLGYSLLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYLYLK					
	480	490	500	510	520	530
m951.pep	550	560	570	580	590	600
g951	GDAESALPYLRYSFENDFEPEVA AHLGEVLWALGERDQAVDVWTOAAHLRGDKKIWRETL					
	540	550	560	570	580	590
m951.pep	610					
g951	KRHGIALQPSRKPRK					
	600	610				
	KRYGIALPEPSRKPRKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2907>:

```
a951.seq
1  ATGTTACCCG CCCGTTTCAC CATTTTATCT GTGCTCGCGG CAGCCCTGCT
51  TGCCGGGCAG GCGTATGCCG CCGGCGCGGC GGATGCGAAG CCGCCGAAGG
101 AAGTCGGAAG GGTTCACAGA AAGCAGCAGC GTTACAGCGA GGAAGAAATC
151 AAAAACGAAC CGCACGCGCT TCGGCGAGTG GCGGAGCGGG TTAATCAGAT
201 ATTTACGTTG CTGGGAGGGG AAACCGCCTT GCAAAAGGGG CAGGCGGGAA
251 CGGCTCTGGC AACCTATATG CTGATCTTGG AACGCACAAA ATCCCCCGAA
301 GTCGCCGAAC GCGCCTTGGA AATGGCCGTG TCGCTGAACG CGTTTGAACA
351 GCGCGAAATG ATTTATCAGA AATGGCGGCA GATTGAGCCT ATACCGGGTA
401 AGGCGCAAAA ACGGGCGGGG TGGCTGCGGA ACGTGTCTAG GGAAGAGGA
451 AATCAGCATC TAGACGGACT GGAAGAAGTG CTGGCTCAGG CGGACGAAGG
501 ACAGAACCGG AGGGTGTITT TATTGTTGGC ACAAGCCGCC GTGCAACAGG
551 ACGGGTTGGC GCAAAAAGCA TCGAAAGCGG TTCGCCGCGC GGCGTTGAGA
601 TATGAACATC TGCCCCGAAG GCGCGTTGCC GATGTGGTGT TCAGCGTACA
651 GGGACGCGAA AAGGAAAAGG CAATCGGAGC TTTGCAGCGT TTGGCGAAGC
701 TCGATACGGA AATATTGCCC CCCACTTTAA TGACGTTGCG TCTGACTGCA
751 CGCAAAATAT CCGAAATACT CGACGCTTTT TTCGAGCAGA CAGACACCCA
801 AAACCTTTCC GCCGCTCTGC AGGAAATGGA AATTATGAAT CTGGTTTCCC
851 TGCACAGGCT GGATGATGCC TATGCGCGTT TGAACGTGCT GTTGGAACGC
901 AATCCGAATG CAGACCTGTA TATTAGGCA GCGATATTGG CGGCAAAACG
951 AAAAGAAGGT GCTTCCGTTA TCGACGCTA CGCCGAAAAG GCATACGGCA
1001 GGGGACGGG GGAACAGCGG GGCAGGCGCG CAATGACGGC GCGGATGATA
1051 TATGCCGACC GAAGGGATTA CACCAAAGTC AGGCAGTGGT TGAAAAAAGT
1101 GTCCGCGCCG GAATACCTGT TCGACAAAGG TGTGCTGGCG GCTGCGCGCG
1151 CTGTGAGATT GGACGCGCGC AGGGCGGCTT TGCGGCAGAT CGGCAGGGTG
1201 CGGAAACTTC CGAACAGCA GGGGCGGTAT TTTACGGCAG ACAATTGTGC
1251 CAAATACAG ATGTTCCGCC TGTCGAAGCT CCCCACAAA CGGGAGGCTT
1301 TGAGGGGTTT GGACAAGATT ATCGAAAAC CGCCTCCCGG CAGTAATACA
1351 GAGTTACAGG CAGAGGCATT GGTACAGCGG TCAGTTGTTT ACGATCGGCT
1401 TGGCAAGCGG AAAAAATGA TTTAGATCT TGAAAGGGCG TTCAGGCTTG
1451 CACCCGATAA CGCTCAGATT ATGAATAATC TGGGTACAG CCGCTTTTCC
1501 GATTCCAAAC GTTTCGACGA AGGCTTCGCC CTGCTTCAGA CGGCATACCA
1551 AATCAACCCG GACGATACCG CTGTCAACGA CAGCATAGGC TGGGCGTATT
1601 ACCTGAAAGG CGACGCGGAA AGCGCGCTGC CGTATCTGCG GTATTCTGTT
1651 GAAACGACC CCGAGCCCGA AGTTGCCGCC CATTGGGCGG AAGTGTGTG
1701 GGCATTGGGG GAACGCGATC AGGCGGTGTA CGTATGGACG CAGGCGGCAC
1751 ACCTTACGGG AGACAAGAAA ATATGGCGGG AACGCTCAA ACGTCACGGC
1801 ATCGCATTCG CCCAACCTTC CCGAAAACCT CGGAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2908; ORF 951.a>:

```
a951.pep
1  MLPARFTILS VLAAALLAGQ AYAAGAADAK FPKEVGKVF R KQORYSEEEI
51  KNERARLAAR GERNVQIFTL LGGETALQKG CAGTALATYM LMLERTKSPE
101 VAERALEMAV SLNAFEQAEI IYQKWRQIEP IPGKAQKRAG WLRNVLRERG
151 NQHLDGLEEV LAQADEGQNR RVFLLLAQAA VQDGLAQKA SKAVRRRAALR
201 YEHLEPAAVA DVVFSVQGRE KEKAIGALQR LAKLDTEILP PTLMTLRLTA
251 RKYFEILDGF FEQTDTONLS AVWQEMEIMN LVSLHRLDDA YARLNVLLER
301 NPNADLYIQA AILANRKEG ASVIDGYAEK AYGRGTGEQR GRAAMTAAMI
351 YADRRDYTKV RQWLKKSAP EYLFDKCVLA AAAAVELDGG RAALRQIGRV
401 RKLPEQQQRY FTADNLSKIQ MFALSKLPDK REALRGLDKI IEKPPAGSNT
451 ELQAEALVQR SVVYDRLGKR KKMISDLERA FRLAPDNAQI MNNLGYSLLS
501 DSKRLDEGFA LLQTAYQINP DDTAVNDSIG WAYYLGKDAE SALPYLRYSF
551 ENDPEPEVAA HLGEVLWALG ERDQAVDVWT QAAHLTGDKK IWRETLKRHK
600 IALPQPSRKP RK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 951 shows 96.4% identity over a 614 aa overlap with a predicted ORF (ORF 951) from *N. meningitidis*

a951/m951 96.4% identity in 614 aa overlap

```

          10      20      30      40      50
a951.pep  MLPARFTILSVLAAALLAGQAYAAAG--AAAKPPKEVGKVFRRKQORYSEEEIKNERAR
          ||| || :|||:|:|:| ||| | :| | ||||| ||||| |||||
m951      MIMLPNRFKMLTTLTATLIAGQVSAAGGGAGDNKQPKVEGKVFRRKQORYSEEEIKNERAR
          10      20      30      40      50      60
a951.pep  LAAGGERVNVQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE

```

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```

|||||
m951      LAAVGERVNIQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFF
              70      80      90      100     110     120

              120     130     140     150     160     170
a951.pep   QAEMIYQKWROIPIPGKACKRAGWLRNVI.RERGNQHLDGLEEVLAQADEGQNRVFLLL
              |||||
m951      QAEMIYQKWROIPIPGKACKRAGWLRNVI.RERGNQHLDGLEEVLAQADEGQNRVFLLL
              130     140     150     160     170     180

              180     190     200     210     220     230
a951.pep   AQAAVQODGLAQKASKAVRRAALRYEHLPEAAVADVVSFVQGREKEKAI GALQRLAKLDT
              |||||
m951      AQAAVQODGLAQKASKAVRRAALRYEHLPEAAVADVVSFVQGREKEKAI GALQRLAKLDT
              190     200     210     220     230     240

              240     250     260     270     280     290
a951.pep   EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
              |||||
m951      EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
              250     260     270     280     290     300

              300     310     320     330     340     350
a951.pep   LLERNPNADLYIQAAILAANRKEGASVIDGYAEKAYGRGTGEQGRGAAMTAAMIYADRRD
              |||||
m951      LLERNPNADLYIQAAILAANRKEGASVIDGYAEKAYGRGTGEQGRGAAMTAAMIYADRRD
              310     320     330     340     350     360

              360     370     380     390     400     410
a951.pep   YTKVRQWLKKVSAPEYLFDKGVLA AAAA AVELDGGRAALRQIGRVRKLPEQCGRYFTADNL
              |||||
m951      YAKVRQWLKKVSAPEYLFDKGVLA AAAA AVELDGGRAALRQIGRVRKLPEQCGRYFTADNL
              370     380     390     400     410     420

              420     430     440     450     460     470
a951.pep   SKIQMFALSKLPDKREALRGLDKII EKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD
              |||||
m951      SKIQMLALSKLPDKREALRGLDKII EKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD
              430     440     450     460     470     480

              480     490     500     510     520     530
a951.pep   LERAFRLAEDNAQIMNNLGYSLLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYILK
              |||||
m951      LERAFRLAEDNAQIMNNLGYSLLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYILK
              490     500     510     520     530     540

              540     550     560     570     580     590
a951.pep   GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL
              |||||
m951      GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL
              550     560     570     580     590     600

              600     610
a951.pep   KRHGIALPQPSRKPRK
              |||||
m951      KRHGIALPQPSRKPRK
              610

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2909>:

```

g952.seq (partial)
1  ..TTGCTTTATC GTTTGAATGC TGCACCGATG TTTAACGATA ATCCTGTTGT
51  TTACGGAAAA ATCAAAATTGC AGAGTTGGAA AGCGCGGCGG GATTTCARTA
101 TTGTAAAGCA GGATTGGAT TTTCCTGCG GGGCGGCTTC GGTGGCGACG
151 CTTTTGAACA ATTTTACGG GCAAAAGCTG ACGGAAGAAG AACTGTTGGA
201 AAAACTGGGT AAGGAACAGA TCGCGCGGTC GTTTGAGGAT ATGCGGCGCA
251 TTATGCCCGA TTTGGGTTT GAGGCGAAAG GCTATGCCCT GTCTTTCGAA
301 CAGCTCGCGC AGTTGAAAAT CCCCCTCATC GTGTATCTGA AATACCGCAA
351 AGACGACCAT TTTCGGTAT TCGCGGAGT GGATGGCAAT ACGGTTTIGC
401 TTGCCGACCC GTCGCCGGT CATGTTTCGA TGAGCAGGGC GCASTTTTTC
451 GAGGCTTGCC AAACCGTGA GGGAAATTG GCAGGCAAAA TTTTGGCGST
501 CGTGCCGAAA AAAGCGGAGG CGATTTCAAA TAAATTGTTT TTCACACATC
551 ATCCCAAGCG GCAGACGGAG TTTCAGTCG GACAGGTAAA ATGGTGGCGT

```

1363

601 GCTTATTGA

This corresponds to the amino acid sequence <SEQ ID 2910; ORF 952.ng>:

```
g952.pep (partial)
1  ..LSYRLNAAPM FNDNPVVYGR IKLQSWKARR DFNIVKQDLD FSCGAASVAT
51  LLNNFYGQKL TEEEVLEKLG KEQMRASFED MRRIMPDLGF EAKGYALSFE
101 QLAQLKIPVI VYLKYRKDDH FSVLRGVDGN TVLLADPSPG HVSMSRAQFL
151 EAWQTREGNL AGKILAVVPR KAEAISNKL FTHHPKRQTE FAVGQVKWWR
201 AY*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2911>:

```
m952.seq
1  ATGATGAAGT TCAAATATGT TTTTCTGTTG GCGTGTGTTG TCGTTTCTTT
51  ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAG CGCGCGGGA TTTCAATATT
151 GTAAAGCAGG ATTTGGATT TTTCTGTGGG GCGGCTTCGG TGCGCAGCT
201 TTTGAACAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCTCCT TTGAGGATAT GCGGCGCAT
301 ATGCTTGATT TGGGTTTGA GCGGAAGGCG TATGCCCTGT CTTTCGAGCA
351 GCTCGCGCAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAAG
401 ACGACCATTT TTCGGTATTG CGCGGTATAG ACGGCAATAC GGTTTTCGCT
451 GCCGACCCGT CGCTGGGGCA TGTTCAATG AGCAGGCGC AGTTTTGGA
501 TGCTTGGCAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCTGTCA
551 TACCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACAACAC
601 CCAAAACGCG AGACGGAGTT TACAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2912; ORF 952>:

```
m952.pep
1  MMKFYVFL ACVVVLSYR LNAAPMFNDN PVVYGKIKVQ SWKARRDFNI
51  VKQDLDFSCG AASVATLLNN FYGQTLTEE VLKLDKEQM RASFEDMRR
101 MPDLGFEAKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFLDAWQ TREGNLAGKI LAVIPKKAET ISNKLFFTQH
201 PKRQTEFTVG QIRQARAE*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 952 shows 92.5% identity over a 201 aa overlap with a predicted ORF (ORF 952) from *N. gonorrhoeae*

g952/m952; 92.5% identity in 201 aa overlap

```

              10      20      30      40
g952.pep      LSYRLNAAPMFNDNPVVYGKIKLQSWKARRDFNIVKQDLD FSCG
              |||
m952          MMKFYVFLACVVVLSYRLNAAPMFNDNPVVYGKIKVQSWKARRDFNIVKQDLD FSCG
              10      20      30      40      50      60

              50      60      70      80      90      100
g952.pep      AASVATLLNNFYGQKLTEEEVLEKLGKEQMRASFEDMRRIMPDLGFEAKGYALSFEQLAQ
              |||
m952          AASVATLLNNFYGQTLTEEEVLEKLDKEQMRASFEDMRRIMPDLGFEAKGYALSFEQLAQ
              70      80      90      100      110      120

              110     120     130     140     150     160
g952.pep      LKIPVIVYLKYRKDDHFSVLRGVDGNTVLLADPSPGHVSMSRAQFL EAWQTREGNLAGKI
              |||
m952          LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSLGHVMSMSRAQFLDAWQTREGNLAGKI
              130     140     150     160     170     180

              170     180     190     200
g952.pep      LAVVPKKA E AISNKLFFTHHPKRQTEFAVGQVKWWRAYX
              |||
m952          LAVIPKKAETISNKLFFTQHHPKRQTEFTVGQIRQARAE
              190     200     210
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2913>:

```
a952.seq
1  ATGATGAAGT TCAAATATGT TTTTCTGTTG GCGTGTGTTG TCGTTTCTTT
```

1364

```

51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAG AAAGGCGGGA TTTCATATT
151 GTAAAGCAGG ATTTGGATT TTCCTGCGG GCGGCTTCGG TGGCGACGCT
201 TTTGAACAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCTCGT TTGAGGATAT GCGGCGCATT
301 ATGCCAGATT TGGGTTTGA AGCGAAAGGC TATGCCCTGT CTTTCGAGCA
351 GCTCGCAGAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAGG
401 ATGATCATT CTGCGTATG CGCGGGATAG ACGCAATAC GGTTTTGCTT
451 GCCGACCCGT CGCTGGGTCA TGTTTCAATG AGCAGGGCGC AGTTTNGGA
501 TGCTTGGCAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCGGTCG
551 TGCCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACATCAT
601 CCCPAGCGGC AGACGGAGTT TGCAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2914; ORF 952.a>:

```

a952.pep
1  MMKFKYVFL ACVVVLSYR LNAAPMFNDN PVVYGKIKVQ SWKERRDFNI
51 VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLKKLDKEQM RASFEDMRRI
101 MPDLGFEEKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFXDAWQ TREGNLAGKI LAVVPKKAET ISNKLFFTHH
201 PKRQTEFAVG QIRQARAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 952 shows 97.7% identity over a 218 aa overlap with a predicted ORF (ORF 952) from *N. meningitidis*

```

a952/m952 97.7% identity in 218 aa overlap

a952.pep      10      20      30      40      50      60
MMKFKYVFLACVVVLSYRLNAAPMFNDNPNVVYGKIKVQSWKERRDFNIVKQDLDFSCG
|||||
m952          10      20      30      40      50      60
MMKFKYVFLACVVVLSYRLNAAPMFNDNPNVVYGKIKVQSWKARRDFNIVKQDLDFSCG
|||||

a952.pep      70      80      90      100     110     120
AASVATLLNNFYGQTLTEEEVLKKLDKEQMRASFEDMRRI MPDLGFEEKGYALSFEQLAQ
|||||
m952          70      80      90      100     110     120
AASVATLLNNFYGQTLTEEEVLKKLDKEQMRASFEDMRRI MPDLGFEEKGYALSFEQLAQ
|||||

a952.pep     130     140     150     160     170     180
LKIPVIVYLK YRKDDHFSVL RGIDGNTVLLADPSLGHVMSRAQFXDAWQTREGNLAGKI
|||||
m952         130     140     150     160     170     180
LKIPVIVYLK YRKDDHFSVL RGIDGNTVLLADPSLGHVMSRAQFLDAWQTREGNLAGKI
|||||

a952.pep     190     200     210     219
LAVVPKKAETISNKLFFTHHPKROTEFAVGQIRQARAE
|||:|||||
m952         190     200     210
LAVIPKKAETISNKLFFTHHPKROTEFTVQIRQARAE
|||||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2915>:

```

g953.seq
1  ATGAAAAAAA TCATCTTCGC CGCGCTCGCA GCGGCAGCCG TCGGCACTGC
51 CTCCGCCACC TACAAAGTGG ACGAATATCA CGCCAACGTC CGTTTCGCCA
101 TCGACCACTT CAACACCAGC ACCAACGTCG GCGGTTTTTA CGGTCGTACC
151 GGTTCGGTCG AGTTCGATCA AGCAAAACGC GACGGCAAAA TCGACATCAC
201 CATTCCCGTC GCCAACCTGC AAAGCGGTTT GCAACCTTC ACCGGCCACC
251 TGAAATCCGC CGACATCTTC GATGCCGCTC AATATCCGGA CATCCGCTTC
301 GTTTCACACA AATTCAACTT CAACGGCAAA AAAGTTGTTT CCGTTGACGG
351 CAACCTGACC ATGCGCGGCA AAACCGCCCC CGTCAAACTC AAAGCCGAAA
401 AATTCAACTG CTACCAAGC CCGATGGCGG AAACCGAAGT TTGCGCGCGC
451 GACTTCAGCA CCACCATCGA CCGCACCAAA TGGGGCGTGG ACTACCTCGT
501 TAACGCCGGT ATGACCAAAA ACGTCCGCAT CGACATCCAA ATCGAAGCTG
551 CAAAACAATA A

```

1365

This corresponds to the amino acid sequence <SEQ ID 2916; ORF 953.ng>:

```
g953.pep
1  MKKIIFAALA AAAGVTASAT YKVDEYHANV RFAIDHENTS TNVGGFYGLT
51  GSVEFDQAKR DGKIDITIPV ANLQSGSQPF TGHLSADIF DAAQYPDIFR
101 VSTKFNFNKG KLVSVVDGNLT MRGKTAPVKL KAEKFNCYQS PMAETEVCQG
151 DFSTTIDRTK WGVVDYLVNAG MTKNVRIDIQ IEAAKQ*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2917>:

```
m953.seq
1  ATGAAAAAAA TCATCTTCGC CGCACTCGCA GCCGCCGCCA TCAGTACTGC
51  CTCGCCGCCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCG
101 CCATCGACCA TTTCAACACC AGCACCAACG TCGGCGGTTT TTACGGTCTG
151 ACCGGTTCCG TCGAGTTTCA CCAAGCAAAA CGCGACGGTA AAATCGACAT
201 CACCATCCCC ATTGCCAACC TGCAAGCGG TTCGCAACAC TTTACCGACC
251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC
301 TTTGTTTCCA CCAATTCAA CTTCAACGGC AAAAACTGG TTTCCGTGTA
351 CGGCAACCTG ACCATGCACC CCAAAACCGC CCCCGTCAA CTCAAAGCCG
401 AAAAATTCAA CTGCTACCAA AGCCCGATGG AGAAAACCGA AGTTTGTGGC
451 GCGGACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
551 CAGCCAAACA ATAA
```

This corresponds to the amino acid sequence <SEQ ID 2918; ORF 953>:

```
m953.pep
1  MKKIIFAALA AAAISTASAA TYKVDEYHAN ARFAIDHENT STNVGGFYGL
51  TGSVEFDQAK RDGKIDITIP IANLQSGSQH FTDHLKSADI FDAAQYPDIFR
101 FVSTKFNFNKG KLVSVVDGNLT TMHGKTAPVK LKAEKFNCYQ SPMEKTEVCQ
151 GDFSTTIDRT KWMMDYLVNV GMTKSVRIDI QIEAAKQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 953 shows 93.0% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. gonorrhoeae*

```
m953/g953    93.0% identity in 187 aa overlap

          10      20      30      40      50      60
m953.pep    MKKIIFAALAAAAAISTASAATYKVDEYHANARFAIDHENTSTNVGGFYGLTGSVEFDQAK
g953         MKKIIFAALAAAAAVGTASA-TYKVDEYHANVRFAIDHENTSTNVGGFYGLTGSVEFDQAK
          10      20      30      40      50
          70      80      90     100     110     120
m953.pep    RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIFRVSTKFNFNKGKLVSVVDGNL
g953         RDGKIDITIPVANLQSGSQPFTGHLKSADIFDAAQYPDIFRVSTKFNFNKGKLVSVVDGNL
          60      70      80      90     100     110
          130     140     150     160     170     180
m953.pep    TMHGKTAPVKLKAKEKFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI
g953         TMHGKTAPVKLKAKEKFNCYQSPMAETEVCVGGDFSTTIDRTKWGVVDYLVNAGMTKNVRIDI
          120     130     140     150     160     170
m953.pep    QIEAAKQX
g953         QIEAAKQX
          180
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2919>:

```
a953.seq
1  ATGAAAAAAA TCATCATCGC CGCGCTCGCA GCAGCCGCCA TCGGCACTGC
51  CTCGCCGCCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCT
101 CTATCGACCA TTTCAACACC AGCACCAACG TCGGCGGTTT TTACGGTCTG
151 ACCGGTTCCG TCGAGTTTCA CCAAGCAAAA CGCGACGGTA AAATCGACAT
201 CACCATCCCC GTTGCCAACC TGCAAGCGG TTCGCAACAC TTTACCGACC
251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC
301 TTTGTTTCCA CCAATTCAA CTTCAACGGC AAAAACTGG TTTCCGTGTA
```

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```

351 CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCCTCAAA CTCAAAGCCG
401 AAAAAATTCAT CTGCTACCAA AGCCCCGATGT TGAAAACCGA AGTTTTCGGC
451 GCGGACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGC
551 CAGCCAAACA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2920; ORF 953.a>:

a953.pep

```

1  MKKIIIAALA AAAIGTASAA TYKVDEYHAN ARFSIDHENT STNVGGFYGL
51  TGSVEFDQAK RDGKIDITIP VANLQSGSQH FTDHLKSADI FDAAQYPDIR
101 FVSTKFNENG KKLVSVDGNL TMHGKTAPVK LKAKEFNICY SPMLKTEVCG
151 GDFSTTIDRT KWGMDYLVNV GMTKSVRIDT QIEAAKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 953 shows 97.3% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. meningitidis*

a953/m953 97.3% identity in 187 aa overlap

```

a953.pep      10      20      30      40      50      60
               MKKIIIAALAAAAIGTASAATYKVDEYHANARFSIDHENTSTNVGGFYGLTGSVEFDQAK
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m953           10      20      30      40      50      60
               MKKIIIFAALAAAAISTASAATYKVDEYHANARFAIDHENTSTNVGGFYGLTGSVEFDQAK
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

a953.pep      70      80      90      100     110     120
               RDGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNENGKKLVSDGNL
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m953           70      80      90      100     110     120
               RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNENGKKLVSDGNL
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

a953.pep      130     140     150     160     170     180
               TMHGKTAPVKLKAKEFNICYQSPMLKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDT
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m953           130     140     150     160     170     180
               TMHGKTAPVKLKAKEFNICYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDT
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

a953.pep      QIEAAKQX
               |||||
m953           QIEAAKQX

```

g954.seq not found yet

g954.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2921>:

m954.seq

```

1  ATGAAAAAGT TTTATTTTGT GCTGCTGCGG TTGGGTTTGG CAGCGTGTGG
51  GCAAGAACAA TCGCAGAAAG CTGATGCGGA GCAGTATTTT TTTGCCAATA
101 AATATCAATT TGCAGATGAG AAACAGCCTT TTTATTTTGA ACGCGCCGCC
151 CGTTTCCGTG TATTGCAACA AGGCCTTGGC GGGGATTTTG AGAGGTTTTT
201 AAAAGGAGAA ATACCTAATC AAGAAAATCT TSCAAAGTAT CGTGAAAATA
251 TTAICTAAGC AGTCGCTTAT TATGCGGACA CSAATGGAGA TGATGACCCA
301 TACCGCGTCT GCAAACAGGC TGCGCAAGAT GCAGAAATCC TGATGAAGAG
351 TATGGTAACA AGCGGTGGAG GCGGTACAAC TGATTTAGAT AAGGAAAGTT
401 ATCAAAATTA CCGAAAATCA ATGCAAGAAT GCGTAAAC AATAACGGAA
451 GCTGAAGCCA ATTTGCCGAA AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2922; ORF 954>:

m954.pep

```

1  MKKFFVLLA LGLAACGQEQ SQKADAEQYF FANKYQFADE KQAFYFERAA
51  RFRVLQQSLG GDFERFLKE IPNQENLAKY RENITQAVAY YADTNGDDDD
101 YRVCKQAAQD AEILMKSMVT SGGGGTTDLD KESYQNYRKS MQECRKTITE
151 AEANLPKK*

```

a954.seq not found yet

a954.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2923>:

```

g957.seq (partial)
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTGTCG GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAT GTGTACGGCG GAACGGCTCA
501 CCGGGAAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTTCGG ATTTGATGCG GCGGGGCGCG GGAATAATCG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCCG GGGGatgaaG gcgaacagtc ttgtggtcgg
801 ctatgatgcg gacggtCtgc CgcaAAAagt ctattggagt gtcgacaatg
851 gaaaaaaacc ccaaagtgtc gaattattt tgaaaaacgg aaatcttttt
901 attgcccaat cttcgacggt aaccttgaaa acggatggcg taacggcgga
951 tatgcaaaacc tatcatgcgc aacaaacgtt ctatttggat ggg...

```

This corresponds to the amino acid sequence <SEQ ID 2924; ORF 957.ng>:

```

g957.pep (partial)
1  MFKKFKPVLL SFFALVFVAFW LGTGIAYEIN PRWFLSDTAT EVPENPNVAFV
51  AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLOSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFVNAEYL
151 YRNDRPFVSU VYGGTAHGEN YETTGEYRVV WQPDGVSFVA AGRGKIGEDV
201 YEHCLGCVQM AQVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYQN
251 MRELMPRGNK ANSLVVGYYDA DGLPKQVYWS VDNKKPKQSV EYYLKNGNLF
301 IAQSSTVTLK TDGVTADMOT YHAQOTLYLD G...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2925>:

```

m957.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAAATCT TGCCGGAACG GTGGATGACG
251 GTCCSTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAT GTGTACGGCG GAACGGTCA
501 CCGGGAAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTTCGG ATTTGATGCG GCGGGGCGCG GGAATAATCG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAAAG
701 AGAGCAACCG AATTGCGTCT GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCCG AGGGATCAAG GCGAACAGTC TTGTGGTCCG
801 CTATGATGCG GACGGTCTCG CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAAACG CCAGAGTTTC GAATATATTT TGAATAACCG AAATCTTTTT
901 ATTGCACAAAT CTTGACGGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTGGAT GCGGGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TSCCTGATT TCCTTTGAAC
1051 TTGGAAAATT TGGAAAAGA GGTGCGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG ACCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2926; ORF 957>:

```

m957.pep
1  MFKKFKPVLL SFFALVFVAFW LGTGIAYEIN PRWFLSDTAT EVPKNPVAFV
51  AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFVNAEYL
151 YRNDRPFVSU VYGGTVHGEN YETTGEYRVV WQPDGVSFVA AGRGKIGEDV
201 YEHCLGCVQM AQVYLAKYRD VANDEQKVWD FRKESNRIAS DSRNSVFYQN

```


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251 MRELMPRGNK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
 301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
 351 LENLEKEVRR YAEAAARRSG GRRDLSH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 957 shows 95.2% identity over a 331 aa overlap with a predicted ORF (ORF 957) from *N. gonorrhoeae*

g957/m957 95.2% identity in 331 aa overlap

g957.pep	10	20	30	40	50	60
m957	10	20	30	40	50	60
g957.pep	70	80	90	100	110	120
m957	70	80	90	100	110	120
g957.pep	130	140	150	160	170	180
m957	130	140	150	160	170	180
g957.pep	190	200	210	220	230	240
m957	190	200	210	220	230	240
g957.pep	250	260	270	280	290	300
m957	250	260	270	280	290	300
g957.pep	310	320	330			
m957	310	320	330	340	350	360
m957						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2927>:

a957.seq

1	ATGTTTAA	AAATCAAACC	GGTACTGTTG	TCATTTTTC	CACTTGTATT
51	TGCCTTTT	GGCTGGGAAC	GGTATTGCCTA	TGAGATTAA	CCGCGTTGGT
101	TTTTGAGCGA	TACGGCAACT	GAAAATCCGA	ATGCTTTTGT	GGCGAAACTT
151	GCCCGCCTGT	TCCGAAATGC	CGACAGGGCG	GTTGTCATCG	TGAAGGAATC
201	GATGAGGACG	GAGGAAAGTC	TTGCCGGAGC	IGTGGATGAC	GGTCCGTTGC
251	AGTCGGAGAA	GGATTATCTT	GCACTCGCTG	ICCGGCTCAG	TCGTTTGAAA
301	GAAAAGGCGA	AATGGTTTCA	CGTAACGGAG	CAGGAACATG	GGGAAGAGGT
351	TTGGCTGGAT	TACTATATCG	GCGAGGGCGG	TTTGGTTGCG	GTTTCGCTTT
401	CGCAACGCTC	GCCGGAAGCG	TTTGTAAATG	CCGAATATCT	GTATCGGAAC
451	GATCGTCCGT	TTTCTGTAAA	TGTGTACGGC	GGAACGGTTC	ACGGGGAAAA
501	TTGATGAAAC	ACAGGAGAAT	ATCGGGTTGT	TTGGCAACCG	GACGGTTCGG
551	TATTGATGTC	GTCGGGGCGC	GGGAAAATCG	GGGAAGATGT	TTATGAGCAT
601	TGCCICGGGT	GTTATCAGAT	GGCCAGGTA	TATTGGCGA	AAATCGGGA
651	TGTCGCGAAT	GATGAGCAGA	AGGTTTGGGA	CTTCCGCGAA	GAGAGTAACC
701	GGATTGCGCT	GGACTCGCGC	GATTCTGTGT	TTTATCAGAA	TATGCGGGAA
751	TTGATGCCCC	GAGGGATGAA	GGCAAAACGT	CTTGTGGTCG	GCTATGATGC
801	GGACGGTCTG	CCGCAGAAAG	TCTATTGGAG	TTTCGACAA	GGGAAAAAAC
851	GCCAGAGTTT	CGAATATTAT	TGAAAAACG	GAAATCTTTT	TATTGCACAA
901	TCTTCGACGG	TAGCATTGAA	AGCGGATGGC	GTAACGGCGG	ATATGCAGAC

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951 CTATCATGCG CAACAGACGT GGTATTAGA TGGCGGGCGG ATTGTCGCGG
1001 AAGAGAAACA GGGGGACAGA CTGCCTGATT TTCCTTGAA CTGGGAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCCGG
1101 CGGCAGCGCG GACCTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2928; ORF 957.a>:

```

a957.pep
1  MFKKFKPVLL SFFALVFVFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51  ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYI ALAVRLSRLK
101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLYRN
151 DRPFVSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGICYMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL POKVYWSFDN GKQRQSFYFY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QOTWYLDGGR IVREEKQGRD LPDFPLNLED
351 LEKEVSRVAE AAARRSGGRR DLSH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

```

a957/m957 96.3% identity in 377 aa overlap

      10      20      30      40      50
a957.pep MFKKFKPVLLSFFALVFVFWLGTGIAYEINPRWFLSDTATE---NPNAFVAKLARLFNA
      |||
m957      MFKKFKPVLLSFFALVFVFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFNA
      |||
      10      20      30      40      50      60
a957.pep DRVVIVKESMRTEESLAGAVDDGPLQSEKDYIALAVRLSRLKEKAKWFHVTEQEHGEEV
      |||
m957      DRVVIVKESIRTEENLAGTVDDGPLQSEKDYIALAIRLSRLKEKAKWFHVTEQEHGKEV
      |||
      60      70      80      90      100     110
a957.pep WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
      |||
m957      WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
      |||
      120     130     140     150     160     170
a957.pep WQPDGVSVDASGRGKIGEDVYEHCLGICYMAQVYLAKYRDVANDEQKVWDFREESNRIAS
      |||
m957      WQPDGVSVDAAAGRGKIGEDVYEHCLGICYMAQVYLAKYRDVANDEQKVWDFRKNRIAS
      |||
      180     190     200     210     220     230
a957.pep DSRDSVFYQNMRELMPRGMKANSLVVGYDADGLPOKVYWSFDNGKKRQSFYFYLKNGNLF
      |||
m957      DSRNSVFYQNMRELMPRGMKANSLVVGYDADGLPOKVYWSFDNGKKRQSFYFYLKNGNLF
      |||
      240     250     260     270     280     290
a957.pep IAQSSTVALKADGVTADMQTYHAQOTWYLDGGRIVREEKQGRDLPDFPLNLEDLEKEVSR
      |||
m957      IAQSSTVALKADGVTADMQTYHAQOTWYLDGGRIVREEKQGRDLPDFPLNLENLEKEVRR
      |||
      300     310     320     330     340     350
a957.pep YAEAAAARRSGGRRDLSHX
      |||
m957      YAEAAAARRSGGRRDLSHX
      |||
      360     370
a957.pep YAEAAAARRSGGRRDLSHX
m957      YAEAAAARRSGGRRDLSHX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2929>:

```

g958.seq
1  TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTTCGGCAGC CATTGCGCCG CCGATACCGT TCGCGCGGAA GAGCGGACG

```

```

101 GCGGTGTCGC AGAAGGCGGT GCGCAGGGCG CGTCCGAATC CGCACAAGCT
151 TCCGATTGTA CCCTCGGTTT GACCTGCCTG TTTTGCACTA ACAGAAAGCGG
201 CAGCCCGGAG AGAACCAGAG CCGCCGTCGA AGGCAGCGGC GAAGCATCCG
251 TCCCGAAGA CTATACGCGC ATTGTTGCCG ACAGGATGGA AGGACAGTCG
301 AAGGTTAAGG TGCGCGCGGA AGGAAGCGTT ATCATCGAAC GGGACGGCGC
351 AGTCCTCAAT ACCGATTGGG CGGATTACGA CCAGTCGGGC GACACCGTTA
401 CCGTAGGCGA CCGGTTTCGC CTCCAACAGG ACCGTACGCT GATTTCGGGGC
451 GAAACCTGTA CCTACAATCT CGATCAGCAG ACCGGCGAAG CGCACAACGT
501 CCGTATGGAA ACCGAACAAG GCGGACGGCG GCTGCAAGC GTCAGCCGCA
551 CCGCCGAAAT GTTGGGCGAA GGGCGTTACA AACTGACGGA AACCCAAATC
601 AACACCTGTT CCGCCGGAGA TGCCGGCTGG TATGTCAAGG CCGCCTCTGT
651 CGAAGCCGAT CCGGGAAAAG GCATAGGCGT TGCCAAACAC GCCGCCCTTCG
701 TGTTCCGCGG CGTTCCCTTT TTCTATACGC CTTGGGCGGA CTTCCCGCTT
751 GACGSCAACC GCAAAAGCGG ACTGCTCGTC CCGTCCGTAT CTGCCGGTTC
801 GGACGCGGTT TCCCTTTCCG TCCCTTATTA TTTCAACCTT GCCCCCAACT
851 TCGATGCCAC TTTCGCCCCC GGCATTATCG GCGAACGCGG CGCGACGTTT
901 GACGSAACAA TCCGTTACCT GCGTCCCGAT TACAGCGGAC AGACCGACCT
951 GACCTGGTTG CCGCACGATA AGAAAAGCGG CAGGAACAAC CGCTATCAGG
1001 CAAAATGGCA GCACCGGCAC GACATTTCCG ACACGCTTCA GCGGGGTGTC
1051 GATTTCGAAC AAGTCTCCGA CAGCGGCTAC TACCGCGACT TTTACGGCGG
1101 CGAAGAAATC GCCGCAACG TCAACCTCAA CCGCCGCGTA TGCTGGATT
1151 ATGGCGGCAG GCGGCGGGA GGCAGCCTGA ATGCCGGCCT TTCGGTTCAG
1201 AAATACCAGA CGCTGGCAA CCAAAGCGGC TACAAAGACG AACCTTACGC
1251 CATCATGCCC CGCCTTTCTG CCGATTGGCA TAAAAACGCA GGCAGGGCGC
1301 AAATCGGCGT GTCCGCACAA TTTACCCGCT TCAGCCACGA CGGCCGCCAA
1351 GACGSCAGCC GACTGGTCTG GTATCCCGGT ATCAATGGG ATTTCAGCAA
1401 CAGCTGGGGC TACGTCCGCC CCAAACCTCG GCTGCAGGCC ACTTATTACA
1451 GCCTCGACAG TTTCCGCGGC AAAGCATCCC GCAGCGTCGG CCGCGTTTGT
1501 CCCGTTGTCA ATATCGACGG CCGCACAAAC TTCGAACGCA ATACGCGCCT
1551 GTTCGGCGGC GGAGTCGTGC AAACCATCGA GCCGCGCCTG TTCTACAAC
1601 ATATTCCTGC CAAATCTCAA AACGACCTGC CCAATTTCGA TTCGTCGGA
1651 AGCAGCTTCG GCTACGGGCA GCTTTCCGCG GAAAACCTCT ATTACGGCAA
1701 CGACCGCATC AACGCCGCCA ACAGCCTTTC CACCGCGCTG CAGAGCCGTA
1751 TTTTGGACAG CGCGACGGGG GAGGAGCGTT TCCGCGCCGG TATCGGTCAG
1801 AAATTCTATT TCAAGGATGA TCGGGTGATG CTTGACGGCA GCGTCGGCAA
1851 AAATCCGCGC AGCGTTCGCG ACTGGGTGGC ATTGCGCTCC GCGCGCATAG
1901 ETLTYNLDQQ TGEAHNVME TEQGGRRLOS VSRTAEMLGE GRYKLTETQF
1951 CCGCGCCGAA ATTACGCGCT CCGCGCAGGC TACCGCCCGC CCCCCGGA
2001 AGTGTGAAC GCCCGCTACA AATACGGGCG CACGAAAAAA ATCTACCTGC
2051 AGCGGACGG TTCTATTTT TACGACAAAC TCAGCCAGCT CGACCTGTCC
2101 GCACAATGGC CGCTGACGCG CAACCTGTCT GCGTCTGTCC GCTACAAC
2151 CGGTTTGTAA GCCAAAAAAC CGATAGAAAT GTTGCCTGGT GCAGAATACA
2201 AAAGCAGTTG CGGCTGCTGG GCGCGGGGCG TGTACGCCCA ACGCTACGTT
2251 AACGGCGAAA ACACCTACAA AAACGCGGTC TTTTTCAC TTCAAGTTGA
2301 AGACCTCAGC AGCGTCGGCA GAAACCCCGC AGGACGATG GATGTGCGCG
2351 TTCCCGGCTA CATCCCCGCC CACTCTCTTT CCGCGGACG CAACAAACGG
2401 CCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2930; ORF 958.ng>:

```

g958.pep
1  LARLFLSKPL VLALGFCEGT HCAADTVAAE EADGRVAEGG AQGASESAQA
51  SDLTLGSTCL FCSNESGSPE RTEAAVCGSG EASVPEDYTR IVADRMEGQS
101 KVKVRAEGSV IIERDGAVLN TDWADYDQSG DTVTVGDRFA LQQDGTLLRG
151 ETLTYNLDQQ TGEAHNVME TEQGGRRLOS VSRTAEMLGE GRYKLTETQF
201 NTCSAGDAGW YVKAASVEAD RKGIGVAKH AAFVFGGVPL FYTPWADFPL
251 DGNRKSGLLV PSVSAGSDGV SLSVPYYFNL APNFDATFAP GIIGERGATF
301 DGQIRYLRPD YSGQDLDLWL PHDKKSGRNN RYQAKWQHRH DISDTLQAGV
351 DFNQVSDSGY YRDFYGGEEI AGNVNLRNRV WLDYGGRAAG GSNAGLSVQ
401 KYQTLANQSG YKDEPYAIMP RLSADWHKNA GRAQIGVSAQ FTRFSDHGRQ
451 DGSRLVVYPG IKWDFNSWG YVRPKLGLHA TYSLDSFGG KASRSVGRVL
501 PVVNIDGTTT FERNTLFGG GVVQTIETPL FYNYPKASQ NDLPNFDSS
551 SSFGYGQLFE ENLYYNDRI NAANSLSTAV QSRILDGATG EERFRAGIGQ
601 KFYFKDDAVM LDGSGVGNPR SRSDWVAFAS GGIGGRFTLD SSIHYNQNDK
651 RAEHYAVGAG YRPAPGKVLN ARYKYGRNEK IYLDAGDSYF YDKLSQLDLS
701 AQWPLTRNLS AVVRYNYGFE AKKPIEMLAG AEYKSSCGCW GAGVYAQRVY
751 TGENYKNAV FFSLLQLDLS SVGRNPAGRM DVAVPGYIPA HSLSAGRNRK
801 P*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2931>:

```

n958.seq
1  TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTCTTG
51  CTTCCGCGAC CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGAA AGCGTTCGGA GCGTGTCCGA ACCCATACAG

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1371

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151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTTCGA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCGAAGCAT
251 CCATCCCCGA AGACTATACG CGCATTTGTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTGC AACGCAACCG
351 GACGACCCCTC AATACCGATT GGGCGGATTA CGACCAAGTC GGCACACCCG
401 TTACCGCAGG CGACCGGTTT GCCCTCCAAC AGGACGGTAC GCTGATTTCG
451 GGCAGAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGCATG GAAATCGAAC AAGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACTGAC GGAACCCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA ACGCAGCCTC
651 TGTCAAGGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCT
701 TCGTGTTCGG CGCGGTTCCC ATTTTCTACA CCCCTTGGGC GGACTTCCCG
751 CTCGATTTCA ACCGCAAAAG CGGCCTGCTT GTTCCCTCAC TGTCCGCCGG
801 TTCGACGGCG GTTCCCTTTT CCGTTCCCTA TTATTTCAAC CTTGCCCCCA
851 ATCTCGATGC CACGTTTCGG CCCAGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTTGACGGCG AGGTACGCTA CCTGCGGGCG GATTATGCCG GCCAGTCCGA
951 CCTGACCTGG CTGCCGCACG ACAAGAAAAG CGGCAGGAAT AACCCTATC
1001 AGGCGAAATG GCAGCATCGG CACGACATT CCGACACGCT TCAGCGCGGT
1051 GTCGATTTCA ACCAAGTCTC CGACAGCGCG TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCGGT GTATGGCTGG
1151 ATTTATGGCG CAGGGCGGCG GCGCGCAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAATAACC AGACGCTGGC AAACCAAAGC GGCTACAAAG ACAAAACGTA
1251 TGCCCTCATG CCGCGCCTTT CGGTGAGTGC GCGTAAAAAC ACCGGCAGGG
1301 CGCAATTCGG CGTGTCCGCA CAATTTACCC GATTTCAGCA CGACAGCCGC
1351 CAAGACGGCA GCGCGCTGGT CGTCTATCCC GACATCAAT GGGATTTTAC
1401 CAACAGCTGG GGCTATGTCC GTCCCAAAC CTGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAG CCCGACGCGT CAGCGCACT
1501 CTGCCCATTC TCAACATCGA CAGCGCGCGA ACTTTTGAGC GGAATACGCG
1551 GATGTTTCGG GGAGAAGTCC TGCAAAACCT CGAGCCGCGC CTGTTCTACA
1601 ACTATATTCG TGCCAAATCC CAARAACGAC TGCCCAATTT CGATTGCTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTCTTT CGCGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAACAGCCTT TTCCGCCGCC GTGCAAAAGCC
1751 GTATTTTGGG CGGCGCGACG GGGGAAGAGC GTTTCGCGCG CGGCATCGGT
1801 CAGAAATTCG ATTTCAAGGA TGATGCGGTG ATGCTTGACG GCAGCGTCGG
1851 CAAAAAACCG CGCAACCGTT CCGACTGGGT GGCATTTGCC TCCGGCAGCA
1901 TCGGCAGCGC CTTCATCCTC GACAGCAGCA TCCACTACAA CCAAAACGAC
1951 AAACCGCGCG AGAATACGCG CSTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGTCT AACGCCCCGT ACAATAACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCCCTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAAT GGCCGCTGAC GCGCAACCTG TCGGCGCTCG TCCGTTACAA
2151 CTACGCTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAGCAG TTGCGGCTGC TGGGCGCGCG GCGGTACGCG CCAACGCTAC
2251 GTTACCGCGG AAAACACCTA CAAAACGCT GTCTTTTCTC CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTGC GCAGAAACCC CGCAGACAGG ATGGATGTGC
2351 CCGTTCCCGG CTATATCACC GCCCACCCTC TTTCCGCCGG ACGCAACAAA
2401 CGACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2932; ORF 958>:

```

m958.pep
1  LARLFSLKPL VLALGLCFGT HCAAADAVAA EETDNPTAGE SVRSVSEPIQ
51  PTSLSLGSTC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEOG
101 SQVQVRAEGN VVVERNRTTL NTDWADYDQS GDTVTAGDRF ALQQDGTLLR
151 GETLTYNLEQ QTGEAHNVRM EIEQGGRRLO SVSRTAEMLG EGHYKLTETO
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFFVGGVP IFYTPWADFP
251 LDGNRKSGLL VPSLSAGSDG VSLSVPPYYFN LAPNLDATFA PSVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSINAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSVEWRN TGRAQIGVSA QTRFSDSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQAARRVSRT
501 LPIVNIIDSGA TFERNTRMFG GEVLQTLFPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGQLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKDDAV MLDGSGVKKP RNRSDWVAFS SGSIGSRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVKL NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVLG GAELYKSSCGG WAGVYAORY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIT AHSLSAGRNR
801  RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 958 shows 89.3% identity over a 802 aa overlap with a predicted ORF (ORF 958) from *N. gonorrhoeae*

1372

m958/g958 89.3% identity in 802 aa overlap

m958.pep	10	20	30	40	50	60
	LARLFSLKPLVLALGLCFGTHCAAADAVAAEETDNPTAGESVRSVSEPIOPTSLSLGSTC					
g958	LARLFSLKPLVLALGLCFGTHCAA-DTVAEEADGRVAEGGAQGAESAQASDLTLGSTC					
	10	20	30	40	50	
m958.pep	70	80	90	100	110	120
	LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGSQVQVRAEGNVVVVERNRTTL					
g958	LFCSNESGSPERTEAAVQGSGEASVPEDYTRIVADRMEGSQVQVRAEGSVIIERDGAVL					
	60	70	80	90	100	110
m958.pep	130	140	150	160	170	180
	NTDWADYDQSGDVTVTAGDRFALQQDGLIRGETLTYNLEOOTGEAHNVNRNEIEQGRRRLQ					
g958	NTDWADYDQSGDVTVTGDRFALQQDGLIRGETLTYNLDQQTGEAHNVNRNETEQGRRRLQ					
	120	130	140	150	160	170
m958.pep	190	200	210	220	230	240
	SVSRTAEMLGEGHYKLTETCFNTCSAGDAGWYVKAASVEADREKIGVAKHAAFFVGGVVP					
g958	SVSRTAEMLGEGRYKLTETCFNTCSAGDAGWYVKAASVEADRGKIGVAKHAAFFVGGVVP					
	180	190	200	210	220	230
m958.pep	250	260	270	280	290	300
	IFYTPWADFPDGNRKSGLLVPSLSAGSDGVSLSVPYYFNLPNLDATFAPSVIGERGAV					
g958	IFYTPWADFPDGNRKSGLLVPSVSAGSDGVSLSVPYYFNLPNFDATFAPGIIGERGAT					
	240	250	260	270	280	290
m958.pep	310	320	330	340	350	360
	FDGQVRYLRPDYAGQSDLTWLPKDKKSGRNNRYQAKWQHRHDSITLQAGVDFNQVSDSG					
g958	FDGQIRYLRPDYSGQDLTWLPKDKKSGRNNRYQAKWQHRHDSITLQAGVDFNQVSDSG					
	300	310	320	330	340	350
m958.pep	370	380	390	400	410	420
	YYRDFYGNKEIAGNVNLRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM					
g958	YYRDFYGGEEIAGNVNLRVWLDYGGRAAGGSLNAGLSVQKYQTLANQSGYKDEPYAIM					
	360	370	380	390	400	410
m958.pep	430	440	450	460	470	480
	PRLSVEWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLVVPDIKWDFSNSWGYVRPKLGLH					
g958	PRLSADWHKNAGRAQIGVSAQFTRFSHDSRQDGSRLVVPDIKWDFSNSWGYVRPKLGLH					
	420	430	440	450	460	470
m958.pep	490	500	510	520	530	540
	ATYYSLNREFSQEARRVSRTLPIVNI DSGATFERNTRMFGGEVLQTLERLFYNYIPAKS					
g958	ATYYSLDSFGGKASRSVGRVLPVVNIDGGTTFERNTRLFGGGVVQTIERLFYNYIPAKS					
	480	490	500	510	520	530
m958.pep	550	560	570	580	590	600
	QNDLPNFDSESSFGYGQLFRENLYYGNDRINTANSLAAVQSRILDGATGEERFRAGIG					
g958	QNDLPNFDSESSFGYGQLFRENLYYGNDRINAANSLSTAVQSRILDGATGEERFRAGIG					
	540	550	560	570	580	590
m958.pep	610	620	630	640	650	660
	QKFYFKDDAVMLDGSVGKKPRNRSDWVAFASGSIGSRFILDSSIHYNQNDKRAENYAVGA					
g958	QKFYFKDDAVMLDGSVGKNPRSRSDWVAFASGGIGGRFTLDSSIHYNQNDKRAEHYAVGA					
	600	610	620	630	640	650
m958.pep	670	680	690	700	710	720
	SYRPAQGKVLNARYKYGRNEKIYLSQDGSYFYDKLSQDLDSAQWPLTRNL SAVVRNYGF					
g958	GYRPAQKVLNARYKYGRNEKIYLSQDGSYFYDKLSQDLDSAQWPLTRNL SAVVRNYGF					
	660	670	680	690	700	710

1373

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              730      740      750      760      770      780
m958.pep      EAKKPIEVLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKOLSSVGRNPADR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g958           EAKKPIEMLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKOLSSVGRNPAGR
              720      730      740      750      760      770

              790      800
m958.pep      NDVAVPGYITAHSLSAGRNRKP
              |||||:|||||:|||||:|||||:
g958           NDVAVPGYIPAHSLSAGRNRKPX
              780      790      800

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2933>:

```

a958.seq
1  TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTTCGGCACG CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGGA AGCGTTCGGA GCGTGTCCGA ACCCATACAG
151 CCTACCGACC TGAGCCTCGG TTCGACCTGC CTGTTTTCGA GTAACGAAAG
201 CGGCAGCCCG GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCAGACAT
251 CCATCCCCGA AGACTATACG CGCATTTSTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTCG AACGCAATCG
351 GACGACCTTC AATGCCGATT GGGCGGATTA CGACCAGTCG GCGGACACCG
401 TTACCGCAGG CGACCGGTTT GCCCTCCAAAC AGGACGGTAC GCTGATTCCG
451 GGCGAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGACAA
501 CGTCCGTATG GAAACCGAAC ACGGCGSACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACTGAC GGAAACCCAA
601 TTCACACCTT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCCGCTTC
651 CGTCGAAGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCT
701 TCGTGTTCCG CGGCGTTCCC ATTTTCTACA CCCCTTGGGC GGACTTCCCG
751 CTTGACGGGC ACCGCAAAAG CGGCCTGCTC GTTCCCTCAC TGTCCGCCGG
801 TTCGGACGGC GTTTCCTTTT CCGTCCCTTA TTATTCAAC CTTGCCCCCA
851 ATCTCGATGC CACGTTTCGG CCCGGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTTGACGGGC AGGTACGCTA CCTGCGGCGG GATTATGCCG GCCAGTCCGA
951 CCTGACCTGG CTGCGGCACG ACAAGAAAAG CGGCAGGAAT AACCGCTATC
1001 AGGCGAAATG CGACACCCGG CACGACATTI CCGACACGCT TCAGGCGGCT
1051 GTCGATTTCG ACCAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTTATGGCG CAGGCGCGCG GCGCGCAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAAGC GGCTACAAAG ACAAAACGTA
1251 TGCCCTGATG CCGCGCCTTT CCGCCGATTG CCGCAAAAAC ACCGGCAGGG
1301 CGCAATCCGG CGTGTCGCCC CAATTTACCC GCTTCAGCCA CGACAGCCGC
1351 CAAGACGGCA GCCGCTCGT CGTCTATCCC GACATCAAAAT GGGATTTCAG
1401 CAACAGCTGG GGTACGTCC GTCCCAAACCT CGGACTGCAC GCCACCTATT
1451 ACACCTTCAA CCGCTTCGGC AGCCAAGAAG CCCGACCGCT CAGCCGCACT
1501 CTGCCCATCG TCAACATCGA CAGCGGCATG ACCTTCGAAC GCAATACGCG
1551 GATGTTCCGG GCGCGAGTCC TGCAAACCTT CGAGCCGCGC GTGTTCTACA
1601 ACTATATTCG TGCCAAATCC CAAAACGACC TGCCCAATT CGATTCTGTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTTTT CGTGAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCCGCC GTGCAAAGCC
1751 GTATTTTGGA CGGCGCGACG GGGGAAGAGC GTTTCGCGC CGGCATCGGG
1801 CAGAAATCTT ACTTCAAAA CGACGCAGTC ATGCTTGACG GCAGTGTGCG
1851 CAAAAAACCG CGCAGCCGTT CCGACTGGGT GGCATTGCGC TCCAGCGGCA
1901 TCGGCAGCCG CTTTATCCTC GACAGCAGCA TCCACTACAA CAAAACGAC
1951 AAACGCGCCG AGAATACGG CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGCTG AACGCCCGCT ACAATAACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCCTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAAT GGCCGCTGAC GCGCAACCTG TCGGCCGTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAGCAG TTGCGGCTGC TGGGCGCGCG GCGGTGACGC CCAACGCTAC
2251 GTTACCGCGC AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTG GCAGAAACCC CGCAGACAGG ATGGATGTG
2351 CCGTTCCCGG CTATATCCCC GCCCACTCTC TTTCCGCCGG ACGCAACAAA
2401 CGGCCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2934; ORF 958.a>:

```

a958.pep
1  LARLFSLKPL VLALGFCFGT HCAAADAVAA EETDNPTAGG SVRSVSEPIQ
51  PTSLSLGSTC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEGQ
101 SQVQVRAEGN VVVERNRTTL NADWADYDOS EDTVTAGDRF ALQQDGLTIR
151 GETLTYNLEQ QTGEAHNVRM ETEHGRRRLQ SVSRFAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFTVFGVP IFYTPWADFP

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251 LDGNRKSGLL VPSLSAGSDG VSLSVPYFFN LAPNLDTFA PGVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGS LNAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSADWRKN TGRAQIGVSA QFTRFSDSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSRT
501 LPIVNIDSGM TFERNTRMFG GGVLTLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGOLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKNDV MLDGSVGKKP RSRSDWVAF SSGIGSRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVK NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF FAKKPTFVLA GA EYKSSCGC WGAGVYAQRY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIP AHSLSAGRKN
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a958/m958 98.1% identity in 802 aa overlap

	10	20	30	40	50	60
a958.pep	LARLFS	LKPLVL	LALGFC	FGTHCAA	ADAVAAE	ETDNPTAGGS
	10	20	30	40	50	60
m958	LARLFS	LKPLVL	LALGFC	FGTHCAA	ADAVAAE	ETDNPTAGGS
	70	80	90	100	110	120
a958.pep	LFCSNES	GS	SPERTEA	AVQSGE	ASIPEDY	TRIVADRME
	70	80	90	100	110	120
m958	LFCSNES	GS	SPERTEA	AVQSGE	ASIPEDY	TRIVADRME
	130	140	150	160	170	180
a958.pep	NADWADY	DQSGD	VTAGDR	FALQD	GT	LIRGETLT
	130	140	150	160	170	180
m958	NADWADY	DQSGD	VTAGDR	FALQD	GT	LIRGETLT
	190	200	210	220	230	240
a958.pep	SVSR	TAEM	LGE	GHYKLT	TETQ	FNTCSAG
	190	200	210	220	230	240
m958	SVSR	TAEM	LGE	GHYKLT	TETQ	FNTCSAG
	250	260	270	280	290	300
a958.pep	IFYTP	WADF	PLD	GNRKS	G	LLVPSLS
	250	260	270	280	290	300
m958	IFYTP	WADF	PLD	GNRKS	G	LLVPSLS
	310	320	330	340	350	360
a958.pep	FDGQ	VRYLR	PDYAG	QSDLT	WLP	HDKKSG
	310	320	330	340	350	360
m958	FDGQ	VRYLR	PDYAG	QSDLT	WLP	HDKKSG
	370	380	390	400	410	420
a958.pep	YYRDF	YGNKE	IAGNV	NLNRR	VWLDY	GGRAAG
	370	380	390	400	410	420
m958	YYRDF	YGNKE	IAGNV	NLNRR	VWLDY	GGRAAG
	430	440	450	460	470	480
a958.pep	PRLS	ADWR	KNTG	RAQIG	VSAQ	FTRF
	430	440	450	460	470	480
m958	PRLS	ADWR	KNTG	RAQIG	VSAQ	FTRF
	490	500	510	520	530	540
a958.pep	ATYY	SLNRF	GSQ	EARRV	SR	TLPIV
	490	500	510	520	530	540
m958	ATYY	SLNRF	GSQ	EARRV	SR	TLPIV

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	490	500	510	520	530	540
a958.pep	550	560	570	580	590	600
	QNDLPNFDSESSFGYGQLFRENLYYGNDRIANTANSLSAAVQSRILDGATGEERFRAGIG					
m958	QNDLPNFDSESSFGYGQLFRENLYYGNDRIANTANSLSAAVQSRILDGATGEERFRAGIG					
	550	560	570	580	590	600
a958.pep	610	620	630	640	650	660
	QKFYFKNDVAVMLDGSVGKKPRSRSDWVAFASGIGSRFILDSSIHYNQHEKRAENYAVGA					
m958	QKFYFKDDAVMLDGSVGKKPRSRSDWVAFASGIGSRFILDSSIHYNQHEKRAENYAVGA					
	610	620	630	640	650	660
a958.pep	670	680	690	700	710	720
	SYRPAQGVNLNARYKYGRNEKIYLSKSDGSYFYDKLSQDLDSAQWPLTRNLSAVVRNYGF					
m958	SYRPAQGVNLNARYKYGRNEKIYLSKSDGSYFYDKLSQDLDSAQWPLTRNLSAVVRNYGF					
	670	680	690	700	710	720
a958.pep	730	740	750	760	770	780
	EAKKPIEVLAGAEYKSSCGCWGAGVYAQRVVTGENTYKNAVFVSLQLKDLSSVGRNPADR					
m958	EAKKPIEVLAGAEYKSSCGCWGAGVYAQRVVTGENTYKNAVFVSLQLKDLSSVGRNPADR					
	730	740	750	760	770	780
a958.pep	790	800				
	MDVAVPGYI PAHSLSAGRNRKPX					
m958	MDVAVPGYI PAHSLSAGRNRKP					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2935>:

g959.seq

```

1  ATGAACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51  CATTTCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCGCAAGCCG AAAAAGCCGC TTGGCGCGT GTCGGCGGCA AAATCACCAG
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2936; ORF 959.ng>:

g959.pep

```

1  MNIKHLLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR
51  AQAEKAARAR VGGKITDIDL EHDDGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2937>:

m959.seq

```

1  ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51  CATTTCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCGCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCAG
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2938; ORF 959>:

m959.pep

```

1  MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 959 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. gonorrhoeae*

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m959/g959 95.4% identity in 108 aa overlap

	10	20	30	40	50	60
m959.pep	MN	NI	KH	LL	LT	SA
g959	MN	NI	KH	LL	LT	SA
	10	20	30	40	50	60
	70	80	90	100	109	
m959.pep	V	G	G	K	I	D
g959	V	G	G	K	I	D
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2939>:

a959.seq

1	AT	GA	AA	CT	TCA	AAC	GC	CT	TCT	CTT	GA	CC	GC	CC	GCC	GC	AA	CC	G	CAC	T	G	A	T	G	G	G		
51	CAT	TT	CC	GC	CC	CC	GC	CA	CT	CG	CCC	ACC	AC	GA	CGG	AC	AC	GC	GC	GAT	G	A	C	G	A	C	C		
101	AC	GG	AC	AC	GC	CG	CA	CA	CC	AA	CAC	AG	CA	AA	AC	AAG	AC	AA	AA	T	CAT	C	A	G	C	C	C	C	
151	G	C	C	A	A	G	C	A	G	C	G	T	T	G	G	C	G	C	G	T	G	T	C	G	G	C	G	C	A
201	CAT	C	G	A	T	C	T	C		GA	C	A	C	A	G	A	C	A		AC	G	G	C	C	G	T	C	C	
251	T	C	A	A	A	A	C	G	G	A	C	A	G	A	A	T	A	C		AA	A	G	T	C	G	T	T	G	
301	G	T	G	A	T	T	C	C	T	C	C	C	G	C	G	C	G	A		C	G	A	C	T	G	A			

This corresponds to the amino acid sequence <SEQ ID 2940; ORF 959.a>:

a959.pep

1	MN	FK	RL	LL	TA	AAT	AL	MG	IS	A	PAL	AH	HD	GH	G	DD	DH	GH	AA	HQ	HS	KQ	D	K	I	I	S	R
51	AQ	AE	KA	AL	AR	V	G	G	K	I	D	I	D	L		E	H	D	N	G	R	P	H	Y	D			
101	V	I	S	S	R	R	D	D	*																			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 959 shows 94.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. meningitidis*

a959/m959 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a959.pep	MN	FK	RL	LL	TA	AA
m959	MN	FK	RL	LL	TA	AA
	10	20	30	40	50	60
	70	80	90	100	109	
a959.pep	V	G	G	K	I	D
m959	V	G	G	K	I	D
	70	80	90	100		

g960.seq not found yet

g960.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2941>:

m960.seq

1	AT	G	C	A	A	G	T	A	A	A	T	A	T	C	A	G	A	T		T	C	C	T	G	T	A	T	G
51	T	A	A	G	C	C	C	C	C	T	T	G	T	T	G	A	A	G		C	T	C	G	C	G	G	C	T
101	C	C	G	T	T	G	T	C	C	C	A	A	G	C	T	C	T		G	C	T	C	C	G	C	G	C	
151	A	A	A	G	G	C	A	A	T	C	G	A	A	A	C	C	G	A	A	A	T	C	G	A	A	A	G	
201	T	G	C	T	A	T	C	T	G	A	A	C	A	G	C	T	C		A	A	A	C	G	T	C	A	A	
251	T	G	C	A	A	C	T	G	G	A	A	A	A	A	A	A	A		A	A	C	C	T	C	A	A	G	
301	G	C	C	G	T	G	C	A	G	C	G	A	T	A	T	C	G		G	C	T	G	G	C	T	G	T	
351	G	G	A	C	T	C	G	A		G	C	C	G	C	A	T	A		C	G	C	A	G	C	C	G	C	
401	A	T	G	C	C	G	C	T		T	G	C	T	C	A	C	T		C	G	T	T	C	T	C	A	G	
451	A	A	T	A	A	G	G	C		A	T	G	T	C	G	C	A		A	A	C	C	T	C	A	A	G	
501	G	G	T	A	A	A	A	A		C	T	G	T	T	G	T	A		C	G	C	G	C	A	A	A	A	

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551 TCGGTGCCCTC TTCCCTTGCC ACTTGGAGCG AAACCCCTTG GGTAACAAC
601 CTCACCGTTA ACCTGGCCAA TGGGGCAGT GCCCGCTGA TCAACACCGC
651 TGTTAACGGC GGCAGCCTGA AAGACAATCT GGAGGCAAT ATCCTGGCGG
701 CATTGGTGAA TACCGCGCAT GGGGAGGCGG CGAGTAAGAT CAAAGGACTG
751 GATCAGCACT ATGTCGCCCA CAAATCGCT CATGCCGTAG CGGGCTGTGC
801 GGCTGCAGCG CGGAATAAGG CCAATGTCA GGACGGCGCG ATCGGTGCGG
851 CTGTGGGTGA GATTGTGCGG GAGGCTTTGG TAAAAATAC CGATTTTAGC
901 GATATGACCC CGGAACAATT AGATCTGGAA GTTAAGAAA TTACCGCCTA
951 TGCCAACTTT GCGGCAGGTA CAGTTGCAGG CGTAACGGGA GGAGATGTCA
1001 ATACTGCTCT ACAACCCGCA CAAAACGCGG TAGAAAAATA TCGCGTTAAA
1051 GCTGTGTGTA CTGCTGCAAA AGTGGTTTAT AAGGTAGCCA GAAAAGGATT
1101 AAAAAACGGG AAAATCAACG TTAGAGATT AAAACAGACG TTGAAAGACG
1151 AAGGTTATAA TTTAGCCGAC AACCTGACCA CCTTATTGGA CGAAACATTG
1201 GATTGGAACG ATGCCAAAGC CGTTATTGAT ATTGTCGTCG GAACAGAGCT
1251 GAAATCGCGCT AATAAAGGGG AAGCGGCACA AAAGGTCAAG GAAGTTTATG
1301 AAAAAAATCG TCCTTATATC CCTAATAAAG GTGCTGTACC GAATATGAGT
1351 ACATACATGA AAAATAATCC TTTTGAAAAA CAGCTGGCTC AAATTCAGA
1401 AAAGACAACG CTTCCGACGC AGCAAGGACA GTCTGTCTCT TTGGTAAAAA
1451 GAAACCAAGC GTTATTAAAA ACCGGTGATA GGTTTATTT AGATGGCCAA
1501 CATAAAATC ATTTAGAGGT TTTTGATAAA AATGGGAAC TTAAGTTTGT
1551 TCTAAATATG GATGGTTCGC TTAACCAAT GAAAACTGGG GCAGCAAAAA
1601 GTCGTAAATT AAACCTAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2942; ORF 960>:

```

m960.pep
1  MQVNIQIPCM LYRRGSVKPP LFEAPRLIPS FTDPVVPKLS APGGYIVDIP
51  KGNLKEIEK LAKQPEYAYL KQLOVAKNVN WNQVQLAYDK WDKQEGLTR
101 AGAAIIALAV TVVTAGAGVG AALGLNGAAA AAADAASFSL ASQASVSLIN
151 NKGDVGGPKL ELGRSRTVKN LVVAATAGV SNKLGAASSL TWSETPWVNN
201 LNVNLANAGS AALINTAVNG GSKDNLEAN ILAALVNTAH GEAAASKIKGL
251 DQHYVAHKIA HAVAGCAAAA ANKGKCDJGA IGAAVGEIVG EALVKNTDFS
301 DMTPEQLDLE VKKITAYAKL AAGTVASVTG GDVNTAAQTA QNAVENNAVK
351 AVVTAAKVYV KVARGLKNG KINVRDLKQT LKDEGYNLAD NLTLFDUETL
401 DWNDKAVID IVVGTELNRA NKGEAAQVKV EVLEKNRPYI PNKGAVPNMS
451 TYMKNNPFCK QLAQISEKTT LPTQQGQSVF LVKRNQGLLK TGDRFYLDGQ
501 HKNHLEVFCK NGNFKFVLENM DGSLNQMKTG AAKGRKLNK *

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a960.seq not found yet

a960.pep not found yet

g961.seq not found yet

g961.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2943>:

```

m961.seq
1  ATGAGCATGA AACACTTTCC AGCCAAAGTA CTGACCACAG CCATCCTTGC
51  CACTTTCTGT AGCGGCGCAC TGGCAGCCAC AAGCGACGAC GATGTTAAAA
101 AAGCTGCCAC TGTGGCCATT GTTGCTGCCT ACAACAATGG CCAAGAAATC
151 AACGGTTTCA AAGCTGGAGA GACCATCTAC GACATTGGTG AAGACGGCAC
201 AATTACCCAA AAAGACGCAA CTGCAGCCGA TGTGAAGCC GACGACTTIA
251 AAGGTCTGGG TCTGAAAAAA GTCGTGAATA ACCTGACCAA AACCGTCAAT
301 GAAPACAAAC AAAACGTCGA TGCCAAAGTA AAAGCTGCAG AATCTGAAAT
351 AGAPAAAGTT ACAACCAAGT TAGCAGACAC TGATGCCGCT TTAGCAGATA
401 CTGATGCCGC TCTGGATGAA ACCACCAACG CCTTGAATAA ATTGGGAGAA
451 AATAATAACGA CATTGTCTGA AGAGACTAAG ACAAAATATCG TAAAAATTGA
501 TGAPAAATTA GAAGCCGTGG CTGATACCGT CGACAAGCAT GCCGAAGCAT
551 TCAACGATAT CGCCGATTCA TTGGATGAAA CCAACACTAA GGCAGACGAA
601 GCCGTCAAAA CCGCCAATGA AGCCAAACAG ACGGCCGAAG AAACCAACAA
651 AAACGTCGAT GCCAAGTAA AAGCTGCAGA AACTGCAGCA GGCAAGCCG
701 AAGCTGCCGC TGGCACAGCT AATACTGCAG CCGACAAGGC CGAAGCTGTC
751 GCTGCAAAAG TTACCGACAT CAAAGCTGAT ATCGCTACGA ACAAGCTGA
801 TATTGCTAAA AACTCAGCAC GCATCGACAG CTTGGACAAA AACGTAGCTA
851 ATCTGCGCAA AGAAACCCGC CAAGGCCTTG CAGAACAAGC CGCGCTCTCC
901 GGCCTGTTCC AACCTTACAA CGTGGGTCGG TTCAATGTAA CGGCTGCAGT
951 CGGCGGCTAC AAATCCGAAT CGGCAGTCGC CATCGGTACC GGCTTCCGCT
1001 TTACCGAAAA CTTTCCCGCC AAAGCAGGCG TGGCAGTCGG CACTTCGTCC
1051 GGTCTCTCCG CAGCCTACCA TGTCGGCGTC AATTACGAGT GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 2944>:

```

m961.pep
1  MSMKHPEPAKV LTTAILATFC SGALAAATSDD DVKKAATVAI VAAVNNQGEI

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```

51  NGFKAGETIY DIGEDGTITQ KDATAADVEA DDFKGLGLKK VVTNLTKTVN
101 ENKQNVDAKV KAAESEIEKL TTKLADTDAA LADTDAALDE TTNALNKLGE
151 NITTFAEETK TNIVKIDEKL EAVADTVDKH AEA FNDIADS LDETNTKADE
201 AVKTANEAKQ TAEETKQNV D AKV KAAETAA GKAEAAA GTA NTAADKAEAV
251 AAKVTDIKAD IATNKADIAK NSARIDSLDK NVANLRKETR OGLAEQAAALS
301 GLFQPINVGR FNVTAAVGGY KSESAVAIGT GFRFTENFAA KAGVAVGTS
351 GSSAAYHVG V NYEW*

```

a961.seq not found yet
a961.pep not found yet

g972.seq not found yet
g972.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2945>:

```

m972.seq
1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
151 GTTGATTGGA TTTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA
251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTTCG GARGTGACGC CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATT CATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTGTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCAGCATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTGT TCGTGTATAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAGAA AGCAAATGGG TAAGGTTTCA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTAATAA ATCAGGTTTC
801 GTATTCTGT GGAGCTTTTC CAATTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA AGCTTAATT AACTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTCA
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAGGCGAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTATT CATGAACAGC CGGATATTGA
1101 TTTGAAATG GAACCTGATG AATTGGGGGT TATTGCTTTT AAAAATCTG
1151 ACAAATTCGA TAGGAAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTAAAGT AAAGTTTATC ATCAAATGT
1251 AGATTATGAT TATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2946; ORF 972>:

```

m972.pep
1  LTNRGGAKLK TXSKSSERMS EVEYFSHFIS DGKGLLEIP QRRGKQDGVF
51  VDWISFTFHE DTLLKVSGCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFQXQRTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RTITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNORPKSE
201 TIGTAWRNE DSGKTFYVGR KKNRSFVRVY EKGRQLGDKE SKWVRFEIQF
251 NYGDIPIPLD ILINQGSYFC GAFFICRKFK NMPVPERFDQ RKXKLNLTFE
301 HKLHYAKNAV GKLNVFMIEM GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLSPDYDVE
401 KERKQYEYLS KVIYHONVDYD YF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2947>:

```

a972.seq
1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CGGGGTTTTT
151 GTTGATTGGA TTTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA

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251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATCTTGA
351 TTATGGAGAG GTGCATTTTC GAGGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTGT TCGTGTTTAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAGAA AGCAAATGGG TAAGGTTCTGA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA CGCTTAATTT AACTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAAACCTGG TCAATTTTCA
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAAATT GAACCTGATG AATTGGGGGT TATTGCTTTT AAAAAATCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAATGT
1251 AGATTATGAT TATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2948; ORF 972.a>:

```

a972.pep
1  LTNRGGAKLK TNSKSSERMS EVEYFSHFIS DGKKGKLEIP QRRGKQDGVF
51  VDWFSTFHE DTLKVSVCPLFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VFHGGQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RTITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TGTAWRNED GSGKTFYVGR KKNRFRVRYV EKGRLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFICKRKF NMPVPERFDQ RKKTLLNLTFE
301 HKLHYAKNAV GKLVNFIEM GFDNSEIVES LKADSGFPG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKYQEYLS KVIHQNVDDYD YF*

```

m972/a972 99.3% identity in 422 aa overlap

m972.pep	10	20	30	40	50	60
a972	10	20	30	40	50	60
m972.pep	70	80	90	100	110	120
a972	70	80	90	100	110	120
m972.pep	130	140	150	160	170	180
a972	130	140	150	160	170	180
m972.pep	190	200	210	220	230	240
a972	190	200	210	220	230	240
m972.pep	250	260	270	280	290	300
a972	250	260	270	280	290	300

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	310	320	330	340	350	360
m972.pep	HKLHYAKNAVGKLVNEMIEMGFNDSEIVESLKADSGFPKGLEPEKYALEMLRDGLKHGFI					
a972	HKLHYAKNAVGKLVNEMIEMGFNDSEIVESLKADSGFPKGLEPEKYALEMLRDGLKHGFI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m972.pep	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPDYDVEKERKYQEYLSKVYHQNVVDYD					
a972	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPDYDVEKERKYQEYLSKVYHQNVVDYD					
	370	380	390	400	410	420
m972.pep	YFX					
a972	YFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2949>:

g973.seq

```

1  ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCG
51  actCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA ACAGGAAGTT TTTGATGCCG ACACACTGAC CCGCTGGAA
151 AAAGTATTGG ACTTTGCCGA GCTGGAAGTG CGCGATGCGA TGATTACGCG
201 CAGCCGCATG AACGTATTGA AAGAAAACGA CAGCATCGAA CGCATACCG
251 CCTACGTCAT CGATACCGCC CATTCGCGCT TCCCGTCAT CGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTCAACCCC GAGCAGTTCC ACCTGAAATC CGTCTTGCGC CTGCGCGTTT
401 TCGTGCCCGA AGGCAAATCT TTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
501 TTTGGTCACC TTTGAAGACA TCATCGAGCa aatcgtcggt gacaTCGAAG
551 ACGAGTTTGA CGAAGACGAA AGCGccgacg acatCCACTC cgTTTccgCC
601 GAACGCTGGC GCATCCacgc ggctaCCGAA ATCGAAGaca TCAACGCCTT
651 TTTCCGTACG GAatacggca gcgaaagaagc cgacaccatc ggcggtTGG
701 TCATTCAGGA ATTGGGACAC CTGCCCGTGC GCGGCGAAAA AGTCCTTatc
751 ggcgGTTTGC agttcaccgt CGCCCGCGCC GACAACCGCC GCCTGCACAC
801 GCTGATGGCG ACCCGCGTGA AGTAAGCAGA GCCTGCCcgc accgcggttT
851 CTGCacAGTT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2950; ORF 973.ng>:

g973.pep

```

1  MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLTRLE
51  KVLDFAELEV RDAITRSM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFPN EQPHLKSIVLR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGLVF FEDIIEQIVG DIEDEFDEDE SADDIHSVSA
201 ERWRIHAATE IEDINAFPGT EYGSEEDTI GGLVIQELGH LPVRGEKVL
251 GGLQFTVARA DNRRHLTLMA TRVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2951>:

m973.seq

```

1  ATGGACGGCG CACAACCGAA AACGAATTTT TTTGAACGCC TGATTGCCCG
51  ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA GCAGGAAGTT TTTGATGCCG ATACGCTTTT AAGATTGGAA
151 AAAGTCTCTG ATTTTCCGA TTTGGAAGTG CGCGACGCGA TGATTACGCG
201 CAGCCGTATG AACGTTTTAA AAGAAAACGA CAGCATCGAG CGCATACCG
251 CCTACGTTAT CGATACCGCC CATTCGCGCT TCCCGTCAT CGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTTAACCCC GAGCAGTTCC ACCTCAAATC CATTCTCCGC CCCGCCGTCT
401 TCGTCCCGCA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCGAT TGTATCGAC GAATACGGCG GCACATCCGG
501 CTTGGTCACC TTTGAAGACA TCATCGAGCA AATCGTCGGC GAAATCGAAG
551 ACGAGTTTGA CGAAGACGAT AGCGCCGACA ATATCCATGC CGTTTCTTcm
601 GaACGcTGGC GCATCCATGC AGTACCAGAA ATCGAAGACA TCAACACCTT

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651 CTTCCGGCAGC GAATACAGCA kCGAAGAAGC CGACACCATT GCGCGCCTGG
 701 TCATTCAAGA GTTGGGACAT CTGCCCGTGC GCGCGGAAAA AGTCCTTATC
 751 GCGCGTTTGC AGTTCACCGT CGCACGCGCC GACAACCGCC GCCTGCATAC
 801 GCTGATGGCG ACCCGCGTGA AGTAA

This corresponds to the amino acid sequence <SEQ ID 2952; ORF 973>:

m973.pep

1 MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLRLLE
 51 KVLDFSDLEV RDAMITSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
 101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
 151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG EIEDEFDEDD SADNIHAVSS
 201 ERWRIHAATE IEDINTFFGT EYSXEEADTI GGLVIQELGH LPVRGEKVLIT
 251 GGLQFTVARA DNRRLHTLMA TRVK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 973 shows 95.6% identity over a 274 aa overlap with a predicted ORF (ORF 973.ng) from *N. gonorrhoeae*:

m973/g973

	10	20	30	40	50	60
m973.pep	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLLEKVLDFSDLEV					
g973	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLLEKVLDFAELEV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m973.pep	RDAMITSRMNVLKENDSIE RITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
g973	RDAMITSRMNVLKENDSIE RITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m973.pep	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
g973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m973.pep	EIEDEFDEDD SADNIHAVSS ERWRIHAATE IEDINTFFGT EYSXEEADTI GGLVIQELGH					
	:					
g973	DIEDEFDEDESADDIHSVAERWRIHAATE IEDINAFFGT EYGESEADTI GGLVIQELGH					
	190	200	210	220	230	240
	250	260	270			
m973.pep	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
g973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2953>:

a973.seq

1 ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCG
 51 ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTGACC CTGTTGCCGC
 101 AAGCGCACGA ACAGGAAGTA TTTGATGCGG ATACGCTTTT AAGATTGGAA
 151 AAAGTCCTCG ATTTTCTGA TTTGGAAGTG CGGACGCGA TGATTACGCG
 201 CAGCCGTATG AACGTTTAA AAGAAAACGA CAGCATCGAA CGCATCACC
 251 CCTACGTTAT CGATACCGCC CATTGCGGCT TCCCCGTCAT CGGTGAAGAC
 301 AAAGACGAAG TTTTGGGTAT TTGACGCGC AAAGACCTGC TCAAATATAT
 351 GTTCAACCCC GAGCAGTTC ACCTCAAATC GATATTGCGC CCTGCCGTCT
 401 TCGTCCCGA AGGCAAAATCG CTGACCGCCC TTTTAAAAGA STTCCGCGAA
 451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
 501 TTTGGTAACT TTTGAAGACA TCATCGAGCA AATCGTCGGC GACATCGAAG
 551 ATGAGTTTGA CGAAGACGAA AGCGCGGACA ACATCCACGC CGTTTCCGCG

1382

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601 GAACGCTGGC GCATCCACGC GGCTACCGAA ATCGAAGACA TCAACGCCTT
651 TTTCGGCACG GAATACAGCA GCGAAGAAGC CGACACCATC GGCGGCCTGG
701 TCATTCAGGA ATTGGGACAC CTGCCCCTGC GCGGGCAAAA AGTCCTTATC
751 GGCGGTTTGC AGTTCACCGT CGCCCGCGCC GACAACCGCC GCCTGCATAC
801 GCTGATGGCG ACCCGCGTGA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2954; ORF 973.a>:

```

a973.pep
1 MDGAQPKTNF FERLIARLAR EPDSAEDVLT LLRQAHEQEV FDADTLRLLE
51 KVLDFSDLEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGLVF FEDIIEQIVG DIEDEFDEDE SADNIHAVSA
201 ERWRIHAATE IEDINAFFGT EYSSEEADTI GGLVIQELGH LPVRGEKVL I
251 GGLQFTVARA DNRRLHTLMA TRVK*

```

m973/a973 97.8% identity in 274 aa overlap

	10	20	30	40	50	60
m973.pep	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLLEKVLDFSDLEV					
a973	MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLRLLEKVLDFSDLEV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m973.pep	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVILGILHAKDLLKYMFP					
a973	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVILGILHAKDLLKYMFP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m973.pep	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
a973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m973.pep	EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH					
	:					
a973	DIEDEFDEDESADNIHAVSAERWRIHAATEIEDINAFFGTEYSSEEADTIGGLVIQELGH					
	190	200	210	220	230	240
	250	260	270			
m973.pep	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
a973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2955>:

```

g981.seq
1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCAC TCGCGCTGTC
51 TGCCTGCGGC GGTCAAGGCA AAGATGCCGC CGCGCCTGCC GCCAACCCCG
101 GCAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GACGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TAAAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCGCCTTG AACAAACGGC ATGCGGACGT TGTGATGTCG
301 GCGTAACCA TTACCGACGA CCGCAAACAG TCTATGGATT TCAGCGACCC
351 GTATTTTGAA ATCACCCAAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTCTCTCCGA AGATTTGAAA AAGATGAACA AAGTCGGCGT GGTACCGGC
451 CACACGGGCG ATTCTCCGT TTCCAAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTCGAAAACG TCCCCCTGAT TATCAAAGAA CTGGAACACG
551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTATCGC CAATTATGTG
601 AAAACAACCC CGGCCAAAGG AATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATCTACG CCAATATTTT TGCCAAAGAG GCGGACAGG CTGCGAAATA
801 A

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1383

This corresponds to the amino acid sequence <SEQ ID 2956; ORF 981.ng>:

g981.pep

```
1 MKKWIAAALA CSALALSACG GQGKDAAAPA ANPGKVYRVA SNAEFAPFES
51 LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS
101 GVTITDDRKO SMDFSDPYFE ITQVVLVPGK KKVSSSEDLK KMNKVGVTG
151 HTGDFSVSKL LGNDNPKIAR FENVPLIIKE LENGGLDSVV SDSAVIANV
201 KNNPAKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE GQAAK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2957>:

m981.seq

```
1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCGC TCGCGCTGTC
51 TGCCTGCGGC GGTCAGGGCA AAGA7ACCGC CGCGCTGCC GCCAACCCCG
101 ACAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAATAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCGCTTTA AACACGGCG ATGCGGACGT TGTGATGTCG
301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACCAGG TCGTCTCTGT TCCGAAAGGC AAAAAAGTAT
401 CTCTCTCCGA AGATTTGAAA AACATGAACA AAGTCGGCGT GGTACCCGGC
451 TACACGGGGC ATTTCTCCGT ATCCAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTTGAAAACG TTCCCTGAT TATCAAAGAA CTGGAACG
551 GCGGCTTGA TTCCGTGGTC AGCGACAGCG CGGTATCGC CAATTATGTG
601 AAAAAAATC CGGCCAAAG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATTACG CCAATATATT TGCAAAAGAA GACGGACAGG CCGCAAAATA
801 A
```

This corresponds to the amino acid sequence <SEQ ID 2958; ORF 981>:

m981.pep

```
1 MKKWIAAALA CSALALSACG GQGKDTAAPA ANPDKVYRVA SNAEFAPFES
51 LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS
101 GVTITDDRKO SMDFSDPYFE ITQVVLVPGK KKVSSSEDLK KMNKVGVTG
151 YTGDFSVSKL LGNDNPKIAR FENVPLIIKE LENGGLDSVV SDSAVIANV
201 KNNPAKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE DGAAK*
```

m981/g981 98.1% identity in 266 aa overlap

	10	20	30	40	50	60
981.pep	MKKWIAAALACSALALSACGGQGKDTAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF					
g981	MKKWIAAALACSALALSACGGQGKDAAPAAANPGKVYRVASNAEFAPFESLDSKGNVEGF					
	10	20	30	40	50	60
981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKSMDFSDPYFE					
g981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKSMDFSDPYFE					
	70	80	90	100	110	120
981.pep	ITQVVLVPGKKVSSSEDLKMNKVGVTGTGDFSVSKLLGNDNPKIARFENVPLIIKE					
g981	ITQVVLVPGKKVSSSEDLKMNKVGVTGTGDFSVSKLLGNDNPKIARFENVPLIIKE					
	130	140	150	160	170	180
981.pep	LENGGLDSVVSDSAVIANVYKNNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
g981	LENGGLDSVVSDSAVIANVYKNNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
	190	200	210	220	230	240
981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
g981	EKVRESGEYDKIYAKYFAKEGGQAAKX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2959>:

```
a981.seq
  1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCCGCGC TCGCGCTGTC
51 TGCCTGCGGC GGTGAGGGTA AAGATGCCGC CGCGCCCGCC GCAAAATCCCG
101 ACAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTCCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCGCCTTG AACACGCGC ATGCGGACGT TGTGATGTCG
301 GGCGTAACCA TTACCGACGA CCGCAAACAG TCTATGGA CTAGCGACCC
351 GTATTTTGAA ATCACCACAG TCGTCTCGT TCCGAAAGGC AAAAAAATAT
401 CTTCTTCCGA AGATTGAAA AACATGAACA AAGTCGGCGT GGTAAACCGGC
451 TACACGGGCG ATTTCTCCGT ATCCAAACTC TTGGGCAACG ACAACCCGAA
501 AATCGCGCGC TTTGAAAACG TTCCCTGAT TATCAAAGAA CTGGAAAACG
551 CGCGCTTGGA TTCCGTGGTC AGCGACAGCG CAGTCATCGC CAATTATGTG
601 AAAACAATC CGACCAAAGG GATGGAATTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG AAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAAATCTACG CCAATATTT TGCAAAAGAA GACGGACAGG CCGCAAAATA
801 A
```

This corresponds to the amino acid sequence <SEQ ID 2960; ORF 981.a>:

```
a981.pep
  1 MKKWIAAALA CSALALSACG GQGKDAAAPA ANPDKVYRVA SNAEFAPFES
51 LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWSLFPAL NNGDADVMS
101 GVTITDDRKQ SMDFSDPYFE ITQVVLVPKG KKISSSEDLK NMNKGVVVTG
151 YTGDFSUSKL LGNDNPKIAR FENVPLIIKE LENGGLDSV SVDSAVIANYV
201 KNNPTKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL KKVRESGEYD
251 KIIYAKYFAKE DGQAAK*
```

m981/a981 98.5% identity in 266 aa overlap

	10	20	30	40	50	60
m981.pep	MKKWIAAALACSALALSACGGQGKDTA	APANPDKVYRVASNAEFAPFESLDSKGNVEGF				
a981	MKKWIAAALACSALALSACGGQGKDA	APANPDKVYRVASNAEFAPFESLDSKGNVEGF				
	10	20	30	40	50	60
	70	80	90	100	110	120
m981.pep	DVDLMNAMAKAGNFKIEFKHQ	PWSLFPALNNGDADVMSGVTITDDRKQ	SMDFSDPYFE			
a981	DVDLMNAMAKAGNFKIEFKHQ	PWSLFPALNNGDADVMSGVTITDDRKQ	SMDFSDPYFE			
	70	80	90	100	110	120
	130	140	150	160	170	180
m981.pep	ITQVVLVPKGKVVSSSEDLKNMNKVG	VVTGYTGDFSUSKLLGNDNPKIAR	FENVPLIIKE			
a981	ITQVVLVPKGKVISSSEDLKNMNKVG	VVTGYTGDFSUSKLLGNDNPKIAR	FENVPLIIKE			
	130	140	150	160	170	180
	190	200	210	220	230	240
m981.pep	LENGGLDSVSVDSAVIANYVKNNPAK	GMDFVTLPDFTTEHYGIAVRKGDE	ATVKMLNDAL			
a981	LENGGLDSVSVDSAVIANYVKNNPTK	GMDFVTLPDFTTEHYGIAVRKGDE	ATVKMLNDAL			
	190	200	210	220	230	240
	250	260				
m981.pep	EKVRESGEYDKIIYAKYFAKEDG	QAAKX				
a981	KKVRESGEYDKIIYAKYFAKEDG	QAAKX				
	250	260				

1385

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2961>:

```

g982.seq
1   atcgcacgcg   aaaaccttcg   attcgacaat   cgattcctcc   aaaaaatggt
51  caacggcgTg   aatatatttcg   cgcccgCga   ttgggtagcC   ttgGGcgCgCA
101 AAGGCCGCAA   CGTGGTGGT   GACCGCGCTT   TCGGCGGCC   GCACATCACC
151 AAAGACGGCG   TAACCGTCGC   CAAAGAAATC   GAACTGAAAG   ACAAGTTTGA
201 AAATATGGGC   GCGCAAATGG   TAAAAGAAGT   CGCGTCCAAA   ACCAAcgaCg
251 tagCCGgcga   cggtagcact   accgCCACCG   TATTGGCACA   ATCCATCGTT
301 GCCGAaggcA   TGAATACGT   TACCGCCGGC   ATGAACCCGA   CCGATCTGAA
351 ACGCGGCATC   GACAAAGccg   ttgCCGCTt   ggttgAAGAg   cTGAAAAACA
401 TCGCCAAACC   TTGCGATACT   TCCAAAGAAA   TCGCCCAAGT   CGGCTCGATT
451 TCCGCCAACT   CCGACGAACA   AGtcgGCGCG   ATTATCGCCG   AAGCGATGGA
501 AAAAGTCGGC   AAAGAAGgcg   tgattacCGT   TGAAGACGGC   AAATCTTTGG
551 AAAACGAGCT   GGACGTGGT   GAAGGTATGC   AGTTCGACCG   CGGCTACCTG
601 TCCCTTACT   TTATCAACGA   CGCGAAAAA   CAAATCGCCG   GTCTGGACAA
651 TCCGTTTGT   TTGCTGTTCG   ACAAAAAAT   CAGCAACATC   CGCGACCTG
701 TGCCCGTGT   GGAACAAGTG   GCGAAAGCCA   GCCGCCGCT   GTTGATTATC
751 GCTGAAGACG   TAGAAGGCGA   AGCCTTGGCG   ACTTTGGTCG   TGAACAACAT
801 CCGCGGCATC   CTGAAAACCG   TTGCCGTCAA   AGCccccggc   tTCGGcGACC
851 GCCGCAAAGC   GATgctgcaa   gaCATCGCCA   TCCTGACcgg   cggcgTagtG
901 ATTtccGAAG   Aagtccgcct   GTCTTGGAA   AAAgcgactT   TGgacgaCTT
951 Gggtcaaacc   aaACGcatCG   AAATCGGtga   agaaaacact   ACCGTcATcg
1001 acgGCTTCGG   CGACGcagcC   CAAAtcgaag   cgCGTGTTCG   CGAAATCCGC
1051 CAACAAATCG   AAACCGCGAC   CAGCGATTAC   GACAAAGAAA   AACTGCAAGA
1101 GCGCGTTGCC   AAATGGCAG   GAGGCGTGGC   AGTGATCAA   STCGGCGCGG
1151 CGACCGAAGT   CGAAATGAAA   GAGAAAAAG   ACCGCGTGA   AGACGCGCTG
1201 CACGCTACCC   GCGCAGCCGT   TGAAGAAGGC   GTGGTTGCAG   SCGGCGGCGT
1251 AGCCCTGTTG   CGCGCCCGTG   CCGCTTTGGA   AAACCTGCAC   ACCGGCAATG
1301 CCGACCAAGA   CGCAGGCGTA   CAAATCGTAT   TCGCGCGCGT   TGAGTCTCCG
1351 CTGCGCCAAA   TCGTTGCCAA   CGCAGGCGGA   GAACCCAGCG   TGGTGGTGAA
1401 CAAAGTGTG   GAAGGCAAAG   GCAactacgG   TTACAACGCa   ggctcCGGCG
1451 AATACGgcga   CATGATCGGA   ATGGGCGTAC   TCGACCCCTG   CAAAGTAACC
1501 CGTTCCGCGC   TGCAACACGC   CGGTCTATc   GCCGGTCTGA   TGCTGACGAC
1551 CGACTGCATG   ATTGCCGAAA   TCCCTGAAGA   AAAACCGGCT   STGCCCGATA
1601 TGGGGGAAT   GGGCGGTATG   GCGGCATGA   TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2962; ORF 982.ng>:

```

g982.pep
1   IASQNLRFDN   RFLQKMVNGV   NILPAADWVA   LGAKGRNVVV   DRAFGGPHIT
51  KDGVTVAKEI   ELKDKFENMG   AQMVKEVASK   TNDVAGDGTT   TATVLAQSIV
101 AEGMKYVTAG   MNPTDLKRG   DKAVAALVEE   LKNIAPCDT   SKEIAQVGS
151 SANSDEQVGA   IIAEAMEKVG   KEGVITVEDG   KSELELDVV   EGMQFDRGYL
201 SPYFINDAEK   QIAGLDNPFV   LFLDKKISNI   RDLLPVLEQV   AKASRPLLI
251 AEDVEGEALA   TLVVNNIRGI   LKTVAVKAPG   FGDRRKAMLQ   DIAILTGGVV
301 ISEEVGLSLE   KATLDDLQGT   KRIEIGEENT   TVIDGFGDAA   QIEARVAEIR
351 QQIETATSDY   DKEKLQERVA   KLAGGVAVIK   VGAATEVEMK   EKKDRVEDAL
401 HATRAAVEEG   VVAGGGVALL   RARAALNLH   TGNADQDAGV   QIVLRAVES
451 LRQIVANAGG   EPSVVVNKVL   EGKNGYGYNA   GSGEYDMIG   MGVLDPAKVT
501 RSLQHAASI   AGLMLTTDCM   IAEIPEEKPA   VPDMGGMGMM   GGMM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2963>:

```

m982.seq
1   ATGGCAGCAA   AAGACGTACA   GTTCGGCAAT   GAAGTCCGTC   AAAAAATGGT
51  AAACGGCGTG   AACATTCTGG   CAAACGCCGT   CCGCGTAACC   TTGGGCCCCA
101 AAGGTCGCAA   CETAAGTCGT   GACCGCGCAT   TCGGCGGCC   GCACATCACC
151 AAAGACGGCG   TAACCGTCGC   CAAAGAAATC   GAACTGAAAG   ACAAGTTTGA
201 AAATATGGGC   GCGCAAATGG   TAAAAGAAGT   TGCGTCCAAA   ACCAACGACG
251 TGGCAGGCGA   CCGTACGACT   ACCGCCACCG   TACTGGCGCA   ATCCATCGTT
301 GCCGAAGGTA   TGAATATGT   TACCGCAGGT   ATGAATCCGA   CCGACCTGAA
351 ACGGGGTATC   GATAAAGCCG   TCGCCGCTTT   GGTGACGAA   CTGAAAAACA
401 TCGCCAAACC   TTGCGACACT   TCTAAAGAAA   TCGCCCAAGT   CGGCTCTATT
451 TCCGCCAACT   CCGACGAACA   AGTCGGCGCG   ATTATCGCCG   AAGCGATGGA
501 AAAAGTCGGC   AAAGAAGGCG   TGATTACCGT   TGAAGACGGC   AAGTCTTTGG
551 AAAACGAGCT   GGACGTAGTT   GAAGGTATGC   AGTTCGACCG   CGGCTACCTG
601 TCTCCTTACT   TCATCAACGA   TCGCGAAAAA   CAAATCGCTG   CTTTGGACAA

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1386

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651  TCCGTTTGTA TTGTTGTTTCG ACAAAAAAAT CAGCAACATC CGCGACCTGC
701  TGCCTGTTTTT GGAACAAGTG GCAAAAGCCA GCCGTCCGCT GTTGATTATC
751  GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801  CCGAGGCATC CTGAAAACCG TTGCCGTCAA AGCCCTGGC TTCCGGCGACC
851  GCCGCAAAGC GATGTTGCAA GACATCGCCA TCCTGACCGG CGGCGTGGTG
901  ATTTCCGAAG AAGTCGGTCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951  GGGTCAAGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001 ACGGCTTTTG CGACGCAGCC CAAATCGAAG CGCGTGTGCG CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTGGCT AAATTGGCAG GCGGCGTGGC AGTCATCAAA GTCGGTGCCG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC CTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CGTGCCCGTG CTGCTTTGGA AAACCTGCAC ACCGCGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTCT TCGCGCGCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401 CAAAGTATTG GAAGGCAAAG GCAACTACGG TTACAACGCT GGCAGCGGCG
1451 AATACGGCGA TATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCTGCGC TGCAACACGC CGCATCTATC GCCGGCTTGA TGCTGACCAC
1551 TGATTGCATG ATCGCTGAAA TCCCCGAAGA CAAACCGGCT GTGCCTGATA
1601 TGGGCGGCAT GGGTGGTATG GCGGCGATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2964; ORF 982>:

```

m982.seq
  1  ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
 51  AAACGGCGTG AACATTCTGG CAAACGCCGT CCGCGTAACC TTGGGCCCCA
101  AAGGTCGCAA CGTAGTCGTT GACCGCGCAT TCGGCGGCCC GCACATCACC
151  AAAGACGGCG TAACCGTCGC CAAAGAAATC GAAGTAAAG ACAAGTTTGA
201  AAATATGGGC GCGCAAAATGG TGAAGAAGT TCGCTCCAAA ACCAACGACG
251  TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
301  GCCGAAGGTA TGAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
351  ACGCGGTATC GATAAAGCCG TCGCCGCTTT GGTTGACGAA CTGAAAAACA
401  TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451  TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCCG AAGCGATGGA
501  AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAGTCTTTGG
551  AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601  TCTCCTTACT TCATCAACGA TCGGGAAGAA CAAATCGCTG CTTTGGACAA
651  TCCGTTTGTA TTGTTGTTTCG ACAAAAAAAT CAGCAACATC CGCGACCTGC
701  TGCCTGTTTT GGAACAAGTG GCAAAAGCCA GCCGTCCGCT GTTGATTATC
751  GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801  CCGAGGCATC CTGAAAACCG TTGCCGTCAA AGCCCTGGC TTCCGGCGACC
851  GCCGCAAAGC GATGTTGCAA GACATCGCCA TCCTGACCGG CGGCGTGGTG
901  ATTTCCGAAG AAGTCGGTCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951  GGGTCAAGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001 ACGGCTTTTG CGACGCAGCC CAAATCGAAG CGCGTGTGCG CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTGGCT AAATTGGCAG GCGGCGTGGC AGTCATCAAA GTCGGTGCCG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CGTGCCCGTG CTGCTTTGGA AAACCTGCAC ACCGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTCT TCGCGCGCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401 CAAAGTATTG GAAGGCAAAG GCAACTACGG TTACAACGCT GGCAGCGGCG
1451 AATACGGCGA TATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCTGCGC TGCAACACGC CGCATCTATC GCCGGCTTGA TGCTGACCAC
1551 TGATTGCATG ATCGCTGAAA TCCCCGAAGA CAAACCGGCT GTGCCTGATA
1601 TGGGCGGCAT GGGTGGTATG GCGGCGATGA TGTA

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m982/g982 95.8% identity in 544 aa overlap

```

              10      20      30      40      50      60
m982.pep  MAAKDVQFGNEVRQKMNNGVNI LANAVRVTLGPKGRNVVVVDRAFGGPHITKDGVTVAKEI
           :|:::| | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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g982	IASQNLRFDNRFLQKMVNGVNILPAADWVALGAKGRNVVVDRAFGGPHITKDGVTVAKEI
	10 20 30 40 50 60
m982.pep	ELKDKFENMGAQMVEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRG
	70 80 90 100 110 120
g982	ELKDKFENMGAQMVEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRG
	70 80 90 100 110 120
m982.pep	DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
g982	DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
m982.pep	KSLENELDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
g982	KSLENELDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
m982.pep	AKASRPLIIAEDVEGEALATLVVNNIRGILKTAVKAPGFGDRRKAMLQDIAILTGCVV
	250 260 270 280 290 300
g982	AKASRPLIIAEDVEGEALATLVVNNIRGILKTAVKAPGFGDRRKAMLQDIAILTGCVV
	250 260 270 280 290 300
m982.pep	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQIETATSDY
	310 320 330 340 350 360
g982	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQIETATSDY
	310 320 330 340 350 360
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
	370 380 390 400 410 420
g982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
	370 380 390 400 410 420
m982.pep	RARAALNLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLEGGKNGYGYNA
	430 440 450 460 470 480
g982	RARAALNLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLEGGKNGYGYNA
	430 440 450 460 470 480
m982.pep	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGM
	490 500 510 520 530 540
g982	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGM
	490 500 510 520 530 540
m982.pep	GGMMX
g982	GGMMX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2965>:

```

a982.seq
1  ATGGCAGCAA AAGACGTACA ATTCGGCAAT GAAGTCCGCC AAAAAATGGT
51  AAACGGCGTG AACATTTTGG CAAACGCCGT GCGCGTAACC TTGGGTCCCA
101 AAGGCCGCAA CGTGGTGTT GACCGCGCTT TCGGCGGCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAAGAAGT CGCGTCCAAA ACCAACGACG
251 TGGCGGGCGA CGGTACGACT ACCGCCACCG TATTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAAATACGT TACCGCCGT ATGAACCGA CCGACCTGAA
351 ACGCGGTATC GACAAAGCCG TCGCGCTTT GGTGAAGAG CTGAAAAACA

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1388

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401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CTGACGAACA AGTCGGCGCG ATTATTGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AATTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TCGGGAAGAA CAAATCGCCG GCTTGGACAA
651 TCCGTTTGTA TTGCTGTTG ACAAATAAT CAGCAATATC CGCGACCTGC
701 TGCCTGTTTT GGAACAAGTG GCCAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATT CTGAAAACCG TTGCCGTTAA AGCTCCGGGC TTCGGCGACC
851 GCCGCAAAGC GATGCTGCAA GACATCGCTA TCCTGACCGG CGGCACAGTG
901 ATTTCCGAAG AAGTCGGCCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAGGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001 ACGGCTTCGG CGACGCAGCC CAAATCGAAG CGCGTGTTCG CGAAATCCGC
1051 CAACAAATCG AAACGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAATGGCAG GCGGCGTGGC AGTAATCAAA GTCGGTGGCG
1151 CGACCGAAGT GGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGCGCT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTCTGGA AAACCTGCAC ACCGGCAATG
1301 CAGACCAAGA CGCAGGCGTA CAAATCGTCT TCGCGCGCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401 CAAAGTGTG GAAGGCAAG GCAACTATGG TTACAACGCT GGCAGCGGCG
1451 AATACGGCGA CATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCGCGC TGCAACACGC CGCGTCTATC GCCGGCCTGA TGCTGACCAC
1551 AGACTGCATG ATTGCTGAAA TCCCTGAAGA CAAACCGGCT ATGCCTGATA
1601 TGGGCGGCAT GGGTGTATG GCGGCATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2966; ORF 982.a>:

a982.pep

```

1  MAAKDVFQGN EVRQKMVNGV NILANAVRVT LGPKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRG I DKAVALVEE LKNIAPCDT SKEIAQVGS I
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KLENELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LFDKKISNI RDLLPVLEQV AKASRPLLI I
251 AEDVEGEALA TLVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGGTV
301 ISEEVGLSLE KATLDDLQQA KRIEIGKENT TIIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALLENH TGNADQDAGV QIVLRAVESP
451 LRQIVANAGG EPSVVVNKVL EGKNGYGYNA GSGEYGDME MGVLDPKAVT
501 RSALQHAASI AGLMLTTDCM IAEIPEKPA MPDMGGMGM GMM*

```

m982/a982 99.3% identity in 544 aa overlap

	10	20	30	40	50	60
m982.pep	MAAKDVQFGNEVRQKMVNGVNILANAVRVT LGPKGRNVVV DRAFGGPHIT KDGVTVAKEI					
a982	MAAKDVQFGNEVRQKMVNGVNILANAVRVT LGPKGRNVVV DRAFGGPHIT KDGVTVAKEI					
	10	20	30	40	50	60
m982.pep	ELKDKFENMGAQMVKEVASKTNDVAGDGT TATVLAQSIVAEGMKYVTAG MNPTDLKRG I					
a982	ELKDKFENMGAQMVKEVASKTNDVAGDGT TATVLAQSIVAEGMKYVTAG MNPTDLKRG I					
	70	80	90	100	110	120
m982.pep	ELKDKFENMGAQMVKEVASKTNDVAGDGT TATVLAQSIVAEGMKYVTAG MNPTDLKRG I					
a982	ELKDKFENMGAQMVKEVASKTNDVAGDGT TATVLAQSIVAEGMKYVTAG MNPTDLKRG I					
	70	80	90	100	110	120
m982.pep	DKAVALVDELKNIAPCDTSKEIAQVGSISANSDEQVG AIIAEAMEKVGKEGVITVEDG					
a982	DKAVALVEELKNIAPCDTSKEIAQVGSISANSDEQVG AIIAEAMEKVGKEGVITVEDG					
	130	140	150	160	170	180
m982.pep	DKAVALVDELKNIAPCDTSKEIAQVGSISANSDEQVG AIIAEAMEKVGKEGVITVEDG					
a982	DKAVALVEELKNIAPCDTSKEIAQVGSISANSDEQVG AIIAEAMEKVGKEGVITVEDG					
	130	140	150	160	170	180
m982.pep	KLENELDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFV LLDKKISNIRDLLPVLEQV					
a982	KLENELDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFV LLDKKISNIRDLLPVLEQV					
	190	200	210	220	230	240
m982.pep	KLENELDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFV LLDKKISNIRDLLPVLEQV					
a982	KLENELDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFV LLDKKISNIRDLLPVLEQV					
	190	200	210	220	230	240

1389

m982.pep	250	260	270	280	290	300
	AKASRPLLI AEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTTGGVV					
a982						
	250	260	270	280	290	300
	AKASRPLLI AEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTTGGTV					
m982.pep	310	320	330	340	350	360
	ISEEVGLSLEKATLDDLGOAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY					
a982						
	310	320	330	340	350	360
	ISEEVGLSLEKATLDDLGOAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY					
m982.pep	370	380	390	400	410	420
	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
a982						
	370	380	390	400	410	420
	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
m982.pep	430	440	450	460	470	480
	RARAALLENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSSVVVNKVLEGKNGYGYNA					
a982						
	430	440	450	460	470	480
	RARAALLENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSSVVVNKVLEGKNGYGYNA					
m982.pep	490	500	510	520	530	540
	GSGEYGDMIEMGVLDPAKVTRSALQHAASIAGLMLTTDCMIAEIPEDKPAVPMGGMGGM					
a982						
	490	500	510	520	530	540
	GSGEYGDMIEMGVLDPAKVTRSALQHAASIAGLMLTTDCMIAEIPEDKPAVPMGGMGGM					
m982.pep	GGMMX					
a982	GGMMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2967>:

g986.seq

1	GTGTTCAAAA	AATACCAATA	CTTCGCTTTG	GCGGCACTGT	GTGCCGCTTT
51	GCTGGCAGGC	TGCGAARAGG	CAGGCAGCTT	TTTCGGTGCG	GACAAAAAAG
101	AAGCATCCTT	CGTAGAACGC	ATCGAACACA	CCAAAGACGA	CGGCASTGTC
151	AGTATGCTGC	TGCCCCGACTT	TGCCCCAATG	GTTCAAAGCG	AAGGCCCGGC
201	AGTCGTCAAT	ATTCAGGCAG	CCCCCGCCCC	GCGCACCCAA	AACGGCAGCG
251	GCAATGCCGA	AACCGATTCC	GACCCGCTTG	CCGACAGCGA	CCCGTTCTAC
301	GAATTTTCA	AACGCCTCGT	CCCGAACATG	CCCGAAATCC	CCCAAGAAGA
351	AGCAGATGAC	GGCGGATTGA	ACTTCGGTTC	GGGCTTCATC	ATCAGCAAAA
401	ACGGCTACAT	CCTGACCAAT	ACCCACGTCG	TTGCCGGTAT	GGGCAGTATC
451	AAAGTCTGCG	TCAACGACAA	GCGCGAATAT	ACCGCCAAAC	TCATCGGTTC
501	GGATGTCCAA	TCCGATGTCG	CCCTTCTGAA	AATCGACGCA	ACGGAAGAGC
551	TACCCGTCGT	CAAAATCGGC	AATCCCAAAA	ATTTGAAACC	GGGCGAATGG
601	GTCGCTGCCA	TCGGCGCGCC	CTTCGGCTTT	GACAACAGCG	TGACCGCCGG
651	CATCGTGTCC	GCCAAAGGCA	GAAGCCTGCC	CAACGAAAgc	tACACACCCT
701	TCATCCAAAC	CGACGTTGCC	ATCAATCCGG	GCAATTCCGG	CGGCCCGCTG
751	TTCAACTTAA	AAGGACAGGt	cgTCGGCATC	AATTTCGCAA	TATACAGCCG
801	CAGCGgcgga	ttCATGGGCA	TCTCCTTTGC	CATCCCGATT	GACGTTGCCA
851	TGAATGTCGC	CGAACAGCTG	AAAAACACCG	GCAAAGTCCA	ACGCGGACAA
901	CTGGGCGTGA	TTATTTCAGGA	AGTATCCTAC	GGTTTGGCAC	AGTCGTTCCG
951	TCTGGATAAA	GCCAGCGGCG	CATTGATTGC	CAAAATCCTT	CCCGGCAGCC
1001	CCGCAGAACG	TGCCGGCCTG	CAGGCGGGCG	ACATCGTCCT	CAGCCTCGAC
1051	GGCGGAGAAA	TACGTTCTTC	CGGCGACCTT	CCCGTCATGG	TCGGCGCCAT
1101	TACGCCGGGA	AAAGAAGTCA	GCCTCGGCGT	ATGGCGCAAA	GGCGAAGAAA
1151	TCACAATCAA	AGCCAAGCTG	GGCAACGCCg	cggagcATAC	CGGCgcatCA
1201	TCCAAAACAG	ATGAAGcccc	ctacaccgAA	CAGCAATCCG	GTACGTTCTC
1251	GGTCGAATCC	GCAGGCATTA	CCCTTCAGAC	ACATACCGAC	AGCAGCGGca
1301	aacacctcgt	cgtcgtacgg	gtttccgacg	cggcagaacg	cGCAGGCTTA

1390

1351 AGgcgcggcg acgaaatcct cgcggtcggg caagtccccg tcaatgacga
 1401 agccgGTTTC cgcaaaGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
 1451 TGGTCatgcg ccgTGGCAAC ACGCTGTTCA TCGCATTAAA CCTGCAATAA

This corresponds to the amino acid sequence <SEQ ID 2968; ORF 986.ng>:

g986.pep
 1 VFKKYQYFAL AALCAALLAG CEKAGSFFGA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVVN IQAAPAPRTQ NGSGNAETDS DPLADSDPFY
 101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKNGYILT N THVVAGMGS I
 151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKNLKPGEW
 201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
 251 FNLKGQVVG I NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
 301 LGVLIQEVSY GLAQSFGLDK ASGALIAKIL PGSPAERAGL QAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKAKL GNAAEHTGAS
 401 SKTDEAPYTE QSGTFSVES AGITLQTHTD SSGKHLVVVR VSDAAERAGL
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLVMRRGN TLFIALNLQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2969>:

m986.seq
 1 GTGTTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCAGCCTC
 51 GCTGGCAGGC TGGCACAAGG CAGGCAGCTT CTTCGTGGCG GACAAAAAAG
 101 AAGCATCCTT CGTAGAACGC ATCGAACACA CCAAAGACGA CGGCAGCGTC
 151 AGTATGCTGC TGCCCGACTT TGCCCAACTG GTTCAAAGTG AAGGTCCGGC
 201 AGTCGTCAAT ATTCAAGCAG CCCCCGCCCC GCGCACCCAA AACGGCAGCG
 251 GCAATGCCGA AAACGATTCC GACCCGATTG CCGACAACGA CCGTTCTAC
 301 GAATTTTTCA AACGCCTCGT CCCGAATATG CCCGAATCC CCCAAGAAGA
 351 AGCAGATGAC GGCAGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
 401 ACGGCTACAT CTTGACCAAT ACCCACGTCG TTACCGGCAT GGGCAGTATC
 451 AAAGTCTCG TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTT
 501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
 551 TGCCCGTCGT CAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
 601 GTCGCGGCCA TCGGCGCGCC CTTCGGCTTC GACAACAGCG TGACCGCCGG
 651 CATCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCT
 701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
 751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
 801 CAGCGGCGGA TTCATGGGCA TTCTCTCGC CATCCCATT GACGTTGCCA
 851 TGAATGTCGC CGAACAGCTG AAAACACCG GCAAAGTCCA ACGCGGACAA
 901 CTGGCGGTGA TTATTCAAGA AGTATCCTAC GGTTCGACAC AATCGTTCGG
 951 TTTGGACAAA GCCGGCGGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
 1001 CCGCAGAACG TCGCGGCTG CAGGCGGGCG ACATCGTCTT CAGCCTCGAC
 1051 GGGCGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
 1101 TACGCGGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAAA GCGGAAGAAA
 1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
 1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTCTC
 1251 GGTCAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
 1301 GACACCTCGT CGTCGTACGG GTTCCGACG CGGCAGAAGC CGCAGGCTTG
 1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
 1401 AGCCGTTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
 1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAA CCTGCAATAA

This corresponds to the amino acid sequence <SEQ ID 2970; ORF 986>:

m986.pep.
 1 VFKKYQYLAL AALCAASLAG CDKAGSFFVA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVVN IQAAPAPRTQ NGSGNAENDS DPLADNDPFY
 101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKNGYILT N THVVAGMGS I
 151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
 201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
 251 FNLKGQVVG I NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
 301 LGVLIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL QAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
 401 SKTDEAPYTE QSGTFSVES AGITLQTHTD SSGHLVVVR VSDAAERAGL
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

Computer analysis of this amino acid sequence gave the following results:

m986.pep	VFKKYQYLALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSGVSM LLPDFAQL	10	20	30	40	50	60
g986	VFKKYQYFALAALCAALLAGCEKAGSFFGADKKEASFVERIEHTKDDGSGVSM LLPDFAQL	10	20	30	40	50	60
m986.pep	VQSEGPVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPMPEIPQEEADD	70	80	90	100	110	120
g986	VQSEGPVVNIQAAPAPRTQNGSGNAETDSDPLADSDPFYEFFKRLVPMPEIPQEEADD	70	80	90	100	110	120
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA	130	140	150	160	170	180
g986	GGLNFGSGFIISKNGYILTNTHVVAGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA	130	140	150	160	170	180
m986.pep	TEELPVVKIGNFKDLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQT DVA	190	200	210	220	230	240
g986	TEELPVVKIGNFKNLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQT DVA	190	200	210	220	230	240
m986.pep	INPGNSGGPFLNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ	250	260	270	280	290	300
g986	INPGNSGGPFLNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ	250	260	270	280	290	300

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	310	320	330	340	350	360
m986.pep	LGVI IQEVS YGLAQS FGLDKAGGALIAKILPGSPAERAGLCAGDIVLSLDGGEIRSSGDL					
g986	LGVI IQEVS YGLAQS FGLDKAGGALIAKILPGSPAERAGLCAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAI TPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
g986	PVMVGAI TPGKEVSLGVWRKGEEITIKVKLGNAAEHTGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQTH TDSGGHLVVVRVSDAAERAGLRGDEILAVGQVPVND EAGFRKAMD KAGKN					
g986	AGITLQTH TDSGGHLVVVRVSDAAERAGLRGDEILAVGQVPVND EAGFRKAMD KAGKN					
	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
g986	VPLLVMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2971>:

```

a986.seq
1  GTGTTCAAAA AATACCAATA CCTCGCTTGT GCAGCACTGT STGCCGCCTC
51  GCTGGCAGGC TGCACAAAG CCGGCAGCTT TTTCGGTGCG GACAAAAAAG
101 AAGCATCCTT TGTAGAACGC ATCAAACACA CCAAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGTCCAACGT GTTCAAAGCG AAGGCCCGGC
201 AGTCGTCAAT ATTACGGCAG CCCCCGCCCC GCGACCCCAA AACGGCAGCA
251 GCAATGCCGA AACCGATTCC GACCCGCTTG CCGACAGCGA CCCGTTCTAC
301 GAATTTTTC AACGCCTCGT CCGGAACATG CCGGAAATCC CCAAGAAGA
351 AGCAGATGAC GNGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
401 ACGGCTATAT TCTGACCAAT ACGCACGTCG TTACCGGCAT GGGCAGTATC
451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTT
501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCCGCCA TCGGCGCGCC CTTCGGCTTC GACAACAGCG TGACCGCCGG
651 CNTCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCT
701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
801 CAGCGGGCGA TTTCATGGCA TTTCCTTCGC CATCCCATT GACGTTGCCA
851 TGAATGTCGC CGAACAGCTG AAAAACACCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTCGGCAC AATCGTTCGG
951 TTTGGACAAA GCCGGCGGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
1001 CCGCAGAACG TGCCGGCCTG CGGGCGGGCG ACATCGTCTT CAGCCTCGAC
1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
1101 TACGCCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAAA GGCGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
1201 TCCAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
1251 GGTCGAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTTCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATCTT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
1401 AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAA CCTGCAATAA

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This corresponds to the amino acid sequence <SEQ ID 2972; ORF 986.a>:

```

a986.pep
1  VFKKYQYLAL AALCAASLAG CDKAGSFFGA DKKEASFVER IKHTKDDGSV
51  SMLLPDFVOL VQSEGPAVVN IQAAPAPRTQ NGSSNAETDS DPLADSDPFY
101 EFFKRLVPNM PEIPQEEADD GGLNFGSGFI ISKDGYILTN THVVTGMGSI
151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGXVS AKGRSLPNES YTPFIQTQDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ

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301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL RAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
 401 SKTDEAPYTE QSGTFSVES AGITLQTHD SSGHLVVVR VSDAERAGL
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGN VPLLIMRRGN TLFIALNLQ*

m986/a986 98.2% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
a986	VFKKYQYLALALCAASLAGCDKAGSFFGADKKEASFVERIKHTKDDGSVSMLLPDFVQL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m986.pep	VQSEGPVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPMPEIPQEEADD					
a986	VQSEGPVVNIQAAPAPRTQNGSSNAETSDPLADSDPFYEFFKRLVPMPEIPQEEADD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
a986	GGLNFGSGFIISKDGYILTNTHVVTGMSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFNSVTAGIVSAKGRSLPNESTPFIQTQVA					
a986	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFNSVTAGXVSAKGRSLPNESTPFIQTQVA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m986.pep	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
a986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m986.pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
a986	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLRAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEETIKVKLGNAAEHIGASSKTDEAPYTEQSGTFSVES					
a986	PVMVGAITPGKEVSLGVWRKGEETIKVKLGNAAEHIGASSKTDEAPYTEQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQTHDSSGGHLVVVRVSDAERAGLRGDEILAVGQVPVNDEAGFRKAMDKAGN					
a986	AGITLQTHDSSGGHLVVVRVSDAERAGLRGDEILAVGQVPVNDEAGFRKAMDKAGN					
	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
a986	VPLLIMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2973>:

g987.seq
 1 ATGAAAACAC GCAGCCTCAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG

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51  TTCTTCATGG TTGCCCCCAG TGGAAGAAGC GACGGAAAGC CGTCATTTTA
101 ATACTTCCAA ACCTGTCTTC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATAACA ACGGGCTATC CGACATCTAC CTGCTCGACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATTTGG CGCAACGACA TTCCGGCAG GCTGCTGTTT
301 AACCTCATGT ACCTTGCCGC agaacgcGGC GTGCGCGTAC GCCTGCTGT
351 ggacgacaAC AACAcgcgcg gcttgacga tctcctGCTC GCCCTCGACA
401 GCCATCCCAA TAtctaagtG CGCCTGTTCa ACCCCTtcgt CCTACGCAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCCTCA ACCGCCGAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCCGCGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA SCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGACGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACATCCA GACACGCGCT CTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACGGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCCT GATCAGCGAC AGCCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAAACCGC CGATTGCCGG GAGGCTGCAA GACGCGCTCA AACAGCCGA
951 AAAAAGCGTC TATCTCGTTT CACCCTATTT CGTCCCTACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCTG
1051 ACCAATCTGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTACGT
1101 CAAATACGCA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGacg gCAAACGCA
1251 CTTTCATCGG TCATTCAACC TCGACCCCGG TTCCGCACGG CTCAATACCG
1301 AAATGGGCGT CGTCATCGAA AGCCCCAAA TCGCAGAACA GATGAGCGC
1351 AccctCGCCG AtacCACACC CGAATACGCC TACCGCGTTA CCTCGACAA
1401 ACACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TCGAAGGTTT ATTATAG

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This corresponds to the amino acid sequence <SEQ ID 2974; ORF 987.ng>:

g987.pep

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1  MKTRSLISLL CLLLSCSSW LPPLEERTES RHFNTSKPVL LDNIQIRIIT
51  PHNGLSDIY LLDDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NIMYLAERG VRVRLLLDN NTRGLDLLLL ALDSHPNI*V RLFNPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG XGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD SPAKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDIVTL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
451 TLADTTPEYA YRVTLDKHNR LQWHPATRK TYPNEPEAKL WKRIAARKILS
501 LLPIEGLL*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2975>:

m987.seq

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1  ATGAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCCAG TGGAAGAAGC GACGGAAAGC CGTCATTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATAACA ACGGGCTATC CGATATCTAT CTGTGGAACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTCCGGCAG GCTGCTGTTT
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTT GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCa ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCCTCA ACCGCCGAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GATTTGACGA TCCTCGCCAC CGGCAGCGTC GTCCGCGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGACGCGG CGACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACAGGATG CATCGACTGG CAGAGCGTCC
851 GAACCCGCCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC

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901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCTATTT CGTCCCCA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTTCTG
1051 ACCAACTCGC TGCAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCC GCCACAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCACGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTTCATCGT TCGTTCAACC TCGACCCCG TTCCGCGCGT CTCAACACCG
1301 AAATGGGCGT TGTATCGAA AGCCCCAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCACACC CGCCTACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAA ACCTACCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAA AATCCTATCC
1501 CTGCTGCCCA TAGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2976; ORF 987>:

```

m987.pep
1 MKTRSLISLL CLLCSCSSW LPPLEERTES RHFNTSKPVR LDNILQIRHT
51 PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAERG VRRLLLDDN NTRGLDDLLL ALDHPNIEV RLFNFFVLRK
151 WRALGYLTF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHAHNA TRIIRSGDIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGCIDW QSVRTRLISD DPAKGLDRDR
301 RKPIIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVI
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVIE SPKIAEQMER
451 TLADTTPAYA YRVTLDRHNR LQWHPATRK TYPNEPEAKL WKRIAAILK
501 LLPIEGLL*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m987/g987 97.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987.pep	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY					
g987	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVLLDNILQIRHTPHNGLSDIY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m987.pep	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNVLVYLAERGVRRLLLDDN					
g987	LLDDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNMYLAERGVRRLLLDDN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m987.pep	NTRGLDDLLLALDHPNIEVRLFPFVLRKWRALGYLTFPRLNRRMHNKSFTADNRATI					
g987	NTRGLDDLLLALDHPNIXVRLFPFVLRKWRALGYLTFPRLNRRMHNKSFTADNRATI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m987.pep	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHAHNATRIIRSGDIG					
g987	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHAHNATRIIRSGNIG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m987.pep	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVRTRLISDPAKGLDRDR					
g987	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDSPAKGLDRDR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m987.pep	RKPIIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLNSLQATDVA					

1396

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|||||
g987      RKPP|IAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVL|TNSLQATEVA
          310      320      330      340      350      360

          370      380      390      400      410      420
m987.pep  AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSV|TSLHAKTFIVDGKRIFIG
          370      380      390      400      410      420
g987      AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSV|TSLHAKTFIVDGKRIFIG
          370      380      390      400      410      420

          430      440      450      460      470      480
m987.pep  SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTT|PAYAYRVTLDRHNLQWHPATRK
          430      440      450      460      470      480
g987      SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTT|PEYAYRVTLDKHNRLQWHPATRK
          430      440      450      460      470      480

          490      500      509
m987.pep  TYPNEPEAKLWKRIA|AAKILSLPIEGLLX
          490      500
g987      TYPNEPEAKLWKRIA|AAKILSLPIEGLLX
          490      500

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2977>:

```

a987.seq
1  ATGAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCCAC TGAAGAAGC GACGGAAGC CGTCATTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTCCCGGCCG ACTGCTGTTC
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGTGTGT
351 GGACGACAAAC AACACGCGCG GATTGGACGA CCTCCTGCTC GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCGCGCTCA ACCGCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTCGACCGC TACTGGGCAA GCCATTCCGC CCACAAGGCC ACGCGCATCA
701 TCCGCAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACAGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCGG GCGGCTGCAA GACGCGTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGTTT CACCCTATT CGTCCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAACTC TACGAGCTGC
1151 AACCCTAACCA TGCCGTCCCT GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTCATCGGC TCATTCAACC TCGACCCCGG TTCCGCACGG CTCAATACTG
1301 AAATGGGCGT TGTATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCTCACC CGAATACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TAGAAAGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 550; ORF 2978.a>:

```

a987.pep
1  MKTRSLISLL CLLLSCSSW LPPLERTES RHFNTSKPVR LDNILQIRHT
51  PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYIYI RNDISGRLLF
101 NLVYLAERG VRVRLLLDDN NTRGLDLLLL ALDSHPNIEV RLFNPFVLRK
151 WRALGYLTD FRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD DPAKGLDRDR
301 RKPP|IAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL

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1397

351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
 401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTMGVVIE SPKIAEQMER
 451 TLAOTSPEYA YRVTLDRHNR LQWHPATRK TYPNEPEAKL WKRIA AKILS
 501 LLPIESLL*

m987/a987 98.8% identity in 508 aa overlap

m987.pep	10	20	30	40	50	60
	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY					
a987	10	20	30	40	50	60
	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY					
m987.pep	70	80	90	100	110	120
	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLLDDN					
a987	70	80	90	100	110	120
	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLLDDN					
m987.pep	130	140	150	160	170	180
	NTRGLDDLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFFRLNRRMHNKSFTADNRATI					
a987	130	140	150	160	170	180
	NTRGLDDLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFFRLNRRMHNKSFTADNRATI					
m987.pep	190	200	210	220	230	240
	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGDIG					
a987	190	200	210	220	230	240
	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIG					
m987.pep	250	260	270	280	290	300
	KGLQALGYNDTSRHALLRYRETVEQSPLYQKIQTGCIDWQSVTRTLISDDPAKGLDRDR					
a987	250	260	270	280	290	300
	KGLQALGYNDTSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRTLISDDPAKGLDRDR					
m987.pep	310	320	330	340	350	360
	RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGDVTVLTNSLQATDVA					
a987	310	320	330	340	350	360
	RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGDVTVLTNSLQATDVA					
m987.pep	370	380	390	400	410	420
	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
a987	370	380	390	400	410	420
	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
m987.pep	430	440	450	460	470	480
	SFNLDPRSARLNTMGVVIESPKIAEQMERTLADTTPAYAYRVTLDRHNR LQWHPATRK					
a987	430	440	450	460	470	480
	SFNLDPRSARLNTMGVVIESPKIAEQMERTLADTSPEYAYRVTLDRHNR LQWHPATRK					
m987.pep	490	500	509			
	TYPNEPEAKLWKRIA AKILSLLPIEGLLX					
a987	490	500	509			
	TYPNEPEAKLWKRIA AKILSLLPIESLLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2979>:

g988.seq
 1 ATGAATAAAA ATATTAAATC TTAAATTTA CGGGAAAAAG ACCCGTTTTT

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51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCCAGT CGGgaATGGA
101 TAATCGAATT GTTGGAGCGC AAAGGTGTGC CTTCAAAAAT CGAATCGCTT
151 GCACGCGAGC TGTGATTAC GGAAGacgag tATGTCTTTT TTGAACGCCG
201 TCTGAaggCG atgGCGCGGG AcggtCAGGT TTTAATCAAC CGCCgaggcg
251 CagtTTGCGc gGCggacaag ctgGATTTGG TCAAATGccg Cgtcgaggcg
301 catAAGGAcg gtttcggctt cgcCGTGCCG CTCATGCCGA TGGACGAAGG
351 GGATTTCGTT TTATACGAAC GCCAgatgcy tggTgtcatG CAcggcgaca
401 ccgttACCGT CCGTCCTGCg ggtatggaCC GCAGGGGccg ccgcGAAGgg
451 acgtttctGG ATATTGTCTGA ACGCGCGCAA AGCAAAGTTG TCGGCCGTTT
501 CTATATCGAT AGGGCGGTGG CGATTTTGA GCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTGTGGAA CCGGACGGCG TGGCGCGTTT CAAACCCGAA
601 TCCGGTCAGG TTATCGTCGG CAAAATTGAG GTTTATCCCG AGCAAAACCG
651 GCCTGCAGTG GCAAAAATCA TTGAAGTTT GGGCGATTAT GCCGACAGCG
701 GGATGGAAAT cgAAATTGCC GTGCGCAAGC ATCATTGGCC GCAccgaTTC
751 AGTGAagcgt gtGcCAAAATC CGcgaAAAAA ATtccccgacc ATGTACGCAA
801 AAGCGATTG AAAGGCCGCG TCGATTTGTG CGACCTTCTT TTGGTAACGA
851 TAGACGGCGA AACGGCGCGC GATTTTCGACG ACGCGGTGTT TGCCGAAAAA
901 GTCGGACGCA ATTACCGCCT GGTCTGGCG ATTGCGGATG TCAGCCATTA
951 TGTCCGCCCT GACGATGCCA TTGATGCAGA TGCTCAAGAA CGCACTACCA
1001 GCGTGTATTT CCGCGCCGT ATGATTCCGA TGCTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCCGATGTC GAGCGTTGT GTATGGTGTG
1101 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTATC
1151 CCGCCGTGAT GCGCTCTCAT GCCCGCTGA CCTACAACCA AGTTTGGAAA
1201 TGGCTTTCAG ACGGCATCGG GAATCCGCAC AAAGCCCAA TCGACACGCT
1251 TTACAAGCTG TTAAAAATTT TGCAGAAAAA ACGTCTGGCG CGCGGGGCGG
1301 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGACGA CAACGGCAAA
1351 ATCGAAAAAA TTGTCCCGT CGTCCGCAAC gatGCCACA AGCTGATTGA
1401 AGAATGTATG CTGGCGGCGA ATGTTTGGCG GCGGATTTT CTGTTGAAAA
1451 ACAACATAC GGCTTTGTTC CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1501 CTCGCCACCC TCGCGGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1551 CCGCGACAAC CCGTCGCGCA AAGACTATGC CGCGCTTGCC GAACAATTCA
1601 AAGGCAGGCC GGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAGCAGCGCG TTTACGAACC GCATTGCGAA GGGCATTTCC GTTTGGCTTA
1701 TGAAGCATA GCCCACTTTA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1751 CCGTCCACCG TGCCATCAAA GCCGTATTGA ACCGGAAGAC CTACACGCCA
1801 AACAAAAGCT GGCAGGCTTT GGGCGTGCAT ACTTCGTTTT GCGAACGCCG
1851 TGCCGACGAT GCTGGCCGCG ATGTGGAAAA CTGGCTGAAA ACTTATTATA
1901 TGCGCGATAA GGTGGTGAA ATATTTGAAG GcaaaatCtc ccggggtgtg
1951 gcaaaTtttg gaATATTGT CACTTTGGAC GATATccata tcgacggtct
2001 ggtacaTATC AGCGatttgg gcgaAGATTA TTTCaacttc cgccccgAAA
2051 TCATGGCAAT CGAAGGCGAA CGCAGCGGCA TCCGTTTCAA TATGGGGGAC
2101 AGGGTTGCCG TCCGGGTCGC GCGTGCCGAT TTGGATGATG GAAAAATCGA
2151 CTTTGTCTTA ATTGCCGGAG AAAGCGGCAG GCGGCGGAAG GTCAAATTAT
2201 CCGCATCTGC CAAACCGGCA GGGGCGGCGG GGAAGGGGAA ATCGAAAACC
2251 ACCGCCGAGA AAAAAACAGC CCGATGCGGC AAAGTAAGGG GAAGGGGCGT
2301 GCCTGCCGTT GCCGAATCGG GGAAAAAGGC AAAGAAACCG GTTCCGATTA
2351 AGGTCAAAAA ACGGAAAGGC AAATCATAA

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This corresponds to the amino acid sequence <SEQ ID 2980; ORF 988.ng>:

g988.pep

```

1  MNKNIKSLNL REKDPFLSRE KORYEHPLPS REWIELLER KGVPSKIESL
51  ARELSITEDE YVFFERRLKA MARDGQVLIN RRGAVCAADK LDLVKCRVEA
101 HKDGFGEFVP LMPMDEGDFV LYERQMRGVM HGDTVTVRPA GMDRRGRREG
151 TFLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSVILE PDGVARFKPE
201 SGQVIVGKIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPFRF
251 SEACAKSAKK IPDHVRKSDL KGRVOLDCLP LVTIDGETAR DFDDAVFAEK
301 VGRNYRLVVA IADVSHYVRP DDAIDADAQE RSTSVYFPRR MIPMLPENLS
351 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPVMRSH ARLTYNQVWK
401 WLSDGIGNPH KAQIDTLYKL FKILQKKRLA RGAVEFESVE TQMIFDDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LATLREQLGL LGLQLGGDN PSPKDYAALA EQFKGRPDAE LLQVMMLRSM
551 QQAVYEPHCE GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNRKTYTP
601 NKSQWALGVH TSFCERRADD AGRDVENWLK TTYMRDKVGE IFEGKISRGV
651 ANFGIFVTL DDIHIDGLVHI SDLGEDYFNF RPEIMAIEGE RSGIRFNMGD
701 RVAVRVARAD LDDGKIDFVL IAGESGRRRK VKLSASAKPA GAAGKGKSKT
751 TAEKKTARCG KVRGRGVPVAV AESGKKAKKP VPIKVKKRKG KS*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2981>:

```
m988.seq (partial)
1  ..ACAGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
51  CTATATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
101 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
151 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
201 GCCGGCAGTG GCAAAAATCA TCGAAGTTTT GGGCGATTAT GCCGACAGCG
251 GCATGGAGAT TGAATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
301 AGTGAAGCGT GTGCCAAAGC TCGGAAAAAA ATTCCCGTCC ATGTACGCAA
351 AAGCGATTTG AAAGGCCGCG TCGATTTGCG CGACCTGCCT TTGGTAACGA
401 TAGACGGCGA AACGGCGCGC GATTTCGACG ACGCGGTGTT TGCCGAAAAA
451 TGCGGACGCA ATTACCGTCT GGTCTGGCG ATTGCGGATG TCAGCCATTA
501 TGTCCGCCCT GACGATGTGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
551 GCGTATATTT CCCGCGCCGT GTGATTCCGA TGCTGCCGGA AAACCTGTCT
601 AACGGCATTG GCTCGCTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
651 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTACC
701 CCGCCGTAAT GCGCTCTCAT GCCGCGCTGA CCTACAACCA AGTTTGGAAA
751 TGGATTTCAG ACGGCATCGA CCA'CCGTAC AAAGCCCAAA TCGACACCCT
801 TTACAAACTC TTCAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGCGCGG
851 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGATGA CAACGGCAAA
901 ATCGAAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCACA AGCTGATTGA
951 AGAATGTATG CTGGCGGCGA ATGTTTGCGC AGCGGATTTT CTGTTGAAAA
1001 ACAAGCATAC GGCTTTGTTC CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1051 CTCGCCACCC TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1101 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGTG GAACAATTCA
1151 AAGGCAGACC TGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1201 CAGCAGGCGG TTTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCCTA
1251 CGAAGCATAC GCCCACTTCA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1301 CCGTACACCG CGCCATCAAA GCCGTGTTGA ATCAGCAAAC CTACACGCCA
1351 AAAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1401 TGCCGACGAC GCCAGCCGCG ACGTGGAAAA CTGGCTGAAA ACCTATTATA
1451 TGCGCGATAA GGTTCGCGAA GTATTCGAAG GTAAAATCTC CGGCATGACC
1501 AGTTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
1551 GCATATCAGC GATTTGGGCG AAGACTATTT CAACTCCGC CCCGAAATCA
1601 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTTCACAT GGGGGACAGG
1651 GTTGGCGTCC GGGTCGCCC GTCGATTG GATGACGGAA AAATCGATTT
1701 TGTCTGTATT GCCGGGGGA GCGGCAGGG GCGGAAAGTT AAATCATCCG
1751 CGTCTGCCAA ACCGCGAGG ACGGCGGGA AAGGAAGCC GAAAACGCC
```


1400

1801 GCCGAGAAAA AACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC
 1851 TGCCGCCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGT CCGATTAAGG
 1901 TAAAAAACG GAAAGGCAAA TCATAA

This corresponds to the amino acid sequence <SEQ ID 2982; ORF 988>:

m988.pep (partial)
 1 ..TVLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
 51 SGQVIVGEIE VYPEQNRPAV AKIEVLGDY ADSGMEIEIA VRKHHLP HQF
 101 SEACAKAAKK IPVHVRKSDL KGRVDLRDLP LVTIDGETAR DFDDAVFAEK
 151 VGRNYRLVVA IADVSHYVRP DDVIDADAQE RSTSVYFPRR VIPMLPENLS
 201 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
 251 WISDGIDHPY KAQIDTLYKL FKILQKKRFE RGAVEFESVE TQMIFDDNGK
 301 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
 351 LATLREQLGL LGLQLGGGDN PSPKDYAALV EQFKGRPD AE LLQVMMLRSM
 401 QOAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQQTYP
 451 KKSQALGVH TSFCERRADD ASRDVENWLK TYMRDKVGE VFEGKISGMT
 501 SFGIFVTL DG IHIDGLVHIS DLGEDYFNFR PEIMAIEGER SGIRENMGDR
 551 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGKPKTA
 601 AEKKTARGGK VRGRGASAAA ESRKAKKPV PIKVKRRKGK S*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m988/g988 94.2% identity in 642 aa overlap

m988.pep				10	20	30
				TVLDIVERAQSKVVGRFYMDRGVAILEPED		
g988	LYERQMRGVMHGDVTVVRPAGMDRRGRREGTFLDIVERAQSKVVGRFYMDRGVAILEPED					
	130	140	150	160	170	180
m988.pep		40	50	60	70	80
		KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIEVLGDYADSGMEIEIA				
g988		KRLNQSIVLEPDGVARFKPESGQVIVGKIEVYPEQNRPAVAKIEVLGDYADSGMEIEIA				
	190	200	210	220	230	240
m988.pep		100	110	120	130	140
		VRKHHLP HQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLP LVTIDGETARDFDDAVFAEK				
g988		VRKHHLP HRFSEACAKSAKKIPDHVRKSDLKGRVDLCDLPLVTIDGETARDFDDAVFAEK				
	250	260	270	280	290	300
m988.pep		160	170	180	190	200
		VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFPRRVI PMLPENLSNGICSLNPDV				
g988		VGRNYRLVVAIADVSHYVRPDDAIDADAQERSTSVYFPRRMIPMLPENLSNGICSLNPDV				
	310	320	330	340	350	360
m988.pep		220	230	240	250	260
		ERLCMVCDMV VTYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL				
g988		ERLCMVCDMV VTYAGNIKEYRFYPAVMRSHARLTYNQVWKWLSDGIGNPHKAQIDTLYKL				
	370	380	390	400	410	420
m988.pep		280	290	300	310	320
		FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF				
g988		FKILQKKRLARGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF				
	430	440	450	460	470	480
m988.pep		340	350	360	370	380
		LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALVEQFKGRPD AE				
g988		LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALAEQFKGRPD AE				
	390					

1401

	490	500	510	520	530	540
	400	410	420	430	440	450
m988 . pep	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYTP					
g988	LLQVMMLRSMQQAVYEPHCEGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNRRKTYTP					
	550	560	570	580	590	600
	460	470	480	490	500	509
m988 . pep	KKSWQALGVHTSFCERRADDASRDVENWLKTYMMDKVGEVFEKGIS-GMTSFGIFVTL					
g988	NKSQWALGVHTSFCERRADDAGRDVENWLKTYMMDKVGEIFEKGISRGVANFGIFVTL					
	610	620	630	640	650	660
	510	520	530	540	550	569
m988 . pep	GIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRENMGDRVAVRVARADLDDGKIDFVL					
g988	DIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRENMGDRVAVRVARADLDDGKIDFVL					
	670	680	690	700	710	720
	570	580	590	600	610	629
m988 . pep	IAGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAESRKKAKKP					
g988	IAGESGRRRKVKLSASAKPAGAAGKGSKTAEKKTARCGKVRGRGVPVAESGKKAKKP					
	730	740	750	760	770	780
	630	640				
m988 . pep	VPIKVKRRKGKXS					
g988	VPIKVKRRKGKXS					
	790					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2983>:

```

a988 . seq
1  ATGAATAAAA ATATTAAATC TTAAATTTA CGGGAAAAAG ACCCGTTTTT
51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCAGT CGGGAATGGA
101 TAATCGAGCT GCTTGAACGT AAAGGCGTAC CATCCAGAT TGAAGCTTTG
151 GTACGCGAAT TGTCGATTAA GGAAGAAGAG TACGAATTTT TCGAACGTCG
201 TCTGAAGGCG ATGGCGGGG ACGGTCAGGT TTTAATCAAC CGTCGGGGCG
251 CGGTTTTCGC GCGGACAAA TTGGATTGG TCAATGCCG TGTCAAGGCG
301 CACAAAGACC GCTTCGGTTT CGCCGTGCCG CTCACGCCCG CCAAAGACGG
351 TGATTTTGTC TTGTACGAAC GCCAGATGCG CGGCATTATG CACGGCGATA
401 TTGTCACTGT TCGTCCTGCC GGCATGGACG GTAGGGGCGG CCGCGAAGGG
451 ACGGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
501 CTANATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTATTGGA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
601 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
651 GCCGGCAGTG GCAAAAATCA TCGAAGTTT GGGCGATTAT GCCGACAGCG
701 GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
751 AGTGAAGCGT GTGCCAAAGC CGCGAAAAAA ATTCCCGACC ATGTACGCAA
801 AAGCGATTTG AAAGGCGCGC TCGATTTCG CGACCTGCCT TTGGTAACGA
851 TAGACGGCGA AACGGCTCGA GATTTTGACG ATGCGGTGTT TGCCGAGAAA
901 ATCGGACGCA ATTACCGTCT GGTCTGGCG ATTGCCGATG TCAGCCATTA
951 TGTCCGCCCC GATGACGCTA TCGACACGGA CGCTCAGGAA CGCAGCACCA
1001 GTGTTTACTT CCCGCGCCGC GTGATTCCTA TGTGCGCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCTCATGTC GAGCGTTTGT GTGTGGTGTG
1101 CGATATGGTT ATCACTTACG CGGGCAATAT CAAAGAATAC CGCTTCTACC
1151 CCGCCGTGAT GCGCTCTCAT GCGCGCTGA CCTACAACCA AGTTTGAAA
1201 TGGCTTTCAG GCGGCATCGA GCATCCGTTT AAAACCCAAA TCGACACGCT
1251 TTACAAACTC TTCAAAATCC TTCAGAAAAA GCGTTTGGAA CGCGGGGCGG
1301 TGAGTTTGA CAGCATCGAA ACCCAAATGC TTTTCGACGA CAACGGTAAA
1351 ATTGAAAAAA TCGTCCCCGT TGTCGCAAC GATGCCACA AGCTGATTGA
1401 AGAATGTATG TTGGCGGCAA ACGTTTGGCG AGCGGATTTT CTGTTGAAA
1451 ACAAGCATAC CGCATTTGTC CGCAACCATT TGGGGCCAC GCCGAAAAA
1501 CTCGCCGCTT TGCGGAGCA GCTCGGCTG TTGGGGCTT ACTTGGCGG
1551 CGGCGACAAC CCGTCGCGGA AAGACTATG CGCGCTTGCC GGACAGTTCA

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1402

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1601 AAGGCAGGCC GGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAACAGGCGG TTTACGAACC GCATTGCGAC GGACACITTG GTCTTGCCCTA
1701 CGAAGCATAC GCCCACTTCA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1751 CCGTACACCG CGCCATCAAA GCCGTGTTGA ATCAGCAAAC CTACACGCCA
1801 AAAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1851 TGCCGACGAC GCCAGCCGCG ACGTGGAAAA CTGGCTGAAA ACCTATTATA
1901 TGCGCGATAA GGTGCGCGAA GTATTGGAAG GTAAAAATCTC CGGCATGACC
1951 AGTTTGGTA TCTTTGTAACT ACTGGACGGC ATCCACATTG ACGGCTTGGT
2001 GCATATCAGC GATTGCGCG AAGACTATTT CAACTTCCGC CCCGAAATCA
2051 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTTCACAT GGGGGACAGG
2101 GTTCCGTCCT GGTGCGCCCG TGCCGATTG GATGACGGAA AAATCGATT
2151 TGTCTGATT GCCGGGGGGA GCGGCAGGGG GCGGAAAGTT AAATCATCCG
2201 CGTCTGCCAA ACCGGCAGG ACGGCGGGGA AAGGGAAGCC GAAACCGCC
2251 GCCGAGAAAA AACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC
2301 TGCGCCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAGG
2351 TAAAAAACG GAAAGGCAAA TCATAA

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This corresponds to the amino acid sequence <SEQ ID 2984; ORF 988.a>:

a988.pep

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1 MNKNIKSLNL REKDFFLSRE KQRYEHLPLS REWIIELLER KGVPSKIEAL
51 VRELSIKEEE YEFFERRLKA MARDGQVLIN RRGAVCAADK LDIVKCRVKA
101 HKDRFGFAVP LTPAKDGDV LYERQMRGIM HGDIVTVRPA GMDGRGRREG
151 TVLDIVERAQ SKVVGFRFXMD RGVAILPEP KRLNQSIVLE PDGVARFKPE
201 SGQVIVGEIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPHQF
251 SEACAKAAKK IPDHVRKSDL KGRVDLRDL LVTIDGETAR DFDDAVFAEK
301 IGRNYRLVVA IADVSHYVRP DDAIDTDAQE RSTSVYFRR VIPMLPENLS
351 NGICSLNPHV ERLCVVCDMV ITYAGNIKEY RFYPAVMRSH ARLTYNQVWK
401 WLSGGIEHPF KTQIDTLYKL FKILQKKRFE RGAVEFDSIE TQMLFDDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LAALREQLGL LGLQLGGGDN PSPKDYAALA GQFKGRPDAA LLQVMMLRSM
551 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQQTYP
601 KKSQWALGVH TSFCERRADD ASRDVENWLK TYMRDKVGE VFEGKISGMT
651 SFGIFVTLDG IHIDGLVHIS DLGEDYFNFR PEIMAEGER SGIRFNMGRD
701 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGKPKTA
751 AEKKTARGGK VRGRGASAAA ESRKKAKPKV PIKVKRKGK S*

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m988/a988 97.0% identity in 641 aa overlap

```

                                10      20      30
m988.pep                                TVLDIVERAQSKVVGFRFYMDRGVAILEPED
                                |||
a988      LYERQMRGIMHGDIVTVRPA GMDGRGRREGTVLDIVERAQSKVVGFRFXMDRGVAILEPED
                                130      140      150      160      170      180

                                40      50      60      70      80      90
m988.pep      KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA
                                |||
a988      KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA
                                190      200      210      220      230      240

                                100      110      120      130      140      150
m988.pep      VRKHHLPHQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK
                                |||
a988      VRKHHLPHQFSEACAKAAKKIPDHVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK
                                250      260      270      280      290      300

                                160      170      180      190      200      210
m988.pep      VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFRRVIPMLPENLSNGICSLNPDV
                                :|||
a988      IGRNYRLVVAIADVSHYVRPDDAIDTDAQERSTSVYFRRVIPMLPENLSNGICSLNPHV
                                310      320      330      340      350      360

                                220      230      240      250      260      270
m988.pep      ERLCMVCDMVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL
                                |||
a988      ERLCVVCDMVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWLSGGIEHPFKTQIDTLYKL

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1403

	370	380	390	400	410	420
	280	290	300	310	320	330
m988.pep	FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
a988	FKILQKKRFERGAVEFDSIETQMLFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
	430	440	450	460	470	480
	340	350	360	370	380	390
m988.pep	LLKNKHTALFRNHLGPTPEKLATLREQLLGLQLGGDNPSPKDYAALVEQFKGRPDAE					
a988	LLKNKHTALFRNHLGPTPEKLAALREQLLGLQLGGDNPSPKDYAALAGQFKGRPDAE					
	490	500	510	520	530	540
	400	410	420	430	440	450
m988.pep	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYTP					
a988	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYTP					
	550	560	570	580	590	600
	460	470	480	490	500	510
m988.pep	KKSWQALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKISGMTSFGIFVTLDG					
a988	KKSWQALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKISGMTSFGIFVTLDG					
	610	620	630	640	650	660
	520	530	540	550	560	570
m988.pep	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDGKIDFVLI					
a988	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDGKIDFVLI					
	670	680	690	700	710	720
	580	590	600	610	620	630
m988.pep	AGGSGRGRKVKSSASAKPAGTAGKGKPKTAAEKKTARGGKVRGRGASAAESRKKAKKPV					
a988	AGGSGRGRKVKSSASAKPAGTAGKGKPKTAAEKKTARGGKVRGRGASAAESRKKAKKPV					
	730	740	750	760	770	780
	640					
m988.pep	PIKVKKRKGKSX					
a988	PIKVKKRKGKSX					
	790					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2985>:

```

g989.seq
1  ATGACCCCTT TCACACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCTT
51  TGCCGCCGCA TCTGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
191 TCAACGCGCA AAGCACGGCA AATGCCGCCG ACGCTCGCAC CATCTTCTAC
151 AATCCCGCCG GCCTGACCAA ACTCGACAGC AGCCAGATTT CCGTCAACGC
291 CAACATCGTG CTGCCAGCA TTCATTATGA AGCAGATTCC GCCACCGACT
251 TTACCGGGCT TCCCGTCCAA GGTTCATAAA ACGGCAAAAT CACCAAAACC
391 ACGGTCGCAC CCCACATTTA CGGCGCATAC AAAGTCAACG ACAATCTGAC
351 CGTGGGCTTG GCGGTGTACG TCCCCTTCGG CTCTGCCACC GAATACGAAA
491 AAGATTCCGT GTTGCGCCAC AACATCAACA AACTCGGTCT GACCAGCATC
451 GCCGTCGAAC CTGTCGCCGC GTGGAAGTCT AACGAACGCC ATTCCTTCGG
591 CGCAGGCATC ATCGCCCAAC ATAATTCGCG CGAATGCGCG AAATATGCCG
551 ACTGAGGAAT CCCAAAAAAA GCGCAAATGC TGCAAGCAAC ACCTTCTAAT
691 CCTACTGCCG CTGCTCAAAT CAAGGCCGAC GGACACGCCG ATGTCAAAGG
651 CAGCGATTGG GCGCTCGGCT ACCAACTGGC GTGGATGTGG GACATCAACG
791 ACCGCGCGCG CGTGGGCGTG AACTACCGTT CCAAAGTTTC ACACACGCTC
751 AAAGGCGATG CCGAATGGGC GGCAGACGGC GCGGCGGCGA AACAACAGTG
801 GAATGACAAT ATGCTCACAC CGCTCGGTTA CACGGCGAAT GAAAAAGCCA
851 GTGTCAAAAT CGTAACGCCT GAGTCTTTGT CCGTACACGG CATGTACAAA

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1404

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901 GTGTCCGACA AAGCCGACCT GTTCGGCGAC GTAACCTGGA CGCGCCACAG
951 CCGCTTCAAT AAGGCGGAAC TGTTTTTTGA AAAAGAAAAA AATATTGCTA
1001 ATGGCAAAAA ATCCGACCGC ACCACCATCA CCCCCAACTG GCGCAACACC
1051 TACAAAGTCG GCTTGGGCGG TTCTTATCAA ATCAGCGAAC CGCTGCAACT
1101 GCGCGTCGGC ATCGCTTTTG ACAAACCGCC TGTCGCGAAC GCCGACTacC
1151 GCATGAACAG CCTGCCCGAC GGCAACCGCA TCTGGTTCTC CGCCGGCATG
1201 AAATACCATA TCGGCAAAAA CCACGTCGTC GATGCCGCCT ACACCCACAT
1251 CCACATCAAC GACACCAGCT ACCGCACGGC GAAGGCAAGC GGCAACGATG
1301 TGGACAGCAA AGGTGCGTCT TCGGCACGTT TCAAAAACCA CGCCGACATC
1351 ATCGGCCTGC AATACACCTA CAAATTCAAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2986; ORF 989.ng>:

g989.pep

```

1 MTPFTLKKT V LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAADASTIFY
51 NPAGLTKLDS SQISVNANIV LPSIHYEADS ATDFTGLPVQ GSKNGKITKT
101 TVAPHIYGAY KVNNDLTVGL GVVVPFGSAT EYEKDSVLRH NINKLGLTSI
151 AVEPVAAWKL NERHSFGAGI IAQHNSAELR KYAD*GIFPK AQMLQATPSN
201 PTAAAIKAD GHADVKGS DW VGYYQLAWMW DINDRARVGV NYRSKVSHTL
251 KGDAEWAADG AAKQQWNND MLTPLGYTAN EKASVKIVTP ESLSVHGMK
301 VSDKADLFGD VTWTRHSR FN KAELFFEKEK NIANGKXSDR TTITPNWRNT
351 YKVLGGSYQ ISEPLQLRVG IAFDKPPVRN ADYRMNSLPD GNRIWFSAGM
401 KYHIGKNHVV DAAYTHIHIN DTSYRTAKAS GNDVDSK GAS CARFKNHADI
451 IGLQYTYKFK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2987>:

m989.seq

```

1 ATGACCCCTT CCGCACTGAA AAAAACCCTC CTGCTGCTCG GCACTGCCTT
51 TGCCGCCGCA TCCGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCACGGCA AATGCCGCGC CCGCAGAGC CGCCGACGCA
151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAAACTCG ACAGCAGCCA
201 GATTTCCTGC AACGCCAACA TCGTGCTGCC CAGCATTTCAT TATGAGGCGG
251 ATTCCGCCAC CCACTTTACC GGGCTTCCCG TCCAAGSTTC GAAAAGCGGC
301 AAAATCACCA AAACACGGT CGCGCCAC ATCTACGCG CATACAAAGT
351 CAACGACAAT CTGACCGTGG GCTTGGGCGT GTACGTCCCC TTCGGCTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA
501 CCGCCATTCC TTCCGCGCAG GCATCATCGC CCAACATACT TCCGCCGAAC
551 TGCGCAAATA TGCCGACTGG GGGATTAAGA GTAAAGCAGA GATATTGACG
601 GCAAAACCGC CCAACCTAA CGGTGTAGCC GAAGCTGCAA AAATTCAGGC
651 CGACGGACAC GCCGATGTCA AAGGCAGCGA TTGGGGCTTC GGCTACCAAC
701 TGGCGTGGAT GTGGGACATC AACGACCGTG CGCGCGTGG CGTGAACATC
751 CGTTCCAAAG TCTCGCACAC GCTCAAAGGC GATGCCGAAT GGGCGGCAGA
801 CGGCGCGGCG GCGAAAGCAA TGTGGAGTAC GATGCTTGCA GCAAACGGCT
851 ACACGGCGAA TGAAAAAGCC CGCGTTAAAA TC GTTACGCC TGAGTCTTTG
901 TCCGTACACG GTATGTACAA AGTGTCCGAT AAAGCCGACC TGTCGGGGA
951 CGTAACCTGG ACGCGCCACA GCCGCTTCGA TAAGGCGGAA CTGGTTTTTG
1001 AAAAAGAAAA AACCGTCTGC AAAGGCAAAT CCGACCGCAC CACCATCACC
1051 CCCAACTGGC GCAACACCTA CAAAGTCGGC TTCGGCGGTT CTATCAAAT
1101 CAGCGAACCG CTGCAACTGC GCGCCGGCAT CGCTTTTGAC AAATCGCCCG
1151 TCCGCAACCG CGACTACCGC ATGAACAGCC TACCCGACGG CAACCGCATC
1201 TGGTTCTCCG CCGGTATGAA ATACCATATC GGTAAAAACC ACGTCGTGCA
1251 TGCCGCTTAC ACCCACATCC ACATCAACGA CACCAGCTAC CGCACGGCGA
1301 AGGCAAGCGG CAACGATGTG GACAGCAAAG GCGCGTCTTC CGCACGTTTC
1351 AAAAACCACG CCGCATCATC CGGTCTGCAA TACACCTACA AATTCAAATA
1401 A

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This corresponds to the amino acid sequence <SEQ ID 2988; ORF 989>:

m989.pep

```

1 MTPSALKKT V LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAAAAEADA
51 STIFYNPAGL TKLDSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNDRHS FGAGIIAQHT SAELRKYADW GIKSKAEILT
201 AKPPKPNVGA EAAKIQADGH ADVKGS DW GYQLAWMW DI NDRARVGVNY
251 RSKVSHTLKG DAEWAAAGAA AKAMWSTMLA ANGYTANEKA RVKIVTPESL
301 SVHGMKVS D KADLFGDVTW TRHSRFDKAE LVFEKEKT VV KGKSDRTTIT

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1405

351 PNWRNTYKVG FGGSYQISEP LQLRAGIAFD KSPVRNADYR MNSLPDGNRI
 401 WFSAGMKYHI GKNHVVDAAI THIHINDTSY RTAKASGNDV DSKGASSARF
 451 KNHADIIGLQ YTYKFK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

g989/m989 90.0% identity in 468 aa overlap

	10	20	30	40	50
g989.pep	MTPFTLKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAA-----DASTIFYNPAGL				
m989	MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEADASTIFYNPAGL				
	10	20	30	40	50
	60	70	80	90	100
g989.pep	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKNGKITKTTVAPHIYGAYKVNND				
m989	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNND				
	70	80	90	100	110
	120	130	140	150	160
g989.pep	LTVGLGVYVFPFSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSFGAGIIAQHN				
m989	LTVGLGVYVFPFSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNRHSFGAGIIAQHT				
	130	140	150	160	170
	180	190	200	210	220
g989.pep	SAELRKYADXGIPKKAQMLQATPSNPTA---AAQIKADGHADVKGSDWGVGYQLAWMWDI				
m989	SAELRKYADWGIKSKAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWGFYQLAWMWDI				
	190	200	210	220	230
	240	250	260	270	280
g989.pep	NDRARVGVNYSKVSHTLKGDAEWAADGAAAKQWQNDNMLTPLGYTANEKASVKIPTPES				
m989	NDRARVGVNYSKVSHTLKGDAEWAADGAAAKAMWS-TMLAANGYTANEKARVKIPTPES				
	250	260	270	280	290
	300	310	320	330	340
g989.pep	LSVHGMVKVSDKADLFGDVTWTRHSRFENKAELFFEKEKNIANGKKS DRTTITPNWRNTYK				
m989	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAEVLFEKEKTVVKGK-SDRTTITPNWRNTYK				
	300	310	320	330	340
	360	370	380	390	400
g989.pep	VGLGGSYQISEPLQLRVGIAFDKPPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVDA				
m989	VGFSGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVDA				
	360	370	380	390	400
	420	430	440	450	460
g989.pep	AYTHIHINDTSYRTAKASGNDVDSKGASCARFKNHADIIGLQYTYKFKX				
m989	AYTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX				
	420	430	440	450	460

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2989>:

a989.seq
 1 ATGACCCCTT CCGCACTGAA AAAAACCGTC CTA CTGCTCG GCACTGCCTT
 51 TGCCGCCGCA TCCGCACAAG CCTCCGGCTA CCACTTCGGC ACACAGTCGG
 101 TCAACGCGCA AAGCACGGCA AATGCCGCG CCGCAGAAGC CGCCGACGCA
 151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAACTCG ACAGCAGCCA
 201 GATTTCGCTC AACGCCAACA TCGTGCTGCC CAGCATTAT TATGAGCGG
 251 ATTCGCCAC CGACTTTACC GGGCTTCCG TCCAAGGTT GAAAAGCGG

1406

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301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTAG GCTTGGGCGT GTACGTCCCC TTCGGTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA
501 ACGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAGC
551 TGCGCAAATA TGCCGACTGG GGGATTATGG AAAAAGCGAA AGCACTAAAA
601 GAAACACCCC CCAATCCAAC TAAAGCCGCC CAAATCAAAG CCGACGGACA
651 CGCCGATGTC AAAGGCAGCG ATTGGGGCTT CGGCTACCAA CTGGCGTGGA
701 TGTGGGACAT CAACGACCGT GCGCGCGTGG GCGTGAAC TA CCGTCCAAA
751 GTCTCACACA CGCTCAAAGG CGATGCCGAA TGGGCGGCAG ACGACGCAAT
801 GGCGAACAG TTATGGGATG CAAACAACT CGCACTGCTC GGCTACACGC
851 CAAGCGAAAA AGCCCGCGTT AAAATCGTTA CGCCCGAGTC TTTGTCCGTA
901 CACGGTATGT ACAAAGTGTC CGACAAAGCC GACCTGTTTG GCGACGTAAC
951 TTGGACGCGC CACAGCCGCT TCGATAAGGC GGAAGTGGTT TTTGAAAAAG
1001 AAAAAACCAT CGTCAACGGC AAATCCGACC GCACCAACAT CACCCCCAAC
1051 TGGCGCAACA CCTACAAAGT CGGCTTCGGC GGTCTTTATC AAATCAGCGA
1101 ACCGCTGCAA CTGCGCGCCG GCATCGCTTT TGACAAATCG CCCGTCCGCA
1151 ACGCCGACTA CCGCATGAAC AGCCTGCCCG ACGGCAACCG CATCTGGTTC
1201 TCCGCCGGCA TGAAATACCA TATCGGCAAA AACCACGTCG TCGATGCCGC
1251 CTACACCCAC ATCCACATCA ACGACACCAG CTACCGCAG GCGAAGGCAA
1301 GCGGCAACGA TGTGGACAGC AAAGGCGCGT CTCCGCACG TTTCAAAAAC
1351 CACGCCGACA TCATCGGCCT GCAATACACC TACAAATTCA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2990; ORF 989.a>:

```

a989.pep
1  MTPSALKKTV LLLGTAFAAA SAQASGYHFG TQSVNAQSTA NAAAAEADA
51  STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVNDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNERHS FGAGIIAQHT SAELRKYADW GIMEKAKALK
201 ETPPNPTKAA QIKADGHADV KGSWGFYQ LAWMWDINDR ARVGVNYSK
251 VSHTLKGADE WAADDAMAKQ LWDANKLALL GYTPSEKARV KIVTPESLSV
301 HGMYKVSDKA DLFQDVTWTR HSRFDKAEV FEKEKTIYNG KSDRTTITPN
351 WRNTYKVGFG GSYQISEPLQ LRAGIAFDKS PVRNADYRMN SLPDGNRIWF
401 SAGMKYHIGK NHVVDAAATH IHINDTSYRT AKASGNDVDS KGASSARFKN
451 HADIIGLQYT YKFK*

m989/a989 93.1% identity in 467 aa overlap

          10      20      30      40      50      60
m989.pep  MTPSALKKTVLLLGTAFAAASVHSAQASGYHFGTQSVNAQSTANAAAAEADASTIFYNPAGL
a989      MTPSALKKTVLLLGTAFAAASVHSAQASGYHFGTQSVNAQSTANAAAAEADASTIFYNPAGL
          10      20      30      40      50      60

          70      80      90      100     110     120
m989.pep  TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
a989      TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
          70      80      90      100     110     120

          130     140     150     160     170     180
m989.pep  LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNDRHSGAGIIAQHT
a989      LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSGAGIIAQHT
          130     140     150     160     170     180

          190     200     210     220     230     240
m989.pep  SAELRKYADWGIKSKAEILTAKPPKPNVGAEEAKIQADGHADVKGSDWGFYQLAWMWDI
a989      SAELRKYADWIMEKAKALKETPPNPT---KAAQIKADGHADVKGSDWGFYQLAWMWDI
          190     200     210     220     230

          250     260     270     280     290     299
m989.pep  NDRARVGVNYSKVSHTLKGADEWAADGAAAKAMW-STMLAANGYTANEKARVKIVTPES
a989      NDRARVGVNYSKVSHTLKGADEWAADAMAKQLWDANKLALLGYTPSEKARVKIVTPES

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1407

	240	250	260	270	280	290
m989.pep	300	310	320	330	340	350
	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAEVFEKEKTIVVKGKSDRTTITPNWRNTYKV					
a989	300	310	320	330	340	350
	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAEVFEKEKTIVVKGKSDRTTITPNWRNTYKV					
m989.pep	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDA					
a989	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDA					
m989.pep	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					
a989	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2991>:

```

m990.seq
1   ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCACCA AAATCGGCGA
51  CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTCCAG CGGTAAACC GATCAAAAT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAATTACAAT AGCGGCATCC TCGCCGTCGA
201 TAATATGCCC GTTGTCAAAA AATATATTAC AGAGAAGTAT GGGGCTGATT
251 TAAAGCAGGC GGTAAAAAGT CAATTACAGG ATTTATACAA AACAAGACCG
301 GAAGCTTGGG CAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGCACA
351 GTTTGGAACA AAATTTAGTA CGCTCAAACA GACGATGCCC GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTC AATCGAAAA
501 CAAATCCAC GTCGCCGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TACGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAAGTAC
651 CGTCCATAAG GATTATGCGG GCGGCGCGGA TTTCTGTTC GGCTACGACG
701 TGCGGGAGTC GGACGAACCC GCCCTGACCT TTGAAGACAA AGTCAGCGGA
751 CAATCCGGCG TGGTTTGGG ACGCCGCGCG GAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CAAAACGGC GGATTCCGGT TCGTTTGCCT
851 TTAAACAAAA TTACCGGCAG GGACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCAAC AGGCTTATGC GGCAAATACT TTGTTTGGGC
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCCT
1051 CAAAAATTGT GGCTGCGCTT CATCGCGGCG CGGTGCGATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GGTGGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGAGGCC GACTGCAAT CCGCGTGATG
1201 GCGGCGAGGG CCGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTGAT TTGTATGGTT ATGGCGGGGG TGTATTGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGGG AACGTACAA
1401 AACCAAAGGT TGGACGGCTT CTGTCGAAGG CGGTACAAC GCGCTTGTGG
1451 CGGAAGGCAT TGTCGGAAAA GGCAATAATG TGCGGTTTTA CCTACAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAGTGGCAA AGCCGCGCCG
1601 GCATTGCGGC AAAAACCCGT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGGCG CTTTAAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCA CTCGAAGGCG
1751 GGTTCGGTAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TATGGCAAAA GGACGGACGG CGACAAAGAA GCCGATTGT CGCTCAAATG
1851 GCTGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2992; ORF 990>:

m990.pep

1408

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQQKKNYN SGILAVDNMP VVKYITEKY GADLKQAVKS QLQDLYKTRP
101 EAWAENKKRT EEAYIAQFGT KFSTLKQTMP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK DYAGGADFLF GYDVRESDEP ALTFEDKVSQ
251 QSGVVLERRP ENLKTLDGRK LIAAKTADSG SFAFKQNYRQ GLYELLKQC
301 EGGFCLGVQR LAIPEAEAVL YAOQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIIRGGA AADGWRKGVQ IGGEVFVRQN EGSRLAIGVM
401 GGRAGQHASV NGKGAAGSD LYGYGGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGIVGK GNNVRFYLPQ
501 QAQFTYLGVN GGFTDSEGA VLLGSGQWQ SRAGIRAKTR FALRNGVNLQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSLKWLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2993>:

a990.seq

```

1 ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCGA
51 CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTTCAG CCGTAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAACATAAT AGCGGCATAC TCGCCGTCGA
201 TAATATGCCC GTTGTAAAGA AATATATTAC AGATACTTAC GGGGATAATT
251 TAAAGGATGC GGTAAAGAAG CAATTACAGG ATTTATACAA AACAAAGCCC
301 GAAGCTTGGG AAGAAATAA AAAACGGACT GAGGAGGCGT ATATAGAACA
351 GCTTGGACCA AAATTTAGTA TACTCAAACA GAAAAACCCC GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCAC GTCGCCGAC AGGTGTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TATGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAACTGAC
651 CGTCCATAAA GCGTATCAGG GCGGTGCGGA TTTCCTGTTC GGCTACGACG
701 TGCGGGAGTC GGACAAACCC GCCCTGACCT TTGAAGAAAA AGTCAGCGGA
751 CAATCCGCGG TGGTTTGGGA ACGCCGCGCG GAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CGGAAAGGC AGACTCTAAT TCGTTTGCCT
851 TTAAACAAAA TTACCGGCAG GGAATGTACG AATTATTGCT CAAGCAATGC
901 GAAGGCGGAT TTTGCTTGGG CGTGACGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAAAATACT TTGTTGCGGC
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCCT
1051 CAAAATTGT GGCTGCGCTT CATCGCGGCG CGGTGCGATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GCGCGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GGCTGGCAAT CGGCGTGATG
1201 GCGGCGAGGG CTGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTTAT TTGCATGGTT ATGGCGGGGG TGTATTATGCT GCGTGCGATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGCGTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCCTGCGG AACGCTACAA
1401 AACCAAAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAC GCGCTTGTGG
1451 CGGAAGGCGT TGTGCGAAAA GGCAATAATG TGCGGTTTTA CTGCAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGAAGTC TCGGCGAGCG TCAGTGCGAA AGCCGCGCCG
1601 GCATTCGGGC AAAAACCCGT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGCCG CTTTAAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCG CTCGAAGGGC
1751 GGTTCGGCAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TACGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
1851 GCTGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2994; ORF 990.a>:

a990.pep

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQQKKNYN SGILAVDNMP VVKYITDITY GDNLKDAVKK QLQDLYKTRP
101 EAWAENKKRT EEAYIEQLGP KFSILKQKNP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHMLE
201 TSDNARIRLN TKDEKLTVHK AYQGGADFLF GYDVRESDEP ALTFEEKVSG
251 QSGVVLERRP ENLKTLDGRK LIAAEKADSN SFAFKQNYRQ GLYELLKQC
301 EGGFCLGVQR LAIPEAEAVL YAOQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIIRGGA AADGRRKGVQ IGGEVFVRQN EGSRLAIGVM

```

1409

401 GGRAGQHASV NGKGAAGSY LHGYGGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKHRINDE NRAERYKTG WTASVEGGYN ALVAEGVVGK GNNVRFYLQP
501 QAQFTYLGVN GGFTDSEGTA VLLGSGQWQ SRAGIRAKTR FALRNGVNLQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSLKWLF*

m990/a990 96.0% identity in 619 aa overlap

	10	20	30	40	50	60
m990.pep	M	F	R	A	Q	L
a990	M	F	R	A	Q	L
	70	80	90	100	110	120
m990.pep	S	G	I	L	A	V
a990	S	G	I	L	A	V
	130	140	150	160	170	180
m990.pep	K	F	S	T	L	K
a990	K	F	S	T	L	K
	190	200	210	220	230	240
m990.pep	M	T	L	K	D	S
a990	M	T	L	K	D	S
	250	260	270	280	290	300
m990.pep	A	L	T	F	E	K
a990	A	L	T	F	E	K
	310	320	330	340	350	360
m990.pep	E	G	G	F	C	L
a990	E	G	G	F	C	L
	370	380	390	400	410	420
m990.pep	R	S	H	Q	N	I
a990	R	S	H	Q	N	I
	430	440	450	460	470	480
m990.pep	L	H	G	Y	G	G
a990	L	H	G	Y	G	G
	490	500	510	520	530	540
m990.pep	A	L	V	A	E	G
a990	A	L	V	A	E	G
	550	560	570	580	590	600
m990.pep	F	A	L	R	N	G
a990	F	A	L	R	N	G

1410

		550	560	570	580	590	600
		610	620				
m990.pep	YGKRTDGDKEAALSLKWLFX						
a990	YGKRTDGDKEAALSLKWLFX						
		610	620				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2995>:

```

g992.seq
1  ATGTTTCAGAC GGCATCGGCA TTTGAAAAAT ATGCAGATTA AAAAAATCAT
51  GAAATGGCTT CCCGTCGCCC TGTCGCTTTT GGGCGCGTTG GGTATACGG
101 GATATGACAG TGAGGCGGTG CGGACGGCGG TTGCCGTA CTACGTA CT
151 G3CACTGCAG GGGACGTGGG TTTGACGCG CCCGTTCCGC GACGGGCATC
201 GCGGAAATCC GGCCACAGCT ACACAGGCAC GGTGTCCAAA GTCTATGACG
251 GCGATACCCCT TCACGTCATC GACGGCGACG GCGCGAAACA TAAATTCGG
301 ATGGCGTATA TCGACGCACC GGAGATGAAA CAGGCTTACG GTACACGTTT
351 GCGCGACAAC CTGCGCGCGG CCGCGGAGGG TAGGAAAGTC AGTGTACGTG
401 TGTTTGAAAC CGACCGCTAT CAGCGCGAAG TGGCGCAGGT ATCCGCCGCG
451 AAAACCGATT TGAACCTGAT GCAGGTGCAG GACGGGCGCG CGTGGCATT
501 TAAAGTTTAT GCTAAAGAAC AGCAGGATAA GCGGGAATTT GCCGACTATG
551 CCGACGCTCA AATTCAGGCG GAAAGGGAAC GCAAAGGATT GTGGAAAGCT
601 AAAAAATCCGC AAGCGCCGTG GCGGTACCGC CGGGCAGGCA GGAGCGGCGG
651 GGGCAATAAG GATTGGATGG ATTCCTGGGG CGAATGGTTG GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2996 ORF 992.ng>:

```

g992.pep
1  MFRRRHRLKN MQIKKIMKWL PVALSLLGAL GYTGVDSEAV RTAVAVLDVL
51  GTAGDVGFDA PVRRRASAKS GHSYTGTVSK VYDGTDLHVI DGDGAKHKIR
101 MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFETDRY QREVAQVSAG
151 KTDNLNMQVQ DGAAWHYKSY AKEQQDKADF ADYADAQIQ A ERERKGLWKA
201 KNPQAPWAYR RAGRSGGGNK DWMDSVGEWL GIW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2997>:

```

m992.seq
1  ATGTTTCAGAC GGCATCGGCA TTTGAAAAAT ATGCAGATTA AAAAAATCAT
51  GAAATGGCTT CCCGTCGCCC TGTCGCTTTT GGGTGCCTTG GGTATACGG
101 GGTACGGCAG CGAGGCGGTG CGGACGGCGG TTGCCGTA CTACGTA CT
151 GCGCGGCGAG GGGACGCGGG TTTCCGACCG CCCGCCCGCC GCCGAGCATC
201 GCGGAAATCC GGCCACCGCT ACACAGGCAC GGTGTCCAAA GTCTATGACG
251 GCGACACCCT TCACGTTATC GACGGCGACG GCGCGAAACA CAAATTCGG
301 ATGGCGTATA TCGACGCGCC GGAGATGAAA CAGGCTTACG GCACGCGTTC
351 GCGCGACAAC CTGCGCGCGG CCGCGGAAGG CAGGAAAGTC AGCGTCCGCG
401 TGTTGCATAC CGACCGCTAC CAGCGCGAAG TGGCGCAGGT TTCTGTCCGG
451 AAAACCGATT TGAACCTGAT GCAGGTGCAG GACGGGCGCG CGTGGCATT
501 TAAAGTTTAT GCTAAAGAAC AGCAGGATAA GCGGGAATTT GCCGATTATG
551 CCGACGCTCA AATTCAGGCG GAAAGGGAAC GCAAAGGATT GTGGAAAGCT
601 AAAAAATCCGC AAGCGCCGTG GCGGTACCGC CGAGCAGGCA GGAGCGGCGG
651 GGGCAATAAG GATTGGATGG ATGCCGTGGG CGAATGGTTG GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2998; ORF 992>:

```

m992.pep
1  MFRRRHRLKN MQIKKIMKWL PVALSLLGAL GYTGVCSEAV RTAVAVLDVL
51  GAAGDAGSDA PARRRASAKS GHRYTGTVSK VYDGTDLHVI DGDGAKHKIR
101 MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFETDRY QREVAQVSAG
151 KTDNLNMQVQ DGAAWHYKSY AKEQQDKADF ADYADAQIQ A ERERKGLWKA
201 KNPQAPWAYR RAGRSGGGNK DWMDAVGEWL GIW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 992 shows 96.1% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. gonorrhoeae*

m992/g992 96.1% identity in 233 aa overlap

1411

	10	20	30	40	50	60
m992 .pep	MFRRRHRLKNNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
g992	MFRRRHRLKNNMQIKKIMKWL PVALSLLGALGYTGYDSEAVRTAVAVLDVLGTAGDVGFDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m992 .pep	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN					
g992	PVRRRASAKSGHSYTGTVSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m992 .pep	LRAAAEGRKVSVRVFD TDRYQREVAQVSVGKTD LNLMOVQDGA AWHYKSYAKEQQDKADF					
g992	LRAAAEGRKVSVRVFET DRYQREVAQVSAGKTD LNLMOVQDGA AWHYKSYAKEQQDKADF					
	130	140	150	160	170	180
	190	200	210	220	230	
m992 .pep	ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRS GGGNKDWM DAVGEWLGIWX					
g992	ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRS GGGNKDWM DSVGEWLGIWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2999>:

```
a992.seq
1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCT  TGTGCGTTT  GGGTGCCTTG  GGTATACGG
101 GGTACGGCAG  CGAGCGCGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GGC GCGGCAG  GGGACGCGGG  TTCCGACGCG  CCCGCCCGCC  GCCGAGCATC
201 GGC GAAATCC  GGCCACCGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGACACCT  TCACGTTATC  GACGCGGACG  GCGCGAAACA  CAAAATCCGG
301 ATGGCGTATA  TCGACGCGCC  GGAGATGAAA  CAGGCTTACG  GCACGCGTTC
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAAGG  CAGGAAAGTC  AGCGTCCGCG
401 TGTTGCGAC  CGACGCTAC  CAGCGCGAAG  TGGCGCAGGT  TTCTGTGCGG
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGCGCG  CGTGGCATTG
501 TAAAAGTTAT  GCTAAAGAAC  AGCAGGATAA  GGCGGATTTT  GCCGATTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAATCCGC  AAGCGCCGTG  GCGGTACCG  CGGGCAGGCA  GGAGCGCGCG
651 GGGCAATAAG  GATTGGATGG  ATGCCGTGGG  CGAATGGTTG  GGCATTGCGT
701 AA
```

This corresponds to the amino acid sequence <SEQ ID 3000; ORF 992.a>:

```
a992.pep
1  MFRRRHRLKN  MQIKKIMKWL  PVALSLLGAL  GYTGYGSEAV  RTAVAVLDVL
51  GAAGDAGSDA  PARRRASAKS  GHRYTGTVSK  VYDGD TLHVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFD TDRY  QREVAQVSVG
151 RTDLNLMQVQ  DGA AWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRS GGGNK  DWM DAVGEWL  GIW*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 992 shows 100.0% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. meningitidis*

a992/m992 100.0% identity in 233 aa overlap

	10	20	30	40	50	60
a992 .pep	MFRRRHRLKNNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
m992	MFRRRHRLKNNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a992 .pep	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN					
m992	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
	130	140	150	160	170	180

1412

```

a992.pep      LRAAAEGRKVSVRVFDTRYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQDKADF
m992          LRAAAEGRKVSVRVFDTRYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQDKADF
              130      140      150      160      170      180

              190      200      210      220      230
a992.pep      ADYADAQIQAERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWM DAVGEWLGIWX
m992          ADYADAQIQAERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWM DAVGEWLGIWX
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3001>:

```

g993.seq
1   CTGAAAGTCG TATTGGGCAG TTTCAAGGC CCTTTGGATC TGCTGCTCTA
51  CCTTATCCGC AAGCAGAACA TCGATGTTCT CGATATTCCG ATGGTGGAAG
101 TTACCGGGCA GTATCTGCAC TATATTGCCC AAATGGAAGC CTATCAGTTT
151 GATTTGGCGG CGGAATATCT TTTGATGGCG GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAGGCGG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCTGCG TTGCCATACGA GCAAATGAAA
301 CTGGCGGCGC AGGGTTTGGA CGCGCTGCCG CGTGCGGGAC GGGATTTCGC
351 GTGGGCTTAC CTGCCGCTGG AAATTGCAGC CGAGACGAAG CTGCCCCGAGG
401 TTTACATCGC CGATTGATG CAGGCATGGT TGGGCATTCT TTCTCGGGCA
451 AAACATACGC GCAGCCACGA AGTAATCCAA GAAACCCCTT CCGTGCGCGC
501 GCAAATGACG GCAATCCTGC GCCGTTTGAA CGAACACGGG ATATGCAGGT
551 TTCACGCCCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GATCGTCAAC
601 TTCATCGCCC TGTGGAGCT TGCCAAAGAA GGATTGGTCG GAATCGTACA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTTCGGC ACACGGGGCG GCGCGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3002 ORF 993.ng>:

```

g993.pep
1   LKVVLSFGQ PLDLLLYLIR KQNI DVLDIP MVEITGQYLH YIAQMEAYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTEAVED EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAAETK LPEVYIADLM QAWLGILSRA
151 KHTRSHEVIQ ETLSVRAQMT AILRLRNEHG ICRFHALFNP EQGAAYVIVN
201 FIALLELAKE GLVGIVQEDG FGEIRISLNH EGAHSDGIFG TRGGRDVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3003>:

```

m993.seq
1   TTGAAAGTCG TATTGGGCAG CTTCCAAGGC CCTTTGGATC TACTGCTGTA
51  TCTGATCCGC AAACAGAATA TCGACGTACT GGATATTCCG ATGGTGGAAG
101 TTACCGGACA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
151 GATTTGGCGG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAAGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCTGCG TGGCTTACGA ACAGATGAAG
301 CTGGCGGCGC AGGGTTTGGA CGCGCTGCCG CGAGCCGGAC GGGATTTCGC
351 GTGGGCTTAC CTGCCGCTGG AAATTGCCGT CGAAGCCAAG CTGCCCGAAG
401 TCTATATTAC CGACTTGACG CAAGCGTGGC TGGGTATTTT GTCTCGGGCA
451 AAACACACGC GCAGCCACGA AGTAATCAAA GAAACCATCT CCGTGCGCGC
501 GCAAATGACG GCAATCCTGC GCCGTTTGAA CGGACACGGA ATATGCAGGT
551 TTCACGACCT GTTCAATCCC AAACAGGGCG CGGCTTACGT GGTCTGCAAC
601 TTCATCGCAC TGTGGAGCT TGCCAAAGAA GGATTGGTCA GAATCGTGCA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTCCGGC ACACGAGGCG GCGCGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3004; ORF 993>:

```

m993.pep
1   LKVVLSFGQ PLDLLLYLIR KQNI DVLDIP MVRITEQYLH YIAQIETIQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTETVED EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLGILSRA
151 KHTRSHEVIK ETISVRAQMT AILRLRNGHG ICRFHDLENP KOGAAYVVVN
201 FIALLELAKE GLVRIVQEDG FGEIRISLNH EGAHSDGISG TRGGRDVF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 993 shows 93.1% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. gonorrhoeae*

1413

m993/g993 93.1% identity in 248 aa overlap

m993.pep	10	20	30	40	50	60
	LKVVLSFGQPLDLLLYLIRKQNI	DVLDIPMVKITEQYLHYIAQI	ETYQFDLAAEYLLMA			
g993	10	20	30	40	50	60
	LKVVLSFGQPLDLLLYLIRKQNI	DVLDIPMVEITGQYLHYIAQME	AYQFDLAAEYLLMA			
m993.pep	70	80	90	100	110	120
	AMLIEIKSRLLLPRTETVEDEE	ADPRAELVRRLAYEQMKLAAQ	GLDALPRAGRDFAWAY			
g993	70	80	90	100	110	120
	AMLIEIKSRLLLPRTAEVEDEE	ADPRAELVRRLAYEQMKLAAQ	GLDALPRAGRDFAWAY			
m993.pep	130	140	150	160	170	180
	LPLEIAVEAKLPEVYITDLTQ	AWLGILSRAKHTRSHEVIKET	ISVRAQMTAILRRLNCHG			
g993	130	140	150	160	170	180
	LPLEIAAETKLPVYIADLMQ	AWLGILSRAKHTRSHEVIQET	LSVRAQMTAILRRLNEHG			
m993.pep	190	200	210	220	230	240
	ICRFHDLFNPQGAAYVVVNF	IALLELAKEGLVRIVQEDGF	GEIRISLNHEGAHSDGISG			
g993	190	200	210	220	230	240
	ICRFHALFNPQGAAYVIVNF	IALLELAKEGLVGIVQEDGF	GEIRISLNHEGAHSDGIEG			
m993.pep	249					
	TRGGRDVFX					
g993						
	TRGGRDVFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3005>:

a993.seq

1	CTGAAAGTCG	TATTGAGCAG	TTTCAAGGC	CCTTTGGATC	TGCTGCTCTA
51	CCTTATCCGC	AAGCAGAACA	TCGATGTTCT	CGATATCCG	ATGGTGAAGA
101	TTACCGAACA	GTATCTGCAC	TACATCGCCC	AAATAGAAAC	CTATCAGTTT
151	GATTTGGCGG	CGGAATATCT	TTTGATGGCA	GCAATGCTGA	TTGAAATCAA
201	ATCGCGCCTG	CTGCTGCCGC	GTACCGAAAC	CGTCGAAGAC	GAAGAAGCCG
251	ACCCGCGTGC	CGAGTTGGTG	CGCCGCTGTC	TGGCTTACGA	GCAGATGAAG
301	CTGGCGGCAC	AAGGGTTGGA	TGCGCTTCCT	CGTGCGGGCC	GGGATTTCSC
351	ATGGGCATAC	CTGCCACTGG	AAATTGCCGT	CGAAGCCAAG	CTGCCCGAAG
401	TCTATATTAC	CGACTTGACG	CAGGCGTGGC	TGAGTATTTT	GTCTCGGGCA
451	AAACATACGC	GCAGCCACGA	AGTTATCAAA	GAAACCATCT	CCGTGCCGSC
501	GCAATGACG	GCAATCCTGC	GCCGTTTGAA	CAAACACGGG	ATATGCAGST
551	TTCACGACCT	GTTCAATCCC	GAACAGGGCG	CGGCTTACGT	GGTCGTCAAC
601	TTCATCGCAC	TGTTGGAGCT	TGCCAAAGAA	GGTTGGTTCG	GAATCGIACA
651	GGAACTCGGT	TTCGGAGAAA	TCCGAATCAG	CCTCAATCAT	GAGGGGGCGC
701	ATTCAGACGG	CATTCCGGC	ACACGGGGCG	GGCGGATGT	GTTCTAA

This corresponds to the amino acid sequence <SEQ ID 3006; ORF 993.a>:

a993.pep

1	LKVVLSFQGP	PLDLLLYLIR	KQNI	DVLDIP	MVKITEQYLH	YIAQIETYQF
51	DLAAEYLLMA	AMLIEIKSRL	LLPRTETVED	EADPRAELV	RRLAYEQMK	
101	LAAQGLDALP	RAGRDFAWAY	LPLEIAVEAK	LPEVYITDLT	QAWLSILSRA	
151	KHTRSHEVIK	ETISVRAQMT	AILRRLNKHG	ICRFHDLFNP	EQGAAYVVVN	
201	FIALELAKE	GLVGIVQEVG	FGEIRISLNH	EGAHSDGISG	TRGGRDVF*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 993 shows 97.6% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. meningitidis*

a993/m993 97.6% identity in 248 aa overlap

a993.pep	10	20	30	40	50	60
	LKVVLSFQGP	PLDLLLYLIRKQNI	DVLDIPMVKITEQYLHYIAQI	ETYQFDLAAEYLLMA		
m993						
	LKVVLSFGQGP	PLDLLLYLIRKQNI	DVLDIPMVKITEQYLHYIAQI	ETYQFDLAAEYLLMA		

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	10	20	30	40	50	60
a993.pep	70	80	90	100	110	120
	AMLEIEIKSRLLLPRTETVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY					
m993	70	80	90	100	110	120
	AMLEIEIKSRLLLPRTETVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY					
a993.pep	130	140	150	160	170	180
	LPLEIAVEAKLPEVYITDLTQAWLSILSRKHTRSHEVIKETISVRAQMTAILRRLNKHG					
m993	130	140	150	160	170	180
	LPLEIAVEAKLPEVYITDLTQAWLGILSRKHTRSHEVIKETISVRAQMTAILRRLNGHG					
a993.pep	190	200	210	220	230	240
	ICRFHDLFNPQGAAYVVVNFIALLELAKEGLVGIVQEVGFGEIRISLNHEGAHSDGISG					
m993	190	200	210	220	230	240
	ICRFHDLFNPQGAAYVVVNFIALLELAKEGLVRIVQEDGFGEIRISLNHEGAHSDGISG					
a993.pep	249					
	TRGGRDVFX					
m993	TRGGRDVFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3007>:

g996.seq

```

1  ATGAACAGAA  GAACCTTCCT  CCTCGGCGCA  GCGCGTTGCG  TTCTTACCGC
51  CTGCGGCAGA  AAATCCGCC  GAACCCACGC  CAAATTTCCC  GAAGGAAGCA
101 CCGTGCTTGC  CTTGGGCGAT  TCGCTCACCT  TCGGCTACGG  AGCAAACCC
151 GCGGAATCCT  ACCCGCGCA  ACTGCAAAA  CTGACGGGTT  GGAATATTGT
201 CAACGGCGGC  GTATCGGGCG  ATACGTCCGC  GCAAGCCCTA  TCGCGCCTGC
251 CCGCGCTGTT  GGCACGCAA  CCAAGCTTG  TGATTGTCGG  CATAGCGGCG
301 AACGACTTTC  TCGCAAAGT  TCCGAGGAG  CAGACCGCG  CCAATATCGC
351 GAAATCATC  GAAACCGTG  AAAAGGAAA  CATTCCTCGC  GTCTCGTCG
401 GCGTGCCGCA  CATCACTG  GCGCGTTGT  TCGGCGATT  GAGCGACCAT
451 CCGCTGTATG  AGGATTTGTC  CGAGGAATAC  GGCATTCCGT  TGTTCGGCGG
501 CCGTGCGGCG  GAAATTTGG  GCAATAATA  TCTGAAATCC  GACCAAATCC
551 ACGCCAACGG  CAAAGGCTAT  CGGAAATTC  CCGAAATTT  GAATCAATTT
601 TTGAGAAAAC  ATGGGTTTAG  ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3008 ORF 996.ng>:

g996.pep

```

1  MNRRTFLLGA  GALLLTACGR  KSARTHAKIP  EGSTVLALGD  SLTFGYGANP
51  GESYPALQK  LTGNIVNGG  VSGDTSAL  SRLPALLARK  PKLVIVGIGG
101 NDFLRKVPEE  QTRANIAKII  ETVQKENIPA  VLVGVPHITL  GALFGHLSDH
151 PLYEDLSEY  GIPLFGGAWA  EILGNLNLK  DOIHANGKGY  RKFAENLNQF
201 LRKHGFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3009>:

m996.seq

```

1  ATGAACAGAA  GAACCTTCCT  CCTCGGCGCA  GCGCGTTGCG  TGCTTACCGC
51  CTGCGGCAGA  AAATCCGCC  GAACCCACGC  CAAATTTCCC  GAAGGAAGCA
101 CCGTACTTGC  CTTGGGCGAT  TCGCTTACCT  TCGGCTACGG  CGCAAACCTT
151 GCGGAATCCT  ACCCGCGCA  ACTGCAAAA  CTGACGGGTT  GGAATATTGT
201 CAACGGCGGC  GTATCGGGCG  ATACATCTGC  CCAAGCCCTG  TCGCGCCTGC
251 CCGCGCTGTT  GGCACGCAA  CCAAGCTTG  TGATTGTCGG  CATAGCGGCG
301 AACGACTTTC  TCGCAAAGT  TCCCAAGGAG  CAGACCGCG  CCAATATCGC
351 GAAATCATC  GAAACCGTG  AGAAGGAAA  CATCCCGGCC  GTCTCGTCG
401 GCGTGCCGCA  CATCACTG  GGTGCGTTGT  TCGGCGATT  GAGCGATCAT
451 CCGCTGTATG  AGGATTTGTC  CGAGGAATAC  GGCATTCCGC  TGTTCGGCGG
501 CCGTGCGGCG  GAAATTTGG  GCGATAATA  TCTGAAATCC  GACCAAATCC
551 ACGCCAACGG  CAAAGGCTAT  CGGAAATTT  CCGAAGATT  GAATCAATTT
601 TTGAGAAAAC  AGGGTTTAG  ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3010; ORF 996>:

m996.pep

```

1  MNRRTFLLGA  GALLLTACGR  KSARTHAKIP  EGSTVLALGD  SLTFGYGANP
51  GESYPALQK  LTGNIVNGG  VSGDTSAL  SRLPALLARK  PKLVIVGIGG

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101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH
 151 PLYEDLSEY GIPFEGGAWA EILGDNNLKS DQIHANGKGY RKFAEDLNQF
 201 LRKQGFR

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 996 shows 98.1% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. gonorrhoeae*

m996/g996 98.1% identity in 207 aa overlap

	10	20	30	40	50	60
m996.pep	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK					
g996	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK					
	10	20	30	40	50	60
m996.pep	70	80	90	100	110	120
	LTGWNIVNGGVSGDTSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII					
g996	LTGWNIVNGGVSGDTSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII					
	70	80	90	100	110	120
m996.pep	130	140	150	160	170	180
	ETVQKENIPAVLVGVPHITLALFGHLSHDHPLYEDLSEYGIPLFGGAWAEILGDNNLKS					
g996	ETVQKENIPAVLVGVPHITLALFGHLSHDHPLYEDLSEYGIPLFGGAWAEILGDNNLKS					
	130	140	150	160	170	180
m996.pep	190	200				
	DQIHANGKGYRKFAEDLNQFLRKQGR					
g996	DQIHANGKGYRKAENLNQFLRKHGFRX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3011>:

a996.seq

1	ATGAACAGAA	GAACCTTCCT	CCTCGGCGCA	GGCGCGTTGC	TCCTTACCGC
51	CTGCGGCAGA	AAATCCGCC	GAACCCACGC	CAAAATTCCC	GAAGGAAGCA
101	CCGTACTTGC	CTTGGGCGAT	TCGCTTACCT	TCGGCTACGG	CGCAAACCCC
151	GGCGAATCCT	ACCCGCGCA	ACTGCAAAA	CTGACGGGTT	GGAATATTGT
201	CAACGGCGGC	GTATCGGGCG	ATACATCCGC	CCAAGCCCTG	TCGCGCCTGC
251	CCGCGCTGTT	GGCAGCGAAA	CCCAAGCTTG	TGATTGTCGG	CATAGGCGGC
301	AACGACTTTC	TGCGCAAAAGT	TCCCAAGGAG	CAGACCCGCG	CCAATATCGC
351	GAAAATCATC	GAAACCGTGC	AGAAGGAAA	CATCCCGGCC	GTCCTCGTCG
401	CGGTGCCGCA	CATTACCTTG	GGCGCGTTGT	TCGGGCATTT	GAGCGATCAT
451	CCGTGTATG	AGGATTTGTC	CGAGGAATAC	GGCATTCGCG	TGTTCCGCGG
501	CGCGTGGCG	GAATTTTGG	GCGATAATA	TCTGAAATCC	GACCAATCC
551	ACGCCAACGG	CAAGGCTAT	CGGAAATTTG	CCGAAGATT	GAATCAATT
601	TTGAGAAAAC	AGGGTTTAG	ATAA		

This corresponds to the amino acid sequence <SEQ ID 3012; ORF 996.a>:

a996.pep

1	MNRRTFLLGA	GALLLTACGR	KSARTHAKIP	EGSTVLALGD	SLTFGYGANP
51	GESYPALQK	LTGWNIVNGG	VSGDTSAQAL	SRLPALLARK	PKLVIVGIGG
101	NDFLRKVPKE	QTRANIAKII	ETVQKENIPA	VLVGVPHITL	GALFGHLSDH
151	PLYEDLSEY	GIPFEGGAWA	EILGDNNLKS	DQIHANGKGY	RKFAEDLNQF
201	LRKQGFR*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 996 shows 100.0% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. meningitidis*

a996/m996 100.0% identity in 207 aa overlap

	10	20	30	40	50	60
a996.pep	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK					

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|||||
m996  MNRRTFLLGAGALLLTACGRKSAATHAKIPEGSTVLALGDSLTFYGYGANPGESYP AOLQK
      10      20      30      40      50      60
      70      80      90      100     110     120
a996.pep LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVIGGGNDFLRKVPKEQTRANIAKII
m996  LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVIGGGNDFLRKVPKEQTRANIAKII
      70      80      90      100     110     120
      130     140     150     160     170     180
a996.pep ETVQKENIPAVLVGVPHITLGALFGHLSDHPLYEDLSEYGIPLFGGAWAEILGDNNLKS
m996  ETVQKENIPAVLVGVPHITLGALFGHLSDHPLYEDLSEYGIPLFGGAWAEILGDNNLKS
      130     140     150     160     170     180
      190     200
a996.pep DQIHANGKGYRKF AEDLNQFLRKQGF RX
      |||||
m996  DQIHANGKGYRKF AEDLNQFLRKQGF R
      190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3013>:

```

g997.seq (partial)
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51  CTGGGCGGCG TTGTCCGCGC CCGTCACCTT GCGCGGCAC GCCGACGTTA
101 CCTGTGTTGA AGCCGGCCGG CAGGCGGGCG GAAGGCGCGC CACACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGCGGTGT TGGCCTGAT GAAACCATC GGTTCAGACC
251 CCCGTGCCGC CTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCGCG CCGCTGCATA TTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAAGTCTTG
401 CCGATATGTC CGATTGTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTTGCAC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTGG CAGCCCTTGG TCTGGGGCGC GCTCAACACG CCTTTGAAA
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCCGCCTTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCTCCCGGA CGGAAAAGTC
751 CTCGTCAACG GCGAAGCCTT CGATGCCGCC ATACTTGCCA CCGCGCCCTA
801 CCACGCCGCG CCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CAGCCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGcCTGc CGCCCGCGTG ACcGGCAtg CCGAcggcAC
951 ggcaCaatgG CTGCTTTgcc cgGGCAGGC tcgggactgc CcccaaAacg
1001 aagTCTCCGC cGTCAAtagc GTTTCGAcc GCGtcggcgC Gtttgcaaac
1051 cga...

```

This corresponds to the amino acid sequence <SEQ ID 3014 ORF 997.ng>:

```

g997.pep (partial)
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51  GNTDGFGLD NGQHILLGAY RGVRLMKTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA FLHILGGVLL ARRVPFAFK KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGCVLT
201 KKSQSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA ILATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGIADGTAQW LCPGQAPDC PQNEVSAVIS VSDRVGAFAF
351 R...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3015>:

```

m997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51  CTGGGCGAGGA CTGTCCGCGC CCGTCACCTT GCGCGGCAC GCCGACGTTA
101 CCTGTGTTGA AGCCGGCCGG CAGGCGGGCG GCAGGCGCGC CACACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGCGGTGT TGGCCTGAT GAAACCATC GGTTCGGATC
251 CCCGTGCCGC CTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCGCG CCGCTGCATA TTTGGGCGG
351 CGTGCTGCTT GCCCGGCGTG CACCGACTGC ATTCAAAGCC AAAGTCTTG
401 CCGATATGTC CGATTGTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTGAT
501 GCAGTTTGG CAGCCCTTGG TTTGGGCGC GCTCAACACG CCTTTGAAA

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```

551 CCGCAAGCCT GCGCGTGTG TGCACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAGCAGGATT TCGGCGCAAT
651 CGTCGCCGAA CCCGCCCTTG CGGATCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCCTCCCGGA CGGGAAAGTG
751 CTCGTCAACG GCGAAGCTTT CGATGCCGCC GTCCCGCCA CCGCCCTTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGCCCTGC CGCCCGCTG ACCGCCCTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGCAGGCT CGGACTGCCT GAAACGAAAG
1001 TGTCCGCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGGCGG ACAAAGCCCA CGCCGACCTC AAACGCATCC TTCCGCATT
1101 GGGCGAACCC GAAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCCGCCGCGG GACTTSTCGT GGTGACACCG GCACCGCATC
1201 TTCGCCGCGG GCGACTACCT CCACCGGAC TACCCGCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGCGGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 3016; ORF 997>:

m997.pep

```

1 MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51 GNTDGFGLD NGQHILLGAY RGVLRMLKTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRAPTAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGVL
201 KKS GSDYLLP KODLGAIVAE PALADLQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLYR
301 AEPVRLPAPL TGLADGTQVW LLCRGRGLP ENEVSAVISV SDRVGFANR
351 AWADKAHADL KRILPHLGEP EAVRVITEKR ATTAADAPP DLNWLHRRHI
401 FPGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 997 shows 96.0% identity over a 351 aa overlap with a predicted ORF (ORF 997) from *N. gonorrhoeae*

g997/m997 96.0% identity in 351 aa overlap

	10	20	30	40	50	60
g997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
	10	20	30	40	50	60
g997.pep	70	80	90	100	110	120
	NGQHILLGAYRGVLRMLKTIGSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
m997	NGQHILLGAYRGVLRMLKTIGSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
g997.pep	130	140	150	160	170	180
	ARRVPSAFKALLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
m997	ARRAPTAFKALLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
g997.pep	190	200	210	220	230	240
	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPAELQRLGADIRLETRVC					
m997	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPAELQRLGADIRLETRVC					
	190	200	210	220	230	240
g997.pep	250	260	270	280	290	300
	RLNTLPDGKVLVNGEAFDAAVILATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLYR					
m997	RLNTLPDGKVLVNGEAFDAAVILATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLYR					
	250	260	270	280	290	300
g997.pep	310	320	330	340	350	
	AEPVRLPAPLTGIADGTQWLLCPGQAPDCPQNEVSAVISVSDRVGFANR					
m997	AEPVRLPAPLTGLADGTQWLLCRGRL-GLPENEVSAVISVSDRVGFANRAWADKAHAD					
	310	320	330	340	350	

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3017>:

```
a997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51  CTGGGCGCGG TTGTCCGCGG CCGTTACCTT GGCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GCAGGGCGCG CGCACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ATATTTTACT
201 CGGCGCATAC CGGGCGGTGT TGCGCCTGAT GAAAACCATC GGTTCAGACC
251 CCCATGCCGC CTTTTTGGCG GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCCGCG CCCCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCCG ATTCAAAGCC AAACGTGCTG
401 CCGATATGTC CGATTTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCCG AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTGG CAGCCCTTGG TTTGGGCGCG GCTCAACACG CCTTTGGAAG
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCCGCCCTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAGC GCGCATATGC CGTCTGAACA CCTTCCCGGA CGGGAAGTGT
751 CTCGTCAACG GCGAACCTTT CGATGCCGCC GTCCCGGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAT CACGCCATCA CCACCGTCTA TCTGCGCTAT
901 GCCGAACCCG TCCGCTTGCC TGCCCGCTG ACCGGACTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGCGAGCT CGGACTGCCT GAAAACGAAG
1001 TGTCCGCCCT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAAACGG
1051 GCGTGGGCGG ACAAAGTTCA CGCCGACCTC AAACGCATCC TTCCGCATTT
1101 GGGCGAACCC GAAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCCGCCGCCG GATTTGTCGT GGTTCGACCG GCACCGCATC
1201 TTCCCGCCCG GCGACTACCT CCACCCAGAC TACCCGCCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCCT CTGA
```

This corresponds to the amino acid sequence <SEQ ID 3018; ORF 997.a>:

```
a997.pep
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARALA
51  GNTDGFGLD NGQHILLGAY RGVLRIMKTI GSDPHAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPFAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSDGVL
201 KKS GSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRIC RLNTLPDGKV
251 LVNGEPPDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLYR
301 AEPVRLPAFL TGLADGTQVQ LLCRGRGLP ENEVSAVISV SDRVGAFANR
351 AWADKVHADL KRILPHLGEP EAVRVITEKR ATTAADAPPP DLSWLHRRHI
401 FPAGDYLHPD YPATLEAAVO SGFASAEACL QSLSDAV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 997 shows 98.2% identity over a 437 aa overlap with a predicted ORF (ORF 997) from *N. meningitidis*

a997/m997 98.2% identity in 437 aa overlap

	10	20	30	40	50	60
a997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARALAGNTDGFGLD					
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
	10	20	30	40	50	60
a997.pep	NGQHILLGAYRGVLRIMKTIGSDPHAAFLRVPLHWHMHGGGLQFRALPLPAPLHILGGVLL					
m997	NGQHILLGAYRGVLRIMKTIGSDPRAAFLRVPLHWHMHGGGLQFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
a997.pep	ARRVPFAFKA KLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
m997	ARRAPTAFAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
a997.pep	PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALAELQRLGADIRLETRIC					
m997	PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALAELQRLGADIRLETRIC					
	190	200	210	220	230	240
a997.pep	PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALAELQRLGADIRLETRIC					
m997	PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALAELQRLGADIRLETRIC					

1419

```

m997      PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALADLQRLGADIRLETRVC
           190      200      210      220      230      240

           250      260      270      280      290      300
a997.pep  RLNTLPDGKVLVNGEPFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLR
           |||
m997      RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLR
           250      260      270      280      290      300

           310      320      330      340      350      360
a997.pep  AEPVRLPAPLTGLADGTVQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKVHADL
           |||
m997      AEPVRLPAPLTGLADGTVQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKAHADL
           310      320      330      340      350      360

           370      380      390      400      410      420
a997.pep  KRILPHLGEPEAVRVITEKRATTAADAPPPDLSSLHRRHIFPAGDYLHPDYPATLEAAVQ
           |||
m997      KRILPHLGEPEAVRVITEKRATTAADAPPPDLSSLHRRHIFPAGDYLHPDYPATLEAAVQ
           370      380      390      400      410      420

           430
a997.pep  SGFASAEACLQSLSDAVX
           |||
m997      SGFASAEACLQSLSDAVX
           430

```

g999.seq Not found yet

g999.pep Not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3019>:

```

m999.seq
1  ATGAATATGA  AAAAATTGAT  TTCCGCAATT  TGTGTTTCAA  TTGTTTTATC
51  AGCCTGCAAC  CAACAATCAA  AAACGGCACA  AGCCGAAGAA  CCTGTCCAAA
101  GTATCCAGGC  TGCTGATTGT  ACCGCCCCAA  TGGACATCAC  AGTTGAACAA
151  TATCTCATCA  ATTTGGAGCA  AGCATTTAAA  ACTCAGAACG  TCTCAACAAA
201  AATCCATAAT  AAAAATATTG  TCAAGACCGA  TTGTGGTTAT  GACCTTACTT
251  TGGAATATGA  TTTTGGGGCG  ATTGCGCTCA  AACTGGACGA  GCAGCAAAAA
301  ATTAGAGCTA  TCTCAGTAGG  CTACATTTTA  AAAACCGACG  GAGAGAAAGG
351  ACAAATCTA  GTCAATAATG  CCATAAATGG  ATTACACAGT  ATTCAGGCAG
401  TTCTGTCTTT  AACTACCACA  GACAAATTGG  GCGAATCGGA  AGCAGGAAAA
451  CAACTTTTAA  CAGCTTTAAC  CGAAGTCGTC  AAAGAATCCA  ATCAGACAGG
501  AGCAACAGCG  CAAAAGACG  TTCCGGCAGA  TGGTATTTTA  TATAGCGTTG
551  TTTTGTAAAA  AGAAACAAAC  ACCATTGCAA  TAATCGGCAG  AAAACAACCC
601  TAA

```

This corresponds to the amino acid sequence <SEQ ID 3020; ORF 999>:

```

m999.pep
1  MNMKKLISAI  CVSIVLSACN  QSKTAQAE  PVQSIQAADC  TAPMDITVEQ
51  YLINLEQAFK  TQNVSTKIHN  KNIVKTDG  DLTLMDFGA  IALKLDEQOK
101  IRAISVGYIL  KTDGEKGQNL  VNNAINGL  IQAVLSLTTT  DKLGESEAGK
151  QLFTALTEVV  KESNOTGATA  OKDVPADG  YSVVFEKETN  TIAIIGRKOP

```

a999.seq Not found yet

a999.pep Not found yet

The foregoing examples are intended to illustrate but not to limit the invention.

CLAIMS

1. A protein comprising a fragment of an amino acid sequence from SEQ ID 2790 wherein said fragment comprises at least 7 amino acids from said sequence.
 2. A protein comprising an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020.
 3. A protein having 50% or greater homology to a protein according to claim 1.
 4. A protein comprising a fragment of an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020, wherein said fragment comprises 7 or more consecutive amino acids from said sequence.
 5. An antibody which binds to a protein according to any one of claims 1 to 3.
 6. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.
 7. A nucleic acid molecule according to claim 5, comprising a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019.
 8. A nucleic acid molecule comprising a fragment of a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019, wherein said fragment comprises 10 or more consecutive nucleotides from said sequence.
 9. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 5.
 10. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 6.
 11. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 7.
 12. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.
 13. A composition according to claim 11 being a vaccine composition or a diagnostic composition.
 14. A composition according to claim 11 for use as a pharmaceutical.
 15. The use of a composition according to claim 11 in the manufacture of a medicament for the treatment or prevention of infection due to Neisserial bacteria.
-

16. A composition comprising a protein of claim 1 wherein said composition is immunogenic.

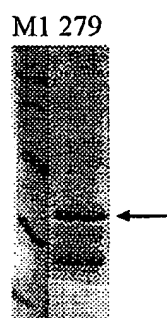
17. A composition comprising a protein of claim 2 wherein said composition is immunogenic.

18. A composition comprising a protein of claim 3 wherein said composition is immunogenic.

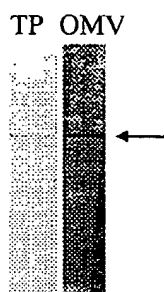
Fig. 2

279 (10.5 kDa)

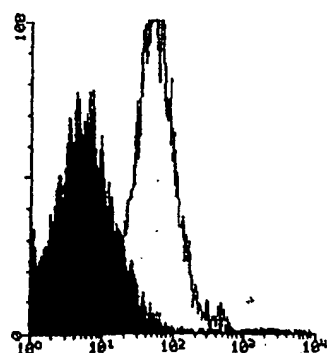
A) PURIFICATION



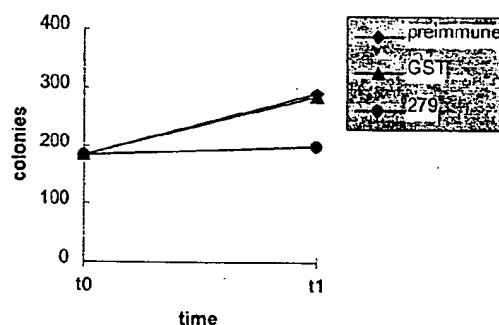
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY

E) ELISA assay: positive

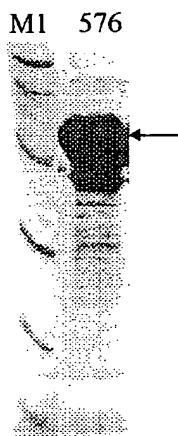
279

The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that protein 279 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

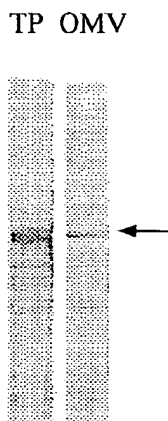
Fig. 3

576 (27.8 kDa)

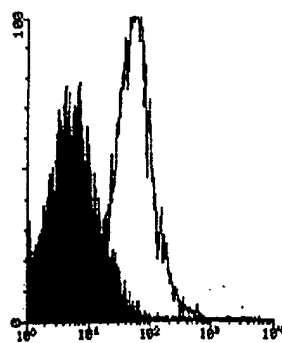
A) PURIFICATION



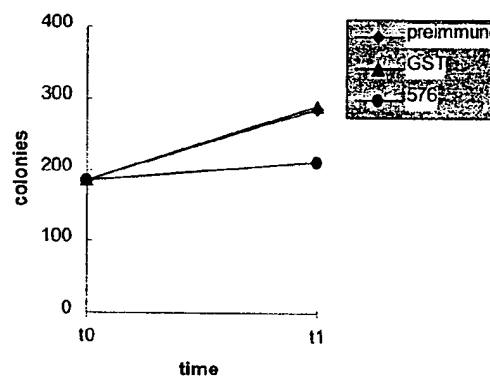
B) WESTERN BLOT



C) FACS

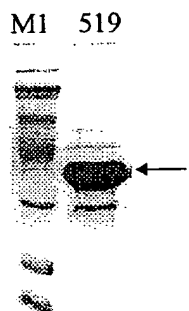
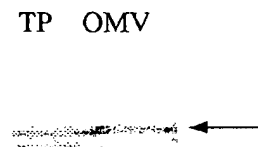
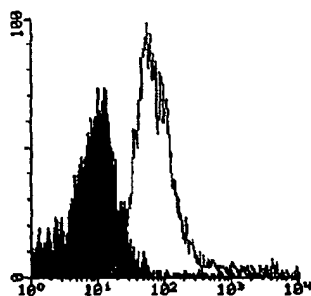
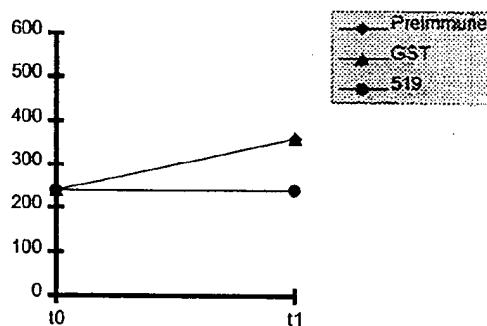


D) BACTERICIDAL ASSAY

E) ELISA assay: positive

576

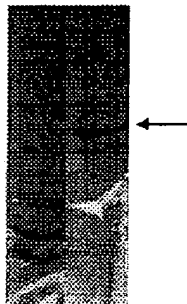
The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 576 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

519 (33 kDa)**Fig. 4****A) PURIFICATION****B) WESTERN BLOT****C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****519**

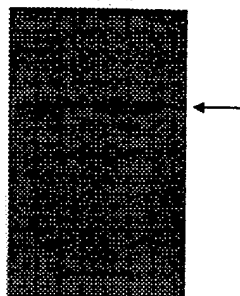
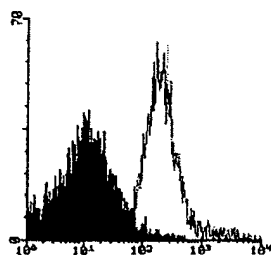
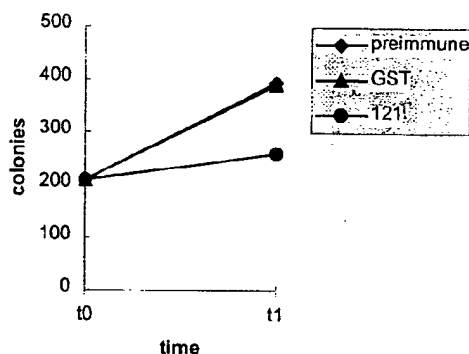
The predicted gene *519* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 519 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

121 (40 kDa)**A) PURIFICATION**

M1 121

**B) WESTERN BLOT**

TP OMV

**C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****121**

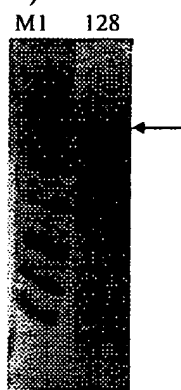
The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 5

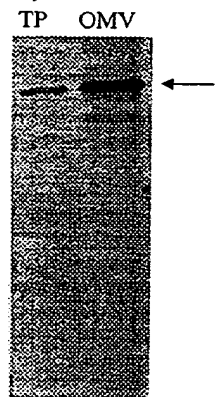
128 (101 kDa)

Fig. 6

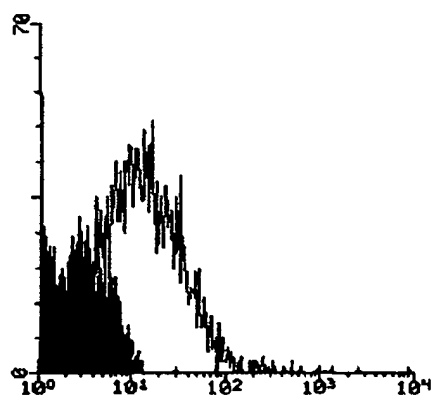
A) PURIFICATION



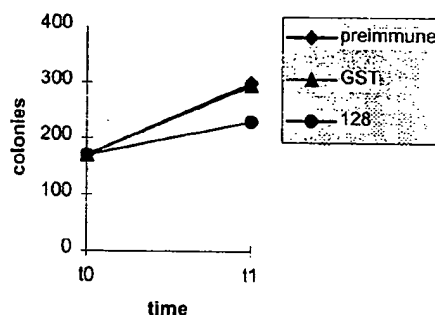
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY



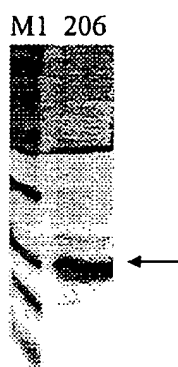
E) ELISA assay: positive

128

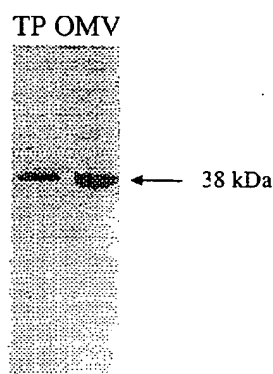
The predicted gene 128 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 7

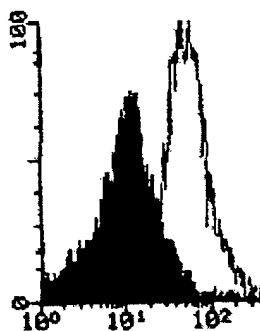
A) PURIFICATION



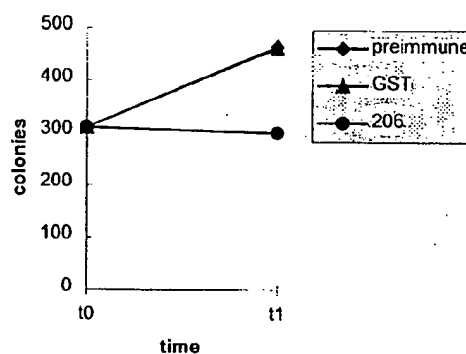
B) WESTERN BLOT



C) FACS



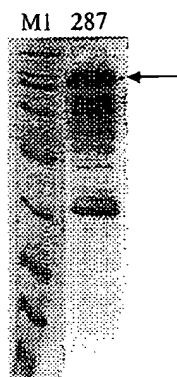
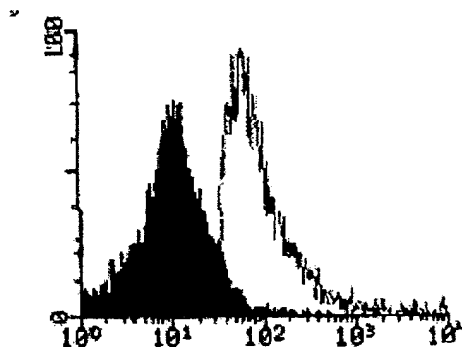
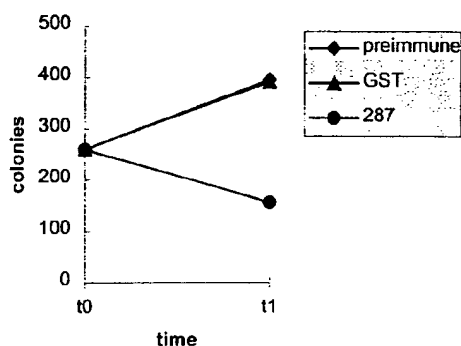
D) BACTERICIDAL ASSAY



E) ELISA assay: positive

206

The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worthnoting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a recative band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C) is shown the FACS analysis, in panel D) the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

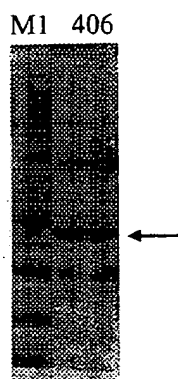
287 (78 kDa)**Fig. 8****A) PURIFICATION****B) FACS****C) BACTERICIDAL ASSAY****D) ELISA assay : positive****287**

The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A).

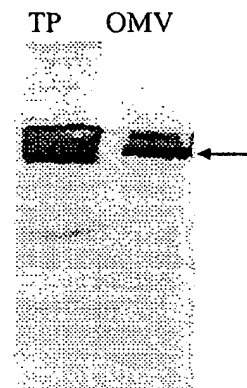
406 (33 kDa)

Fig. 9

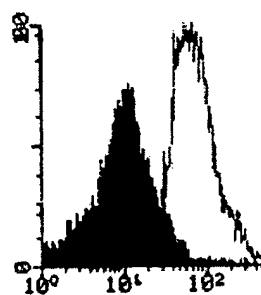
A) PURIFICATION



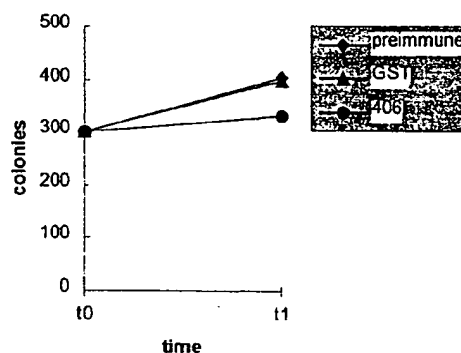
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY

E) ELISA assay : positive

406

The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

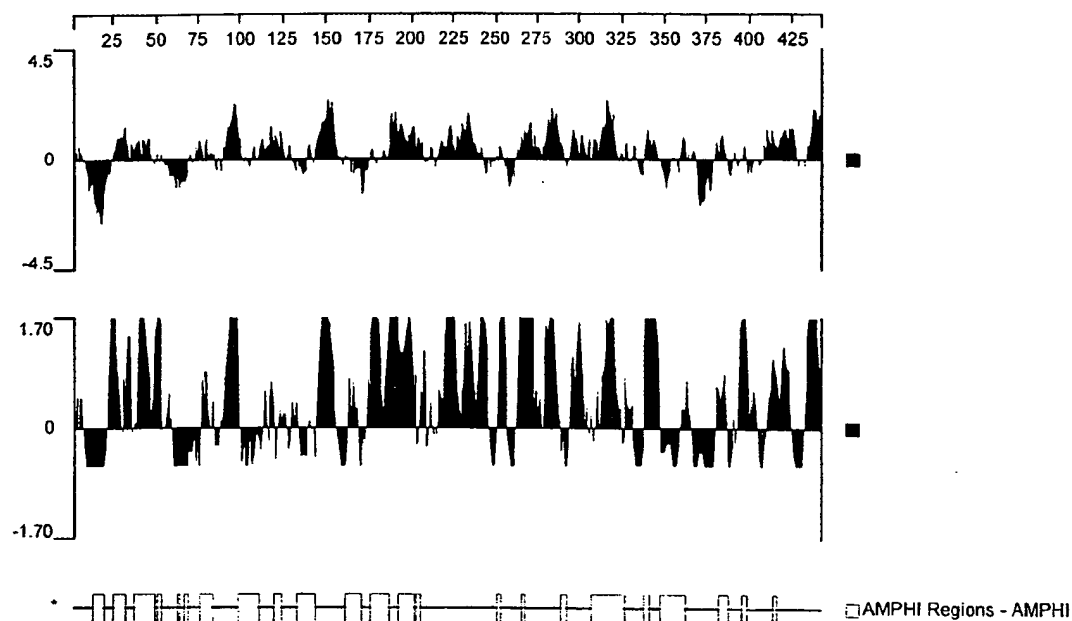
919Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 10

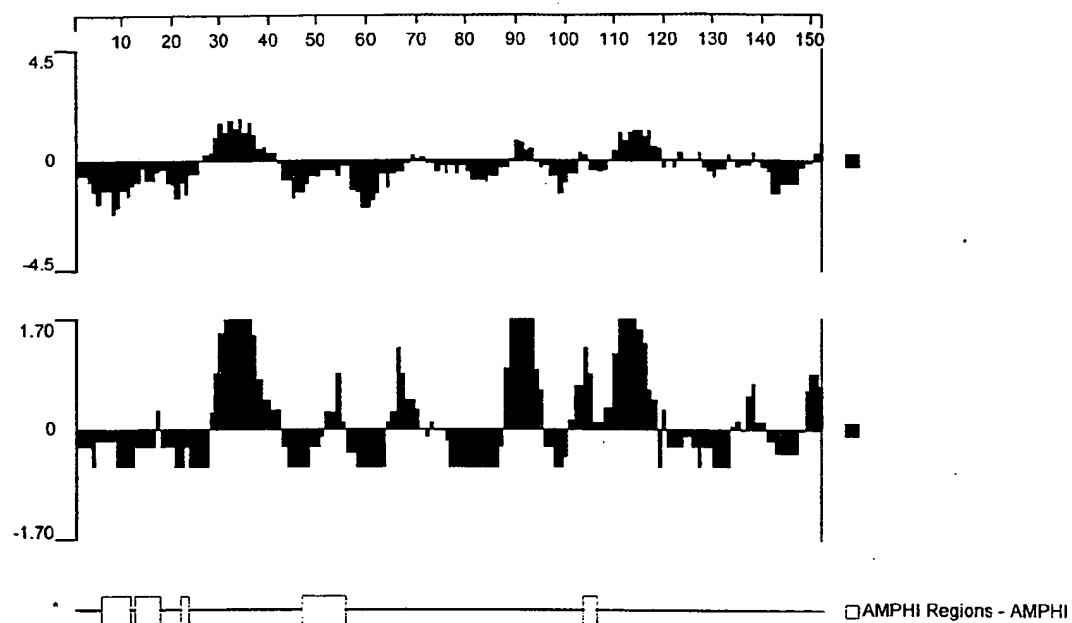
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 11

11/30

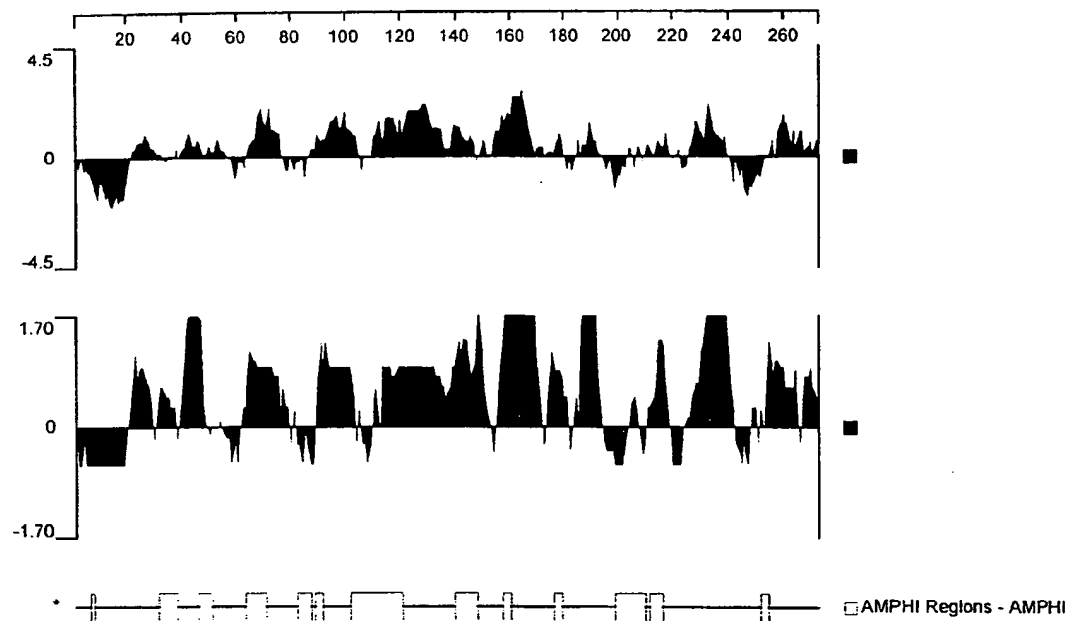
576-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 12

12/30

519-1

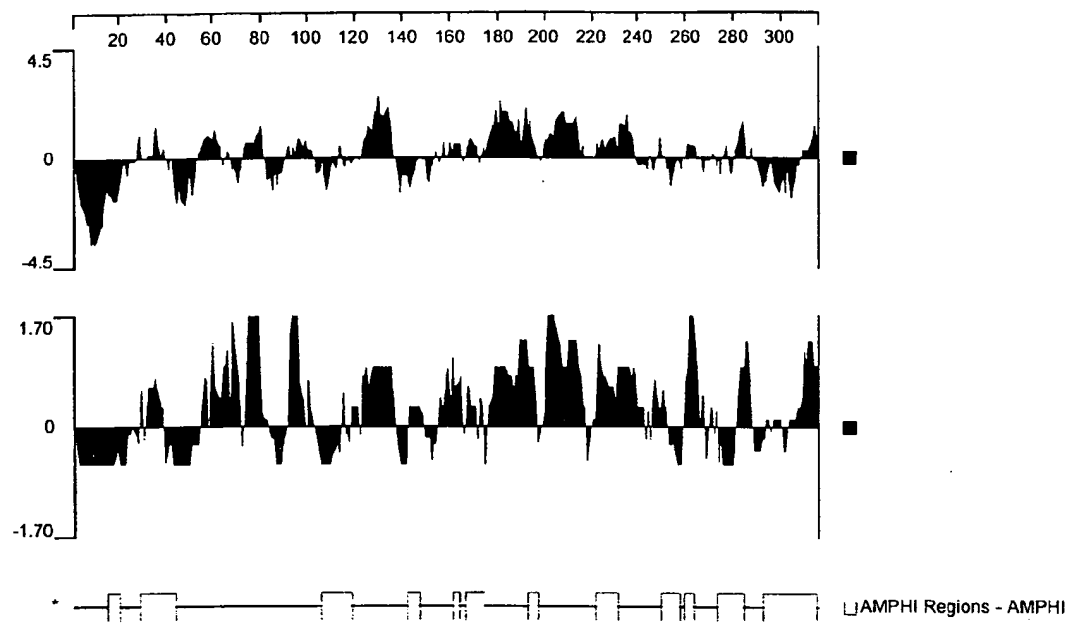
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 13

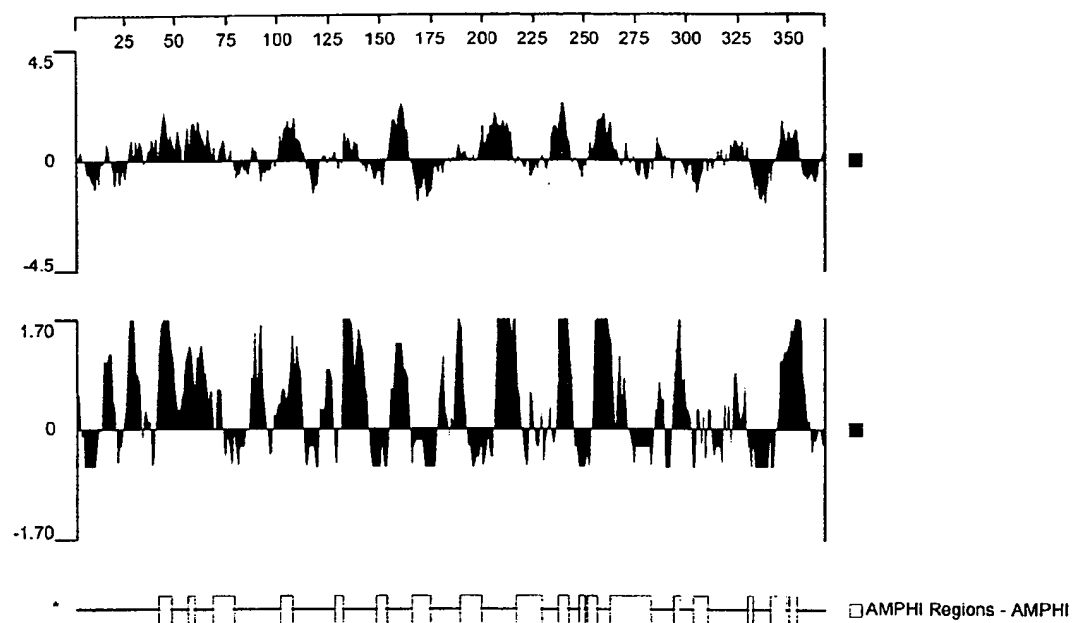
121-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 14

14/30

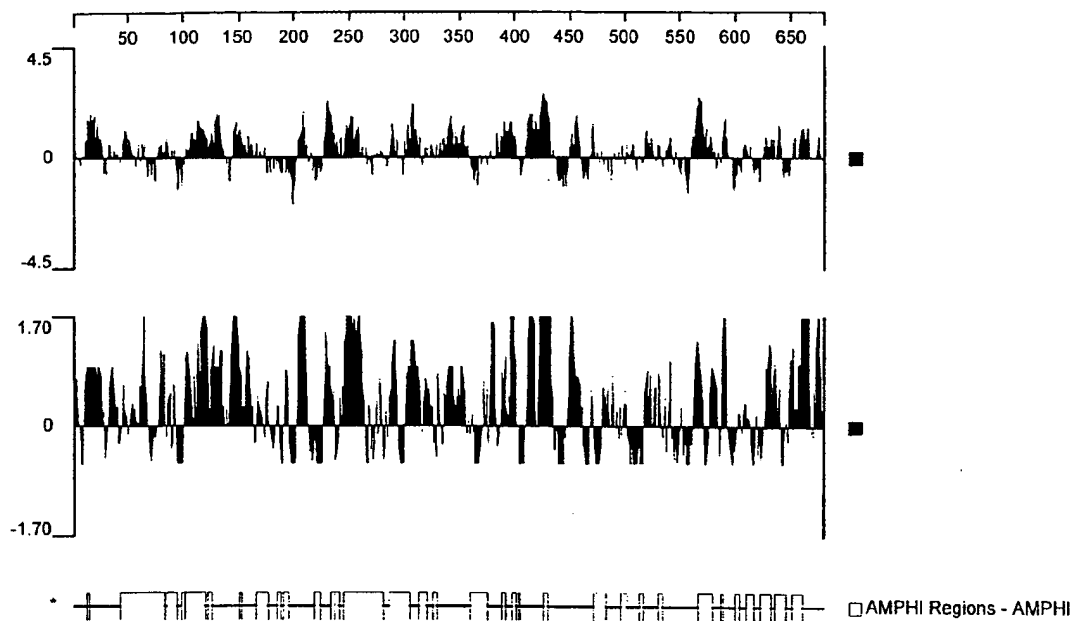
128-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 15

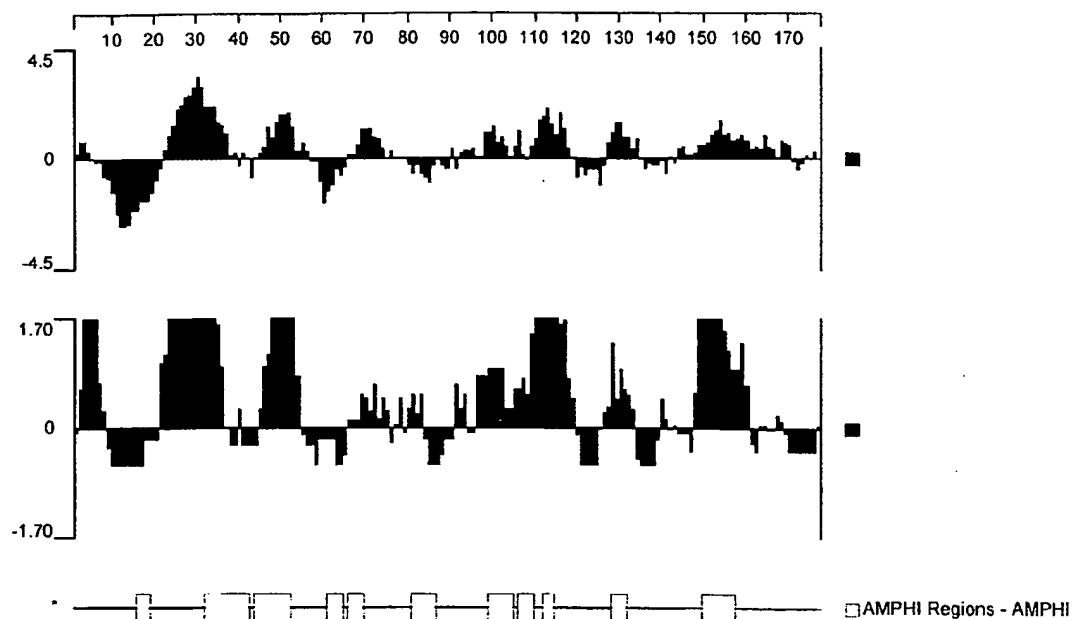
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 16

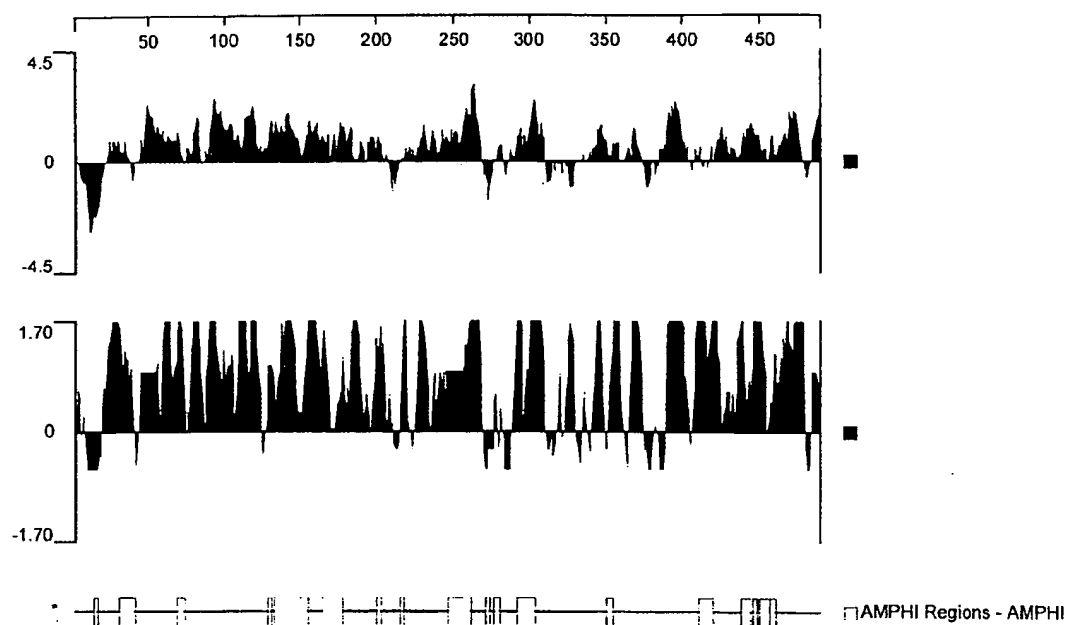
287Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 17

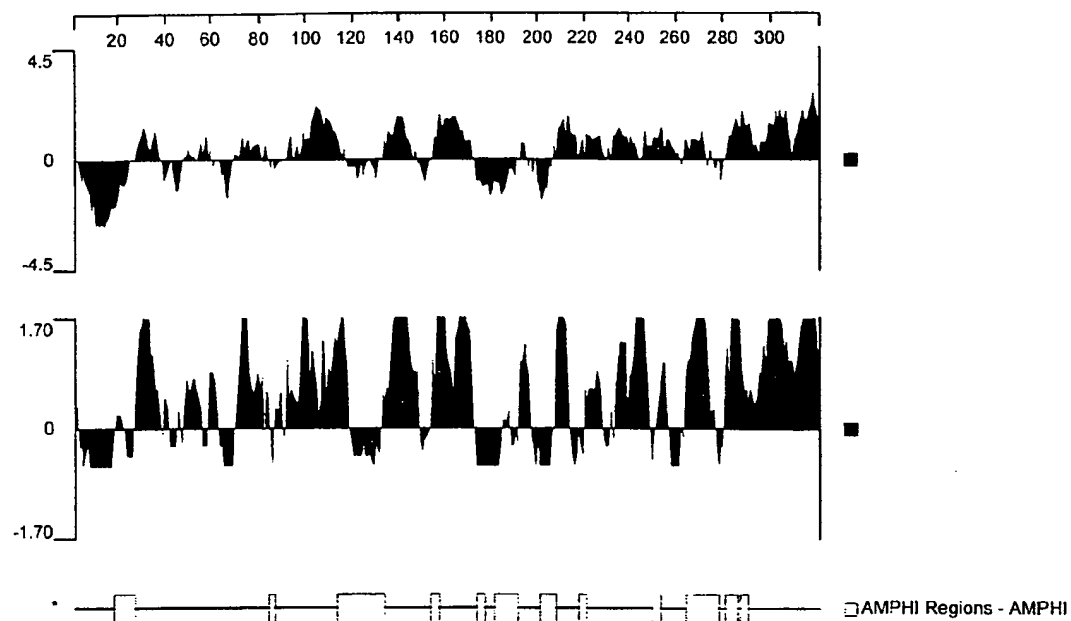
406Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 18

Fig. 19A

Fig. 19B

```
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zo08_225 212 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
z2491 241 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo11_225 241 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
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zo01_225 212 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo09_225 212 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
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zo96_225 212 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
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zo17_225 212 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo18_225 212 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo19_225 212 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo21_225 212 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo27_225 212 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo28_225 212 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo29_225 212 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo13_225 212 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo03_225 212 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo15_225 183 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
fa1090 183 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo32_225 183 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
zo33_225 183 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLN*
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Fig. 19C

Fig. 20A

Fig. 20B

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287_14 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVSE ..... KETEA
287_2 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVSE ..... KETEA
287_21 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVSE ..... KETEA
z2491 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVSE ..... KETEA
287_9 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVSE ..... KETEA
fa1090 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVSE ..... KETEA

287_14 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNCGAATDRPKNEDEGAQNDMFQNAADT
287_2 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNCGAATDRPKNEDEGAQNDMFQNAADT
287_21 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNCGAATDRPKNEDEGAQNDMFQNAADT
z2491 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNCGAATDRPKNEDEGAQNDMFQNAADT
287_9 61 VSGAPQADT...QDATAGKGGQDMAAVSAENTGNCGAATDRPKNEDEGAQNDMFQNAADT
fa1090 61 AGGAPQADT...QDATAGEGSQDMAAVSAENTGNCGAATDRPKNEDEGAQNDMFQNAADT

287_14 110 DSLTPNHPTASNMPAGNMENQAPDAGESEQPANOPDMANTADGMQGGDDPSAGCGENAGNTA
287_2 110 DSLTPNHPTASNMPAGNMENQAPDAGESEQPANOPDMANTADGMQGGDDPSAGCGENAGNTA
287_21 110 DSLTPNHPTASNMPAGNMENQAPDAGESEQPANOPDMANTADGMQGGDDPSAGCGENAGNTA
z2491 110 DSLTPNHPTASNMPAGNMENQAPDAGESEQPANOPDMANTADGMQGGDDPSAGCGENAGNTA
287_9 119 DSLTPNHPTASNMPTRDMGNQAPDAGESAQPANOPDMANTADGMQGGDDPSAGCGENAGNTA
fa1090 117 .....

287_14 170 AQSTNQAEENQTAGSQNPASSINPSATNSGGDFGRNTNNGSVIIDGPSQNTITLTHCKGDS
287_2 170 AQSTNQAEENQTAGSQNPASSINPSATNSGGDFGRNTNNGSVIIDGPSQNTITLTHCKGDS
287_21 170 AQSTNQAEENQTAGSQNPASSINPSATNSGGDFGRNTNNGSVIIDGPSQNTITLTHCKGDS
z2491 170 AQSTNQAEENQTAGSQNPASSINPSATNSGGDFGRNTNNGSVIIDGPSQNTITLTHCKGDS
287_9 178 DQSTNQAEENQTAGSQNPASSINPSATNSGGDFGRNTNNGSVIIDGPSQNTITLTHCKGDS
fa1090 117 .ESANQTAGSQNPASSINPSATNSGGDFGRNTNNGSVIIDGPSQNTITLTHCKGDS

287_14 230 CSCNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNDGKNIKFVGLVADSVQMKGINQYII
287_2 230 CSCNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNDGKNIKFVGLVADSVQMKGINQYII
287_21 230 CSCNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNDGKNIKFVGLVADSVQMKGINQYII
z2491 230 CSCNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNDGKNIKFVGLVADSVQMKGINQYII
287_9 238 QDRD.FLDEEAPPKSEFEKLSDEKIKRYKK....DEQRNFVGLVADSVQMKGINQYII
fa1090 176 CNGDNLFLDEEAPPKSEFEKLSDEKIKRYKK....DEQRNFVGLVADSVQMKGINQYII

287_14 290 FYKPKP...TSFARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_2 290 FYKPKP...TSFARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_21 286 FYKPKP...TSFARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
z2491 286 FYKPKP...TSFARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_9 293 IYKDKSASSSARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
fa1090 232 FYTDKPTT.....RSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG

287_14 348 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFMENGRPSPGRFAA
287_2 348 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFMENGRPSPGRFAA
287_21 344 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFMENGRPSPGRFAA
z2491 344 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFMENGRPSPGRFAA
287_9 353 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGTAVYNGEVLHFMENGRPSPGRFAA
fa1090 285 NYRYLTYGAEKLPGGSYALRVQGEPAKGEMLVGTAVYNGEVLHFMENGRPSPGRFAA

287_14 408 KVDGFSKSDGIIDSGDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGFYGPAGEEVA
287_2 408 KVDGFSKSDGIIDSGDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGFYGPAGEEVA
287_21 404 KVDGFSKSDGIIDSGDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGFYGPAGEEVA
z2491 404 KVDGFSKSDGIIDSGDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGFYGPAGEEVA
287_9 413 KVDGFSKSDGIIDSGDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGFYGPAGEEVA
fa1090 345 KVDGFSKSDGIIDSGDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGFYGPAGEEVA

```

FIG. 21A

287_14	468	GKYSYRPTDAEKGFGVFAGKKEQD*
287_2	468	GKYSYRPTDAEKGFGVFAGKKEQD*
287_21	464	GKYSYRPTDAEKGFGVFAGKKEQD*
z2491	464	GKYSYRPTDAEKGFGVFAGKKEQD*
287_9	473	GKYSYRPTDAEKGFGVFAGKKEQD*
fa1090	405	GKYSYRPTDAEKGFGVFAGKKEQD*

FIG. 21B

z2491_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv26_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv22_519ass 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
fa1090_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv32_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv11_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv28_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv96_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv02_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv03_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv04_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv05_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv01_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv07_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv12_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv18_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv19_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv21_519ass 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv27_519 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv20_519ass 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv06_519ass 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS
zv29_519ass 1 MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRLTAGLNILIPFIDRVAYRHS

z2491_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
zv26_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
zv22_519ass 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
fa1090_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
zv32_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
zv11_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
zv28_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
zv96_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
zv02_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
zv03_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
zv04_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
zv05_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
zv01_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
zv07_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
zv12_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
zv18_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
zv19_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
zv21_519ass 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
zv27_519 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
zv20_519ass 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
zv06_519ass 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG
zv29_519ass 61 KEIPLDVP SQVCITRDNTQLTV DGIIFYQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG

z2491_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv26_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv22_519ass 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
fa1090_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv32_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv11_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv28_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv96_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv02_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv03_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv04_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv05_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv01_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv07_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv12_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv18_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv19_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv21_519ass 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv27_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv20_519ass 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv06_519ass 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv29_519ass 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE

FIG. 22A

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z2491_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv26_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv22_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
fa1090_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv32_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv11_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv28_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv96_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv02_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv03_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv04_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv05_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv01_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv07_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv12_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv18_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv19_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv21_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv27_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv20_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv06_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv29_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR

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z2491_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv26_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv22_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
fa1090_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv32_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv11_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv28_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv96_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv02_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv03_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv04_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv05_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv01_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv07_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv12_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv18_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv19_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv21_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv27_519 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv20_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv06_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv29_519ass 241 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL

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z2491_519 301 ISAGMKIIDSSKTAK*
zv26_519 301 ISAGMKIIDSSKTAK*
zv22_519ass 301 ISAGMKIIDSSKTAK*
fa1090_519 301 ISAGMKIIDSSKTAK*
zv32_519 301 ISAGMKIIDSSKTAK*
zv11_519 301 ISAGMKIIDSSKTAK*
zv28_519 301 ISAGMKIIDSSKTAK*
zv96_519 301 ISAGMKIIDSSKTAK*
zv02_519 301 ISAGMKIIDSSKTAK*
zv03_519 301 ISAGMKIIDSSKTAK*
zv04_519 301 ISAGMKIIDSSKTAK*
zv05_519 301 ISAGMKIIDSSKTAK*
zv01_519 301 ISAGMKIIDSSKTAK*
zv07_519 301 ISAGMKIIDSSKTAK*
zv12_519 301 ISAGMKIIDSSKTAK*
zv18_519 301 ISAGMKIIDSSKTAK*
zv19_519 301 ISAGMKIIDSSKTAK*
zv21_519ass 301 ISAGMKIIDSSKTAK*
zv27_519 301 ISAGMKIIDSSKTAK*
zv20_519ass 301 ISAGMKIIDSSKTAK*
zv06_519ass 301 ISAGMKIIDSSKTAK*
zv29_519ass 301 ISAGMKIIDSSKTAK*

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Fig. 22B

Fig. 23A

Fig. 23B

Fig. 23C

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fa1090      361  IDRRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm33asbc    361  IDRRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm32asbc    361  IDRRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm23asbc    361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm27bc      361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm09        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm10        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm24        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm25        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm14        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm04        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm11asbc    361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm08n       361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm96        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm01        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm02        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm03        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm07        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm12        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm18        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm19        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm20        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm21        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm06        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm17        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm13        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm05        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
z2491      361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm22        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm26        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm28        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm29asbc    361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm16        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm15        361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm31asbc    361  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK

fa1090      421  QKTTGYVWQLLPNCMKPEYRP*
zm33asbc    421  QKTTGYVWQLLPNCMKPEYRP*
zm32asbc    421  QKTTGYVWQLLPNCMKPEYRP*
zm23asbc    421  MKETGYVWQLLPNCMKPEYRP*
zm27bc      421  MKETGYVWQLLPNCMKPEYRP*
zm09        421  QKTTGYVWQLLPNCMKPEYRP*
zm10        421  QKTTGYVWQLLPNCMKPEYRP*
zm24        421  QKTTGYVWQLLPNCMKPEYRP*
zm25        421  QKTTGYVWQLLPNCMKPEYRP*
zm14        421  QKTTGYVWQLLPNCMKPEYRP*
zm04        421  QKTTGYVWQLLPNCMKPEYRP*
zm11asbc    421  QKTTGYVWQLLPNCMKPEYRP*
zm08n       421  QKTTGYVWQLLPNCMKPEYRP*
zm96        421  QKTTGYVWQLLPNCMKPEYRP*
zm01        421  QKTTGYVWQLLPNCMKPEYRP*
zm02        421  QKTTGYVWQLLPNCMKPEYRP*
zm03        421  QKTTGYVWQLLPNCMKPEYRP*
zm07        421  QKTTGYVWQLLPNCMKPEYRP*
zm12        421  QKTTGYVWQLLPNCMKPEYRP*
zm18        421  QKTTGYVWQLLPNCMKPEYRP*
zm19        421  QKTTGYVWQLLPNCMKPEYRP*
zm20        421  QKTTGYVWQLLPNCMKPEYRP*
zm21        421  QKTTGYVWQLLPNCMKPEYRP*
zm06        421  QKTTGYVWQLLPNCMKPEYRP*
zm17        421  QKTTGYVWQLLPNCMKPEYRP*
zm13        421  QKTTGYVWQLLPNCMKPEYRP*
zm05        421  QKTTGYVWQLLPNCMKPEYRP*
z2491      421  QKTTGYVWQLLPNCMKPEYRP*
zm22        421  QKTTGYVWQLLPNCMKPEYRP*
zm26        421  QKTTGYVWQLLPNCMKPEYRP*
zm28        421  QKTTGYVWQLLPNCMKPEYRP*
zm29asbc    421  QKTTGYVWQLLPNCMKPEYRP*
zm16        421  QKTTGYVWQLLPNCMKPEYRP*
zm15        421  QKTTGYVWQLLPNCMKPEYRP*
zm31asbc    421  QKTTGYVWQLLPNCMKPEYRP*

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Fig. 23D

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